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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

#### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

#### 2. BACKGROUND

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Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

#### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

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full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, butilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and form a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compound that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases o disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

### 4. DETAILED DESCRIPTION OF THE INVENTION

#### **4.1 DEFINITIONS**

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

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As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 15 to about 50 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4<sup>20</sup> possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match  $(1 \div 4^{25})$  times the increased probability for mismatch at each nucleotide position  $(3 \times 25)$ . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophobicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

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The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

## 4.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

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The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., Gene 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and Current Protocols in Molecular Biology, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### **4.3 ANTISENSE**

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

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In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

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The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

## 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1350 or (b)

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polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ 10 ID NO:1351-2700.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

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The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat<sup>TM</sup> kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl<sup>TM</sup> or Cibacrom blue 3GA Sepharose<sup>TM</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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# 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

## 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

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For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

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The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

## 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

## 4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

# 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

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Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

## 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

PCT/US01/03800 WO 01/57188

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of 10 stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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## 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

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A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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# 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

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Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β<sub>2</sub> microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

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Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

## 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

PCT/US01/03800 WO 01/57188

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

#### HEMOSTATIC AND THROMBOLYTIC ACTIVITY 4.10.10

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of 25 cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### CANCER DIAGNOSIS AND THERAPY 4.10.11

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the 35

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin,
Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen'mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl,
Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

## 4.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

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The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

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Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

## 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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## 4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### 4.10.16 **LEUKEMIAS**

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Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

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- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
  - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
  - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
  - (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
  - (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
  - (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
  - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

## 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

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The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### **4.11.1 EXAMPLE**

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

# 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

### 4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

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comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

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For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications.

Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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## 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC<sub>50</sub> as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the  $ED_{50}$  (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu$ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1  $\mu$ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

### 4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

#### 4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab'}$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG<sub>1</sub>, IgG<sub>2</sub>, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

### 5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

## 5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

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The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

# 5.13.2 Humanized Antibodies

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The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

## 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

# 5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_{v}$  fragments.

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g.  $F(ab')_2$  bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc R I (CD64), Fc R II (CD32) and Fc R III (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

### 5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HTV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

## 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

#### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}$ Bi,  $^{131}$ In,  $^{90}$ Y, and  $^{186}$ Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

# 4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

# 4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

PCT/US01/03800 WO 01/57188

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide. 10

# 4.16 DIAGNOSTIC ASSAYS AND KITS

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The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

## 4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

## 4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
  - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

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The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

## 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

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Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

# 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude et al. (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

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More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

# 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer et al. (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviII, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI\*\*), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

# 4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

#### 5.0 EXAMPLES

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## 5.1 EXAMPLE 1

# Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

### 5.2 EXAMPLE 2

### Novel Contigs

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

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## TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927
			976 1233 1319
adult brain	GIBCO	ABD003	41 49 74 101 111 120 132 141-142 151
			217 225 238 271 317 404 446 469 503
			513-514 535 550 564 573 666-669 798
			898 910 927 976 1067 1083 1085 1178
			1254
adult brain	Clontech	ABR001	39 216 238 327 356 535 927 1056 1121
	_l		1178-1180 1199 1251
adult brain	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145 147 188 197 208 225 227-239 250 300-
			303 312 316 328-331 340 357-362 374
	<b>,</b>		380 384-391 408 414 446 448 464-467
		,	483 488 495-496 505 512 521 535 550
			566 571 577 585 590 594 598 634 641
			658 666 683 725 742 764 767 786 801
			805 810 823 826 829 831 836 841 887-
			923 927 934 943 950-951 963 976 995
			1000-1001 1006 1026 1034 1048 1057-
		}	1067 1086 1088 1090 1118 1120 1122-
l	j		1128 1142 1162 1181-1192 1199 1204
			1218-1219 1225 1232 1253 1267 1271-
			1306 1342 1347 1349-1350
adult brain	Clontech	ABR011	49 238 1219
adult brain	BioChain	ABR012	74 238
adult brain	Invitrogen	ABR013	868 1268
adult brain	Invitrogen	ABT004	49 117 138 191 217 252 291 305 535
dan oran			566 596 663 670 746 798 816-819 876
	)		892 898 922 943 963 1034-1036 1121
cultured	Strategene	ADP001	41 74 101 138 211 238 304 537 582
preadipocytes	_		740 798 883 943 976 1067
adrenal gland	Clontech	ADR002	49 74 101 111 120 127 151 215 238
			240-247 316 330 363-364 404 414 534- 535 833 924-940 950 963 976 1001
			1003 1067-1070 1118 1156 1193-1200
			1325
		ATTROCI	38 49 71-72 74-77 79 92 99 101 111
adult heart	GIBCO	AHR001	118 129 132 138 151 158-163 182 195-
			203 215 217 238 264 269 353 384 398
			408 434-439 446 504 512-513 519 537
			562-573 577 611-614 616-619 658 661
			671-672 722 734 757-773 815 828-835
		(	874 891 898 919 926-927 976 988
į			1021 1037 1041 1062 1067 1071 1080
	E		1083 1093 1122 1131 1185 1201 1254
			1308 1331 1335
adult kidney	GIBCO	AKD001	41 49 51 71-74 78-85 94 100-101 103-
addit Ridiey			107 111 119-120 138 151 157 215 217-
			218 238 250 264 294 304 384 404 440
			446 454 477 504-505 509 514 518-519
			535 537 564 574-583 620-627 639 653
1	1		673-675 705 753 789 831 844 851 859
}			877 909 918 927 956 963 976 1067
			1074 1083 1095 1178 1302 1331 1335
adult kidnev	Invitrogen	AKT002	1074 1083 1095 1178 1302 1331 1335 11-12 41 49 111-112 215-217 294 316
adult kidney	Invitrogen	AKT002	1074 1083 1095 1178 1302 1331 1335 11-12 41 49 111-112 215-217 294 316 446 487 564 575 844 868 910 927 976
adult kidney	Invitrogen	AKT002	1074 1083 1095 1178 1302 1331 1335 11-12 41 49 111-112 215-217 294 316

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS: 518 537 545 549 580 582 592 594 634
			640 651-652 676-678 725 851 873 918
			952 976 1042 1067 1076 1083 1152
		<u> </u>	8 111 121 151 180-182 188 215 537
ymph node	Clontech	ALN001	545 549 651 679-682 789 804-810 868
, ,			873 927 952 976 1042 1059 1335
			8 64 79 111 186 215-216 238 446 514
young liver	GIBCO	ALV001	519 537 564 653 683-684 698 753 798
,0			813 833 840 858 927 976 1038-1039
			1051 1085 1224 1245 1256 40 71 292-293 305 384 468-469 496
adult liver	Invitrogen	ALV002	505 657 675 714 753 832 844 941-942
		)	505 657 675 714 753 832 844 941-942
			976 1040 1076 1256 1293
adult liver	Clontech	ALV003	976
adult ovary	Invitrogen	AOV001	8 32 36 38 41 49 51 71 74 79-80 101
			104 111 120 122-125 138 140 143-149
			151 188-190 207-212 215-217 238 264
		1	316 384 409 440 445-446 496 504 512
		ì	514 518-519 535 537 549-550 564 566
		(	571 580 582 600 618 638 657 667 681
			685-697 699 705 722 735-744 761 771
	Į		815 833 842-865 868 875-876 918 926-
		}	927 950 952 963 976 1023 1042 1048
		1	1051 1059 1072 1076 1083 1117 1120
			1124 1131 1144 1174 1224 1268 1331
			1335
adult placenta	Clontech	APL001	102 217 238 537 641 700
placenta	Invitrogen	APL002	663 851 1048
adult spleen	GIBCO	ASP001	8 45 74 111 132 140 151 185 217 238
addit spicen	<b>3.2</b> - 3		294 414 446 477 504 514 534 545 549
			592 722 873 883 952 976 1041-1042
		1	1083 1093-1094 1152 1224
testis	GIBCO	ATS001	72 107 111 113 126 140 151 183 215
tesus	0.2.2.2		238 446 497 537 642 701-706 811 877
			927 962 976 1083 1117 1131
adult bladder	Invitrogen	BLD001	41 151 191 402-405 409 414 496 545
adult bladder	mv.zogoz	- 1	592 607 706 873 952 1178 1329-1335
bone marrow	Clontech	BMD001	8 58-62 65-68 74 79 108 111 116 137
Dolle Illanow	Cionico		147 151 164-174 213-215 238 305-307
	i		374 404 446 460 466 516 519 534 538-
			541 544-546 549-554 566 584 586 592
			596 607 610 628-629 643-645 652 707-
			708 774-789 844 866-871 873 919 927
		(	952 963 976 998 1034 1042 1064 1083
			1085 1120 1132 1152 1225 1229 1268
			1307 1310
1	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132
bone marrow	Cioniecii	22002	210 317 510-511 545 549 581 598 628
			638 724 766 789 844 860 868 873 919
(	{	·	927 952 963 968 976 1042 1111 1141
		}	1160-1161 1229 1266 1346
L	Clertach	BMD004	111 238 282 549 1083
bone marrow	Clontech	CLN001	52 260 264 299 494 536 545 564 592
adult colon	Invitrogen	CLINOI	844 873 877 952 976 1042 1152 1268
			1336-1337
		CVVOOL	49 51 129 132 151 205 207 238 332-
adult cervix	BioChain	CVX001	335 365-367 392-401 440 466 470-471
			518 537 597 629 832 877 927 976 1006
	1		1085 1117 1129-1134 1192 1202-1205
			1219 1309-1328
			74 976 1083
	BioChain	DIA002	/4 9 / U 1 U O J

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
endothelial cells	Strategene	EDT001	32 40-41 49 74 79 101 111 120 132
			138 151 204-206 215-217 238 269 316
			414 433 505 510 513 550 555 580 582
			596 675 722 745 798 814 836-841 851
			918 976 1041 1043 1073 1083 1131
	1		1331
Genomic clones	Genomic DNA	EPM001	525-532 927
from the short arm	from Genetic		
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM003	47 525
from the short arm	from Genetic		
of chromosome 8	Research		505.000
Genomic clones	Genomic DNA	EPM004	525 927
from the short arm	from Genetic		
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM005	531
from the short arm	from Genetic	-	
of chromosome 8	Research		74 138 238
esophagus	BioChain	E\$O002	
fetal brain	Clontech	FBR001	441-442 927
fetal brain	Clontech	FBR004	215 893 927 1001
fetal brain	Clontech	FBR006	48 61 101 120 132 138 140 147 208
	}		225 271 317 319 336 359 368 405-414
			519 550 571 594 686 715 722 764 824
		}	829 836 859 909 927 943 947 963 1057
			1067-1068 1104 1135-1140 1162 1206-
	l		1207 1235 1268 1288 1307-1308 1319
			1338-1350
fetal brain	Clontech	FBRs03	111 446 41 51 120 151 192-194 264 504 512
fetal brain	Invitrogen	FBT002	535 683 761 798 820-827 844 876 909
			963 976 1026 1048 1083 1144 1302
i			
fetal heart	Invitrogen	FHR001	446 566 761 51 74 111 127 140 151 184 294 537
fetal kidney	Clontech	FKD001	550 630-631 1319
			111 976 1083
fetal kidney	Clontech	FKD002	238 974
fetal kidney	Invitrogen	FKD007	463 566 976 1074 1083 1093
fetal lung	Clontech	FLG001	41 238 330 407 415-416 537 573 844
fetal lung	Invitrogen	FLG003	859 1048 1083 1116 1192
		<u> </u>	8 14 34-35 37 41 43 49 51 54-56 63-64
fetal liver-spleen	Columbia	FLS001	69-71 74 77 79 87-90 101 107 110-111
	University		114 120 128-131 138 140 147 150-155
			197 210 215 217 225 238 312 367 384
			414 440 446 460 468 483 496 504-507
			511-515 518-519 523 533-535 537 541
			544-545 547-550 555-560 564 566 571
			577 582 585-586 598 636 646-647 649
			652 664 698 709-710 714 722-723 731
			735-736 746-753 761 784 798 823 829
	}		832 844 851 858-859 868 873 876 898
			927 943 949 952 963 976 984 1002
			1021 1023 1040 1042 1044 1050 1083
	Ì		1021 1023 1040 1042 1044 1030 1083
(			1217 1251 1254 1256 1302 1308 1311
1			ł.
			8 36-37 41-46 49 54 64 71 74 79 101
fetal liver-spleen	Columbia	FLS002	8 36-37 41-46 49 34 64 71 74 79 101
_	University		111 120 129 147 207 210 215-216 238
}			250 330 353 359 366 383-384 414 478 505 508-509 511 515-524 534-535 537
1		1	505 508-509 511 515-524 534-535 537 544-545 564 566 571 577 591 598 638
	1		LEAR CAE CEA CEE COT COT COT COVER

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			663 671 698 714 722 725 727 751 798
			851 859 873 876 909 927 949 952 983-
	ļ		984 1002 1023 1042-1044 1085 1095
			1131 1144 1178 1199 1233 1240-1270
	ļ		1331 1340
fetal liver-spleen	Columbia University	FLS003	64 535 976 1256
fetal liver	Invitrogen	FLV001	8 101 120 138 217 446 468 535 566
ietai iivei	Mylhogen		580 722 730 749 844 918 943 976 1051
			1256 1331
fetal liver	Clontech	FLV004	537 926 1256
fetal muscle	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421
ictal muscic			425 535 537 577 598 614 836 857 1141 1208 1268
fetal muscle	Invitrogen	FMS002	537
	Invitrogen	FSK001	13-26 32 41 51 89 107 111 147 151
fetal skin	mon ogen	1512001	225 264 316 405 422-429 488-494 496
			519 534-535 537 566 675 732 859 876-
			877 898 947 949-950 963 976 1001
			1062 1076 1083 1117 1144 1165 1268
			1281
fotal alsim	Invitrogen	FSK002	537 812
fetal skin	BioChain	FSP001	87 549
fetal spleen	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301
umbilical cord	BioChain	100001	316 446 495-503 519 521 534-535 537
	İ		582 634 691 877 883 927 944-950 963
	·		976 1001 1075 1142-1143 1171 1218
			1243 1308
fetal brain	GIBCO	HFB001	41 49 57 79 87 103 111 120 132-135
iciai oram	GIBCO		138 145 151 188 197 207 215 238 264
			271 294 316 367 414 440 446 466 504
			513-514 535 542-543 550 564 571 596
			635 648-654 675 711-715 722-723 798
		Í	832 872 876 883 927 976 1095 1144
			1168 1171 1178 1211 1335
macrophage	Invitrogen	HMP001	238
infant brain	Columbia	IB2002	49-50 77 81 89 105 111 136-138 140
	University		151 161 175-179 185 216-217 264 295
			299 308-310 371-373 462 476 504 511-
			513 533 537 564 566 571 655-657 662
			683 716-720 723 752 790-803 829 832 858-859 876 898 909 949 976 1045-
			1047 1076-1087 1090 1093 1116 1122
			1144 1209-1213 1225 1233 1256 1319
			1
L			1341 41 50 77 104 132 215 238 508 512-513
infant brain	Columbia	IB2003	519 566 655 714 794 918 943 976 1067
	University		
			1092-1093 1233 311 472-473 753 1214
infant brain	Columbia	IBM002	311 472-473 733 1214
	University		51 111 376 474 790 876 949 1144 1204
infant brain	Columbia	IBS001	,
	University		1221 151 316 462 514 534 582 675 939 1131
lung, fibroblast	Strategene	LFB001	1-7 41 74 79 94 115 120 138-139 156
lung tumor	Invitrogen	LGT002	215 217 269 280 296 337 374-375 384
_			404 446 454 475-480 498 514 518-519
			522 537 545 564 577 597 653 658 705
1			721-724 754-756 779 859 868 872-874
			876-877 919 927 949 951-952 959 976
			1002 1042 1048-1053 1076 1083 1088-
			1089 1131 1144-1147 1216-1218 1229
1	1	1	1007 1151 1177 1177 1210 1215 1227

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS: 1293 1311
			41 74 111 132 151 253 316 446 550
lymphocytes	ATCC	LPC001	634 844 927 976 1085 1268
		1110001	8 11 41 74 86 91-98 101 109 111 120
leukocyte	GIBCO	LUC001	147 151 212 215 218 238 252 288 312-
!			314.316.338.359.408.427.443-447.505
			510 512 514 518 534 545 549-550 561
			564 566 571 577 580 582 587-609 615
		}	632-638 658-659 698 714 725-728 832
			836 841 859 866 873-874 882-883 918-
	}	}	836 841 859 866 875-874 862-863 916-
			919 927 943 952 963 976 1042 1076
			1083 1090 1148 1152 1168 1195 1219-
			1220 1224
leukocyte	Clontech	LUC003	74 100 215 232 238 339-341 446 545
Tourson, in			657 660 729 873 883 927 952 963 1008
	1	_	1042 1116 1120 1149-1150 1215 1222
Melanoma from cell	Clontech	MEL004	210 215 238 342 534 545 592 722 873
line ATCC #CRL			919 929 939 952 976 1071 1118 1218
	1		1235 1245
1424	Invitrogen	MMG001	8-10 40-41 49 73 80 114 138-140 147
mammary gland	Hivinogen	1.2.10001	217 250-256 264 297-299 305 377-378
	1		398 446 481-486 505 512 537 545 549
			571 592 725 730-733 816 829 836 844
	}		868 873 876-877 898 926 943 951-960
			963 976 995 1034 1042 1048 1054-
			1055 1076 1083 1091 1093 1116-1117
			1124 1152 1302
		NTDOOL	39 101 111 138 238 361 1225 1251
induced neuron cells	Strategene	NTD001	1319
		170001	74 225 976
retinoid acid induced	Strategene	NTR001	74 223 710
neuronal cells		- I Start VOO.1	129 225 238 304 313 361 657 976
neuronal cells	Strategene	NTU001	976
pituitary gland	Clontech	PIT004	38 976
placenta	Clontech	PLA003	111 188 238 257-258 564 724 961-966
prostate.	Clontech	PRT001	•
•			1067 1095 238 430-431 841 859 868 963 1001
rectum	Invitrogen	REC001	1
			1116 8 151 402 432-433 446 496 868 952
salivary gland	Clontech	SAL001	
J	1		976 1083 1120 1151 1184
small intestine	Clontech	SIN001	8 101 147 215 259-266 446 462 505
Siller Bresser		ļ	545 592 660 789 836 866 873 927 952
		1	963 967-978 1042 1120 1152 1223-
•		{	1224
skeletal muscle	Clontech	SKM001	238 302 927 943 992 1031
spinal cord	Clontech	SPC001	74 111 132 151 215-216 238 264 267-
Spinar coru	Clontoon	1	270 343-344 353 379 516 537 566 740
		{	828 927 976 979-994 1092 1153-1159
			1225 1250
	Clastach	SPLc01	698 859 1042
adult spleen	Clontech	STO001	210 238 271-272 537 580 705 918 952
stomach	Clontech	310001	995 1171
	<del></del>	TILAGO	61 219-220 273-276 312 315 330 596
thalamus	Clontech	THA002	963 996-1007 1059 1093 1160-1162
			8 120 151 208 221 316-317 353 639
thymus	Clonetech	THM001	750 867 874 878-881 927 963 1023
			1083 1094-1096 1124
	+	THMc02	8 61 114 129 132 210 225 231 306
thymus	Clontech	1 I I I I I I I I I I I I I I I I I I I	1
thymus	Clontech	1 HIVICO2	317-319 336 340 359 380 398 446 448
thymus	Clontech	1 MWC02	317-319 336 340 359 380 398 446 448 463 512 519 545 554 587 598 698 724- 725 789 812 836 868 873 927 947 952

0	RNA Source	Hyseq Library Name	SEQ ID NOS:
Tissue Origin	KINA Source	Trysed Energy :	976 1007 1042 1083 1085 1097-1116
			1122 1147 1177 1226-1229 1234 1311
			1313
d wid sland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188
thyroid gland	Clonteen	112.001	210 217 222 253 264 271 277-286 294
	]		320-326 345-352 361 381-382 446 467
			483 514 534 549-550 564 578 602 649
			844 882-883 927 950 956 976 1008-
<u> </u>		1	1028 1076 1083 1117-1120 1142 1163-
	Į.	Í	1175 1230-1238 1308
Aug also o	Clontech	TRC001	223-225 238 287 353-354 514
trachea	Clonteen	THE STATE OF THE S	545 592 611 873 883-884 927
			952 1029-1031 1042 1151-1152
ļ			1170 1176-1177 1239
	Clontech	UTR001	151 226 288-290 355 537 877
uterus	Ciontech	OTROOT	885-886 976 1001 1032-1033
			1232

## TABLE 2

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.	460	100
		L	Human secreted protein, SEQ ID NO: 7645.	111	51
2	G03564	Homo sapiens	Part of Major Yo paraneoplastic antigen	293	76
3	R26173	Homo sapiens	(CDR62) encoded by clone pY2.		
	100536	Homo sapiens	calcium channel L-type alpha 1 subunit	191	65
4	L29536 Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	251	50
5	Y94943	Homo sapiens	sequence SEQ ID NO:92.		
	M11507	Homo sapiens	transferrin receptor	120	95
6	AF099100	Homo sapiens	W/D-repeat protein 6	1941	93
7	Y92338	Homo sapiens	Human cancer associated antigen precursor from	245	82
o	192336	Tomo sup.site	clone NY-REN-45.		91
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	
10	AJ133798	Homo sapiens	conine VII protein	1127	68 99
11	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	
12	X98330	Homo sapiens	ryanodine recentor 2	282	78 100
13	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threonine-protein	293	100
13	711024490	110	kinase (ortholog of mouse and rat MAK (male	1	-
	ļ	}	germ cell-associated kinase))	ļ	36
14	AF045577	Pan	olfactory receptor OR93Ch	191	30
1-4	7 12 0 13 5 1 1	troglodytes		93	39
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	569	89
16	U26595	Rattus	prostaglandin F2a receptor regulatory protein	309	67
		norvegicus	precursor	99	44
17	B08918	Homo sapiens	Human secreted protein sequence encoded by	99	44
• •		_	gene 28 SEQ ID NO:75.	165	75
18	Y36203	Homo sapiens	Human secreted protein #75.	106	40
19	U15647	Mus	reverse transcriptase	100	1
		musculus	1 050 ID NO (702	544	100
20	G02701	Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	1691	100
21	Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ	1031	100
	1		ID NO. 172.	380	96
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 8111.	123	50
23	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	284	90
24	AF036329	Homo sapiens	gonadotropin-releasing hormone precursor,	204	1
	1		second form	96	32
25	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	100	34
26	S80119	Rattus sp.	reverse transcriptase homolog	101	35
27	U83303	Homo sapiens	line-1 reverse transcriptase	135	45
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	133	

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:				83	42
29	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.		72
30	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	116	67
31	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	96	
32	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	58	32
	Y66688	Homo sapiens	Membrane-bound protein PRO1152.	2457	98
33 34	Y87071	Homo sapiens	Human secreted protein sequence SEQ ID NO:110.	348	95
		Trans essions	p126	182	48
35 36	U15131 Y73464	Homo sapiens Homo sapiens	Human secreted protein clone yl4_1 protein sequence SEQ ID NO:150.	982	90
37	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	687	99
38	AC067969	amino acids	Homo sapiens ryanodine receptor 1 (skeletal)	386	66
39	AL031588	3338-4088 Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN, FGENES and GENEWISE)	493	76
			Human secreted protein, SEQ ID NO: 7709.	110	51
40	G03628	Homo sapiens		228	68
41	AF132969	Homo sapiens	CGI-35 protein	220	88
42	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	105	35
43	X61048	Hydra sp.	mini-collagen	110	31
44	M76546	Helianthus annuus	hydroxyproline-rich protein	139	70
45	U82288	Caenorhabditi s elegans	Rac-like GTPase	118	58
46	G03477	Homo sapiens	Human secreted protein, SEQ ID NO: 7558.		63
47	AF090942	Homo sapiens	PRO0657	113	59
48	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	90	56
49	AJ005560	Mus musculus	SPR2B protein	72	98
50	G02450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	98
51	Y91649	Homo sapiens	Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.	973	
52	U93563	Homo sapiens	putative p150	105	38
53	Y55927	Homo sapiens	Human STLK2 protein.	699	85
	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	145	56
55	AB008175	Mus musculus	hepatic nuclear factor 1-beta short form	356	74
	M68941	Homo sapiens	protein-tyrosine phophatase	165	41
56	AL031600	Homo sapiens	17	338	76
57 58	AE031600 AF011417	Mus musculus	putative pheromone receptor	143	55
59	AF167320	Mus	zinc finger protein ZFP113	558	68
		musculus	interferon regultory factor 7	263	96
60	U73036 X07984	Homo sapiens Mus	protein-tyrosine kinase	297	69
<u></u>		musculus	Human secreted protein clone cb98_4.	791	98
62	Y29861	Homo sapiens	- 1 f 4 a m	485	65
63 64	U35376 AF265555	Homo sapiens Homo sapiens		785	74
			1 000 100 100 100 1	88	95
65	G03883	Homo sapiens	antennal specific membrane protein AMP	274	54
66	AF177390	Manduca sexta		614	100
67	AB040800	Homo sapiens		213	26
68	AF030027	Equine herpesvirus 4	24		95
69	G02965	Homo sapien	Human secreted protein, SEQ ID NO: 7040.	261	98
70	W75770	Homo sapien		1144	
71	AB011135	Homo sapien		239	76
72	AB011133 AB014885	Halocynthia roretzi	HrPOPK-1	813	78
73	AF045454	Cavia	phospholipase B	955	73
1				308	61

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
10:	140.	1		Score	<del> </del>
10.		musculus			ļ
5	Y00826	Rattus norvegicus	gp210 (AA 1-1886)	413	84
6	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	351	54
		VVione	Human secreted protein.	468	76
7	Y38422	Homo sapiens	Human T-type voltage-gated Ca channel alpha-	1357	99
18	Y14596	Homo sapiens	1-I (hCavT3).	767	100
79	Y14591	Human papillomaviru s type 68	APM-1 protein		34
80	AL137802	Homo sapiens	dJ798A10.2 (KIAA0445 protein)	71	
31	AP000383	Arabidopsis thaliana	protein arginine N-methyltransferase-like protein	359	65
82	L46815	Mus musculus	DNA binding protein Rc	895	75
	001600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681.	315	96
83 84	G01600 Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	538	71
	1	77	KIAA1079 protein	134	42
85	AB029002	Homo sapiens	Human cw272_7 secreted protein.	325	62
86	Y28678	Homo sapiens	Human PRO1326 (UNQ686) amino acid	156	48
87	Y99368	Homo sapiens	sequence SEQ ID NO:100.  hyperpolarization-activated cation channel,	487	95
88	AJ225124	Mus musculus	HAC3	290	56
89	AF177203	Homo sapiens	cerebral cell adhesion molecule	326	79
90	Y28280	Homo sapiens	Human G-protein coupled receptor GRIR-2. polycystic kidney disease-associated protein	1751	95
91	L39891	Homo sapiens	polycystic kidney disease-associated protein	953	99
92	AF064876	Homo sapiens	ion channel BCNG-1	401	53
93	AF170723	Homo sapiens	protein kinase STK10	151	37
94 .	X13292	Trypanosoma brucei	GPI-phospholipase C (AA 1 - 358)	661	99
95	Y34127	Homo sapiens	Human potassium channel K+Hnov11.	1775	92
96	X03638	Rattus norvegicus	sodium channel protein I (aa 1-2009)		99
97	AF134213	Homo sapiens	ubiquitin-specific protease	1995	38
98	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.		48
99	AF021935	Rattus norvegicus	mytonic dystrophy kinase-related Cdc42-binding kinase	675	_
100	AF279265	Homo sapiens	putative anion transporter 1	867	98
101	AC007878	Homo sapiens	match to nuclear protein, NP220; note: sequence difference at residue 58	160	60
102	U22829	Mus musculus	P2Y purinoceptor	264	42
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	516	99
101	7/04000	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	787	98
104	Y94990 Y87342	Homo sapiens		343	57
	1	11.		212	67
106	AF169312	Homo sapiens	PRO1310	74	52
107	AF116657	Homo sapiens	sialic acid transporter	587	96
108	AE000401	Escherichia coli	d the sea No. 10	693	100
109	Y38395	Homo sapiens		182	94
110	Y78801	Homo sapiens	HP00631 amino acid sequence.	464	85
111	Z25535	Homo sapiens		274	51
112	Y94939	Homo sapiens	sequence SEQ ID NO:84.		
113	AF016365	Homo sapiens		301	71
114	AC007956	Homo sapiens	unknown	520	75
115	M83738 AL157952	Homo sapiens Homo sapiens	protein-tyrosine phosphatase	251 484	92
110	DE13/332	Homo sapiens	domain transcription factor ESE-3A, isoform 1))	546	87

EQ D	Accession No.	Species	Description	Smith- Waterman	% Identity
	No.		1	Score	
O:	141016	Homo sapiens	cam kinase l	407	62
18	L41816		phosphatidylinositol 3-kinase	627	93
19	AJ006710	Rattus	phospitatidy into site of a site of		
		norvegicus	pyruvate dehydrogenase phosphatase regulatory	1646	94
20	AF026954	Bos taurus	pyruvate denydrogenase phosphanase regulatery		1
1	_1		subunit precursor, PDPr	373	68
21	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase {EC	313	
<u> </u>			3.1.3.48}	262	88
122	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit		35
23	Y44403	Homo sapiens	Human truncated tankyrase-1.	111	
124	U88167	Caenorhabditi	contains similarity to C2 domains	219	29
124	033107	s elegans			
	17000(40	Homo sapiens	guanine nucleotide binding protein beta subunit	693	90
125	AF300648	Homo sapiens	4		
			apoptosis signal-regulating kinase 2	153	65
126	AB021861	Mus	apoptosis signal-regulating kinaso 2		ļ
1		musculus	concentrative Na+-nucleoside cotransporter	807	97
127	AF305210	Homo sapiens		601	
	1	[	hCNT3	220	73
128	M90360	Homo sapiens	protein kinase	574	86
129	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2		67
130	AF208043	Homo sapiens	TEL16b	496	
131	AF201734	Mus	testis specific serine kinase-3	800	87
131	AF201/34	musculus			
120	AE112006	Bos taurus	differentiation enhancing factor 1	159	74
132	AF112886	Homo sapiens	phospholipase C-beta-1b	554	85
133	AJ278314	riomo sapiens	Human secreted protein encoded by gene 73	1157	87
134	W74802	Homo sapiens	clone HSQEL25.		
			Pancreas-specific gene	668	96
135	AB020335	Home sapiens	A secreted protein encoded by clone dt674_2.	866	98
136	W80408	Homo sapiens	A secreted protein encoded by crone dio/4_2.	5041	99
137	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95%	3041	"
	1		similarity to P49205 (PID:g1345860)	891	100
138	Y96736	Homo sapiens	PRO3434, a novel secreted protein.	1	55
139	AB024034	Arabidopsis	DNA-damage inducible protein DDI1-like	147	1 33
137	1 2002 100 1	thaliana		1	
140	W97809	Homo sapiens	Human GTPase regulator GRAF.	248	56
	Y51557	Homo sapiens	Human PLA2 protein.	125	46
141	AF090113	Rattus	AMPA receptor binding protein	623	93
142	AF090113	norvegicus	7EM 111000pitt Carrows D 1	1	
	1777		Human RECK cancer-inhibiting protein.	641	82
143	W26642	Homo sapiens	transmembrane receptor UNC5H2	578	84
144	U87306	Rattus	transmentorate receptor of costa	1	
		norvegicus		727	92
145	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein	1	
	1		M160 precursor	140	40
146	W63683	Homo sapiens	Human secreted protein 3.	513	81
147	M96264	Homo sapiens	galactose-1-phosphate uridyl transferase		90
148	D64014	Escherichia	HrsA	818	70
1.70	23.0	coli		<del> </del>	
149	M83316	Escherichia	pppGpp phosphohydrolase	915	95
147	14102210	coli			-+
160	AT 162270	Homo sapiens	homolog to cAMP response element binding and	1261	99
150	AL163279	110mo sabiens	beta transducin family proteins	_	
	1	177		940	99
151	AF179867	Homo sapiens	1 1 - 1 - 1 - 1 - 1	392	61
152	R95332	Homo sapiens	Tumor necrosis ractor receptor 1 deads somalis		
			ligand (clone 3TW).	370	92
153	AF151859	Homo sapiens	CGI-101 protein	489	81
154	X66957	Homo sapiens	hexokinase type 1		92
155	Y16355	Homo sapiens	alternatively soliced form	432	
156	G00857	Homo sapiens	CEO ID NO. 4038	349	78
		Mus	zinc finger protein	352	74
157	AF159455	musculus			
	1		interleukin-1 receptor-associated kinase	537	76
158	L76191	Homo sapiens	1 1 1 1 n - angible duel	670	98
159	AP001743	Homo sapiens	specifity Ser/Thr/Tyr kinase domain	1	1
ì				556	74
160	AJ250425	Rattus	Collybistin I	) 550	' '
	1	norvegicus		270	100
161	G02885	Homo sapiens	Human secreted protein, SEQ ID NO: 6966.	370	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:				610	100
162	Z22968	Homo sapiens	M130 antigen	336	92
163	AF181121	Homo sapiens	ATP-dependent Ca2+ pump PMR1	455	94
164	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	700	96
165	AF160798	Rattus	calcium transporter CaT1	700	90
166	Y76332	norvegicus Homo sapiens	Fragment of human secreted protein encoded by	327	45
100	170000		gene 38.	1072	99
167	Y48607	Homo sapiens	Human breast tumour-associated protein 68.	1072	
168	AB020741	Mus	NIK-related kinase	197	43
		musculus	PAR3	596	44
169	AF252293	Homo sapiens	diacylglycerol kinase eta	481	82
170	U59429	Cricetinae gen. sp.			
171	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	386	42
	AF127085	Mus	semaphorin cytoplasmic domain-associated	507	82
172	AF12/063	musculus	protein 3B	653	99
173	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	033	
	-	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97
174	G02979		embryonic stem cell phosphatase	168	55
175	U36488	Mus musculus	Chioryome stem sen phosphases	1	
176	W95629	Homo sapiens	Homo sapiens secreted protein gene clone	1022	100
		<u></u>	gm196_4.  formiminotransferase cyclodeaminase form D	255	93
177	AF289023	Homo sapiens	T-cell receptor alpha-chain (413 is 2nd base in	710	99
178	X04936	Homo sapiens	(codon)		1
179 `	AF127481	Homo sapiens	non-ocogenic Rho GTPase-specific GTP exchange factor	175	80
		<del></del>	Human secreted protein, SEQ ID NO: 5059.	517	94
180	G00978	Homo sapiens	Membrane-bound protein PRO1310.	671	96
181	Y66645	Homo sapiens	orphan seven-transmembrane receptor	862	100
182	AF110640	Homo sapiens	orphan transporter short splicing variant	766	84
183	AB020854	Bos taurus	cadherin-like protein VR8	375	38
184	AF169691	Homo sapiens	thyrotropin-releasing hormone degrading	985	99
185	AF 126372	Homo sapiens	ectoenzyme		1
186	L20966	Homo sapiens	phosphodiesterase	541	76
187	G02920	Homo sapiens	Human secreted protein, SEO ID NO: 7001.	254	93
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein	301	98
			sequence SEQ ID NO:42.  Membrane-bound protein PRO1309.	694	100
189	Y66713	Homo sapiens	0FO ID MO: 7375	331	73
190	G03244	Homo sapiens	sn-glycerol 3-phosphate acyltransferase	707	92
191	U36771	Rattus norvegicus			
192	R05935	Homo sapiens	Secreted GPIIb subunit of multiple subunit polypeptide (MSP)GPIIb-IIIa.	157	72
			casein kinase II alpha subunit	364	50
193	M92084	Theileria parva		1	
100	100000	Homo sapiens	Membrane-bound protein PRO1310.	448	90
194 195	Y66645 W95631	Homo sapiens	Homo sapiens secreted protein gene clone	382	49
			hj968 2.	680	99
196	AF255614	Rattus	scaffolding protein SLIPR	1 555	
1		norvegicus	La hatidata sharmhahudralase	300	41
Į.	AC021640	Arabidopsis thaliana	putative phosphatidate phosphohydrolase		
197	l l		olfactory receptor	316	43
	AE073067	Mus		1	
197	AF073967	Mus musculus		1	
		musculus domesticus	TIND A 190	617	98
	AF073967 W01730	musculus domesticus Homo sapiens		617	98
198		musculus domesticus Homo sapiens Homo sapiens	pancreas-enriched phospholipase C	625	89
198 199 200	W01730 AF117948	musculus domesticus Homo sapiens	pancreas-enriched phospholipase C CDC42-binding protein kinase beta	625 636	89 94
198 199 200 201	W01730 AF117948 AF128625	musculus domesticus Homo sapiens Homo sapiens	pancreas-enriched phospholipase C  CDC42-binding protein kinase beta	625 636 1303	89 94 100
198 199 200	W01730 AF117948	musculus domesticus Homo sapiens Homo sapiens Homo sapiens	pancreas-enriched phospholipase C CDC42-binding protein kinase beta Link guanine nucleotide exchange factor II Human secreted protein clone qc646_1 protein	625 636	89 94 100 99
198 199 200 201 202	W01730 AF117948 AF128625 AF117946	musculus domesticus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	pancreas-enriched phospholipase C CDC42-binding protein kinase beta Link guanine nucleotide exchange factor II Human secreted protein clone qc646_1 protein sequence SEQ ID NO:48.	625 636 1303	89 94 100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
<u> 10:</u>			(ovarian cancer critical region of deletion)		
		Sus scrofa	parathyroid receptor	122	60
06	U18315		putative pheromone receptor V1RL1 long form	170	96
07	AF255342	Homo sapiens	neurotransmitter transporter	715	94
08	S52051	Rattus sp.	neurotransmitter transporter	840	99
09	W63683	Homo sapiens	Human secreted protein 3.	541	82
10	D79992	Homo sapiens	similar to Drosophila photoreceptor cell-specific protein, calphotin.		99
111	AF117948	Homo sapiens	pancreas-enriched phospholipase C	1348	
12	U81035	Rattus	ankyrin binding cell adhesion molecule	471	69
.12	001033	norvegicus	neurofascin		<del> </del>
213	AF154846	Homo sapiens	zinc finger protein	798	56
214	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	933	93
214	AL 102///	musculus		L	<u> </u>
216	AL163303	Homo sapiens	putative gene containing transmembrane domain	523	89
215	U26595	Rattus	prostaglandin F2a receptor regulatory protein	563	78
216	026393	norvegicus	precursor		<u> </u>
	001005	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	98
217	G04095		protein kinase C mu	314	81
218	X75756	Homo sapiens	Membrane-bound protein PRO1100.	770	98
219	Y66723	Homo sapiens	Kupffer cell receptor	567	40
220	D88577	Mus	Kuhitei cen iccobioi	1	
	<u> </u>	musculus	OTRPC4	853	100
221	AF258465	Homo sapiens	mytonic dystrophy kinase-related Cdc42-binding	636	96
222	AF021935	Rattus		1	
		norvegicus	kinase bA215B13.1 (A kinase (PRKA) anchor protein	693	100
223	AL136527	Homo sapiens		0,0	
	i		11)	690	99
224	AB032417	Homo sapiens	WNT receptor Frizzled-4	703	68
225	AF030430	Mus	semaphorin VIa	1,00	1 -
		musculus	17 Language Lineau (EC 2 7 L2)	297	39
226	AE000218	Escherichia	putative dihydroxyacetone kinase (EC 2.7.1.2)	251	1 "
		coli	l li li li a acetein 2	2080	100
227	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	265	88
228	AB024573	Mus	GTP-binding like protein 2	263	1 50
		musculus		316	40
229	AF122924	Xenopus	Wnt inhibitory factor-1	310	140
		laevis		229	100
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.		92
231	X98260	Homo sapiens	M-phase phosphoprotein 11	265	95
232	R92754	Homo sapiens	Human growth differentiation factor-12.	682	
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific	290	100
233	10,511.		phospholipase-D.		
234	W69431	Homo sapiens	Human secreted protein cw1233_3.	235	97
235	Y08686	Homo sapiens	serine palmitoyltransferase, subunit II	859	81
	AF118275	Homo sapiens	atrophin-related protein ARP	117	37
236		Mus	Embryo Brain Kinase	460	62
237	X81466	musculus			
238	U64857	Caenorhabditi	similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor	284	33
	1	s elegans	precursor (TFPI)		}
	<u> </u>	-	serine/threonine protein kinase	739	63
239	AJ250840	Mus	seimonne proten kinase		
		musculus	transcription elongation factor TFIIS.h	222	38
240	AJ223472	Mus	uanscription ciongadon factor 11 fro.ii		1
		musculus	Human secreted protein clone rb649_3 protein	353	52
241	Y94906	Homo sapiens	Human secreted protein clone rbo49_3 protein sequence SEQ ID NO:18.		-
			OT MT 1	591	99
242	AF169301	Homo sapiens	Na+/sulfate cotransporter SUT-1	667	93
243	L22022	Rattus	orphan transporter v7-3	1 557	1
		norvegicus		1043	98
244	AF016191	Rattus	potassium channel	1043	70
		norvegicus_			98
245	AF097366	Homo sapiens	cone sodium-calcium potassium exchanger	645	
246	Y29868	Homo sapiens		497	98
247	AF180475	Homo sapiens	Not4-Np	188	83
248	Y17227	Homo sapiens		690	99
				182	31

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO:	110.			Score	
<u> </u>	<del></del>	sexta	protein SCLP		
50	AF192756	Kaposi's	Orf73	134	34
:50	AF 192730	sarcoma-	01175	}	
		associated			
	1				1
-	17000001	herpesvirus	MOK protein kinase	209	83
251	AB022694	Homo sapiens	Neural adhesion molecule (ethb0018f2 product).	469	100
252	W55045	Homo sapiens		251	67
253	L46815	Mus	DNA binding protein Rc	251	0,
	j	musculus		173	82
254	W68505	Homo sapiens	Human acid sensing ionic channel.	1201	98
255	AF070066	Mus	Citron-K kinase	1201	76
		musculus		460	100
256	G02491	Homo sapiens	Human secreted protein, SEQ ID NO: 6572.	1	80
257	Z12841	Oryctolagus	Phospholipase	368	1 80
		cuniculus			<del> </del>
258	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1857	99
259	AJ222968	Mus	L-periaxin	430	72
		musculus	·	ļ	1
260	AJ250839	Homo sapiens	serine/threonine protein kinase	861	100
261	AJ249977	Homo sapiens	AMP-activated protein kinase gamma 3 subunit	758	98
262	AF141386	Rattus	SLIT-2	198	40
202	15171500	norvegicus		[	
263	AF022859	Homo sapiens	neuropilin-2(a0)	335	62
264	AF160477	Homo sapiens	Ig superfamily receptor LNIR precursor	387	91
265	Y44662	Homo sapiens	Human 14273 G-protein coupled receptor	636	99
203	1 44002	Homo sapiens	(GPCR).	1	1
266	U27269	Mus	sodium glucose cotransporter	204	56
200	021209	musculus	Sodium Binesse commisperior	1	1
0.00	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	159	75
267			putative taste receptor TR1	209	39
268	AF127389	Rattus	putative taste receptor Tres		
0.60	1/0000/	norvegicus	ubiquitin hydrolase	215	95
269	X98296	Homo sapiens	Fc-gamma receptor	129	26
270	X78482	Streptococcus	re-gamma receptor	1 .27	1
		pyogenes	KED	109	26
271	AB009883	Nicotiana	KED	1 .05	
		tabacum	VPS10 domain receptor protein SORCS	899	97
272	AF137367	Mus	VPS10 domain receptor protein Society	033	1 -
		musculus	i de la contra del la contra de la contra de la contra del la contra del la contra de la contra de la contra del la contra	460	86
273	L34938	Rattus	ionotropic glutamate receptor	, 400	1 00
		norvegicus	TYCOTYC 1 1 (1) Andrews dependent	188	74
274	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent	100	'
		}	Expressed Protein LIKE PUTATIVE protein)	]	1
		<u> </u>	(isoform 1)	177	94
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	173	74
			APOLLON	140	56
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	
277	L40380	Homo sapiens	thyroid receptor interactor	430	61
278	AB046851	Homo sapiens	KIAA1631 protein	283	96
279	AC008075	Arabidopsis	Contains PF 00069 Eukaryotic protein kinase	157	43
		thaliana	domain.		
280	M83738	Homo sapiens	protein-tyrosine phosphatase	181	73
281	AK024397	Homo sapiens	unnamed protein product	439	91
282	AF141326	Homo sapiens	RNA helicase HDB/DICE1	497	84
283	AF156530	Mus	ETS-domain transcriptional repressor PE1	605	76
200	15 150550	musculus			
204	V20226	Homo sapiens	Human secreted protein clone cs756_2 alternate	647	100
284	Y29336	Troute sapiens	reading frame protein.		
201	17772 400	Home conieca	Human secreted protein clone ye25_1 protein	300	90
285	Y73402	Homo sapiens	sequence SEQ ID NO:26.		
		<del></del>		137	100
286	AF016411	Homo sapiens	KČNA3.1B	688	97
287	W89253	Homo sapiens	Human ALP.	750	96
288	AF112886	Bos taurus	differentiation enhancing factor 1		44
289	AF113131	Homo sapiens	host cell factor homolog LCP	367	100
290	U52111	Homo sapiens	plexin-related protein	698	
291	AF026504	Rattus	SPA-1 like protein p1294	603	89

SEQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
<u>10:</u>		norvegicus			<del> </del>
102	AF102854	Rattus	membrane-associated guanylate kinase-	124	53
292	AF 102654	norvegicus	interacting protein 2 Maguin-2		1-20
293	X99211	Drosophila	ubiquitin-specific protease	143	38
293	737211	melanogaster	•		94
294	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	185	94
294	194243	110	sequence SEO ID NO:92.		59
295	Y94890	Homo sapiens	Human protein clone HP02798.	108	96
296	AF019767	Home sapiens	zinc finger protein	154	
297	Y28568	Homo sapiens	Secreted peptide clone bd577_1.	568	97
298	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	182	) 97
290	174743		sequence SEO ID NO:92.		69
299	B08906	Homo sapiens	Human secreted protein sequence encoded by	605	69
237	1 200,00		gene 16 SEQ ID NO:63.	212	97
300	R58890	Homo sapiens	Human-32 cadherin-related molecule.		100
301	AF022859	Homo sapiens	neuropilin-2(a0)	277	97
302	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
303	Y44297	Homo sapiens	Human receptor tyrosine kinase.	228	80
304	D32050	Homo sapiens	alanyl-tRNA synthetase	192	72
305	U43586	Homo sapiens	protein kinase related to Raf protein kinases; Method: conceptual translation supplied by	428	/2
			author	280	95
306	R54872	Homo sapiens	Human H13 viral receptor mutant 4.	199	41
307	D78572	Mus	membrane glycoprotein		1
	<u> </u>	musculus	scaffolding protein SLIPR	639	88
308	AF255614	Rattus	scarroiding protein SER R	l	
		norvegicus	semaphorin homolog=M-Sema F	162	89
309	579463	Mus sp.	ATP-binding cassette sub-family A member 2	736	100
310	AF178941	Homo sapiens	calcium binding protein	151	36
311	U03413	Dictyostelium discoideum			
216	7/07247	Homo sapiens	Human signal peptide containing protein HSPP-	744	100
312	Y87347	nomo sapiens	124 SEO ID NO:124.		
272	707055	Homo sapiens	41299N45 4 (putative GS2 like protein)	789	99
313	Z97055 AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins;	197	38
314	AC004010	Troine sapiens	44% similarity to U42767 (PID:g1736918)	<u> </u>	100
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and	278	38
313	ALU21332	1.05 524.586	GENEWISE)	1.05	38
316	U70209	Mus	polycystic kidney disease 1 protein	165	38
טונ	0,0209	musculus		1222	38
317	AF109643	Rattus	coxsackie-adenovirus-receptor homolog	223	36
317	1 1 1 1 1 1 1 1	norvegicus		138	84
318	AF104923	Homo sapiens	putative transcription factor		38
319	AF100287	Тгурапоѕота	activated protein kinase C receptor homolog	141	36
7.7		vivax		125	51
320	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	459	97
321	Y21591	Homo sapiens	Human secreted protein (clone CC332-33).	232	97
322	D26070	Homo sapiens	human type 1 inositol 1,4,5-trisphosphate	232	1"
		1 .	receptor	306	88
323	Y27918	Homo sapiens		300	55
			123.	209	70
324	AF010144	Homo sapiens		214	97
325	M19650	Homo sapiens	13 273'-cyclic-nucleotide 3'-phosphodiesterase (EC	1 - 1 - 1	- '
			3.1.4.37)	140	70
326	W80396	Homo sapiens		540	78
327	X75756	Homo sapiens		721	99
328	G02292	Homo sapiens		877	99
329	AF168990	Homo sapiens		581	80
330	S67984	Homo sapiens	anti-HIV gp120 antibody heavy chain variable	301	"
	1		region (AA 19 to 4525)	2823	98
331	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	1127	100
332	Y87330	Homo sapien	Human signal peptide containing protein HSPP-	1	
1			107 SEQ ID NO:107.  S HGFH3 Human Growth Factor Homologue 3.	320	98
333	Y28503	Homo sapien	5 1 0 0 1 C CC -1 050/-	327	93
334	AC002563	Homo sapien	s i nutative Kho/kho effector protein, 7570		

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			similarity to P49205 (PID:g1345860)		
			Human signal peptide containing protein HSPP-	1111	67
335	Y87347	Homo sapiens	124 SEQ ID NO:124.  lymphocyte specific formin related protein	193	75
336	AF006466	Mus musculus		632	97
337	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON		
338	Y13443	Homo sapiens	Amino acid sequence of hSlo3-2.	516	100
339	Y07637	Homo sapiens	nutative GABA-gated chloride channel	189	100
340	Y05734	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
341	AE000497	Escherichia coli	L-idonate transcriptional regulator	928	98
342	D90855	Escherichia coli	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	769	99
343	D85613	Escherichia coli	membrane component	399	100
344	M93239	Escherichia	transmembrane protein	232	100
345	M60177	Escherichia	enterobactin	759	99
346	D90699	Escherichia	Sensor protein copS (EC 2.7.3).	638	97
347	D90843	Escherichia	CapB protein.	552	100
348	M13422	Escherichia	49 kd protein	1193	96
349	L10328	Escherichia	similar to drug resistance translocases	340	90
350	X69942	coli Mus	enhancer-trap-locus-1	560	82
351	AF239613	Homo sapiens	apamin-sensitive small-conductance Ca2+-	463	80
352	D90777	Escherichia	activated potassium channel 3-hydroxybutyryl-CoA dehydrogenase (EC	577	100
552		coli	1.1.1.157) (b- hydroxybutyryl-CoA dehydrogenase) (BhbD).	311	98
353	D90863	Escherichia coli	similar to		58
354	Y52386	Homo sapiens	Human transmembrane protein HP02000.	133	55
355	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-		
356	Y58637	Homo sapiens	Protein regulating gene expression PRGE-30.	119	51
357	AF119226	Homo sapiens	dual-specificity tyrosine phosphatase YVH1	1788	100
358	Y87219	Homo sapiens	Human secreted protein sequence SEQ ID NO:258.	165	
359	J00132	Homo sapiens	heta-fibringen	233	93
360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	70
361	R28916	Homo sapiens	Type III procollagen (prior art).	108	40
362	U16655	Rattus norvegicus	phospholipase C delta-4	649	65
363	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	95	34
364	U47276	Gallus gallus	chicken brain factor-2	104	
365	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	65
366	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	118	46
	X98258	Homo sapiens	M-phase phosphoprotein 9	564	75
367		Homo sapiens	1 and anothern	3387	99
368	AL021366 U70932	Peromyscus	reverse transcriptase	92	59
369	ı	leucopus	gamma subunit of sodium potassium ATPase	242	73
	X86400	Homo sapiens	like-		
369 370			like	165	56
369 370 371	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	56 55
369 370 371 372	G03172 U49974	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7253.  mariner transposase	257	
369 370 371	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.  mariner transposase		55

10:		. \		Waterman Score	Identity
	1		SEO ID MO: 6065	221	67
376	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	600	100
77	G00669	Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	1456	91
78	X52574	Mus musculus	GTP binding protein		
179	R69095	Homo sapiens	Anti-HIV Fab tat31 light chain.	68	37
80	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
	AB002405	Homo sapiens	LAK-4p	530	43
81	U64830	Dictyostelium	protein tyrosine kinase	115	44
		discoideum	Human secreted protein, SEQ ID NO: 6997.	618	98
83	G02916	Homo sapiens	Human secreted protein, SEQ ID NO. 5275	617	93
84	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	4560	100
85	AJ245822	Homo sapiens	type I transmembrane receptor	2148	98
86	D86974	Homo sapiens	KIAA0220	142	50
387	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	99	59
388	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.		1 51
889	M12140	Homo sapiens	envelope protein	197	177
390	AJ293309	Homo sapiens	NHP2 protein	461	94
191	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	181	
392	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	241	66
192 193	Y14442	Homo sapiens	olfactory receptor protein	339	54
	W85607	Homo sapiens	Secreted protein clone da228 6.	957	100
39 <b>4</b> 39 <b>5</b>	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	171	34
<u>.</u>	1 22222	Homo sapiens	Human secreted protein, SEQ ID NO: 8011.	250	100
396 397	G03930 AB032904	Hylobates	dopamine receptor D4	105	35
		syndactylus	(00.400)	861	85
398	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	1047	92
399	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.		
400	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	162	37
401	D87002	Homo sapiens	similar to rat integral membrane glycoprotein;	527	78
400	AF100754	Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
402	X74904	Gallus gallus	alpha-2-macroglobulin receptor	258	60
404	AF075462	Mus	ADP-ribosylation factor-directed GTPase activating protein isoform b	545	89
405	X92887	musculus Human endogenous retrovirus K	pol/env	162	30
	1/201/0	Homo sapiens	Human dorsal root receptor 4 hDRR4.	325	72
406	Y30162	Homo sapiens	unnamed protein product	2833	99
407	AK022626		ribosmal protein small subunit	264	92
408 409	L13802 Y91600	Homo sapiens Homo sapiens		1788	89
410	W88745	Homo sapiens	Secreted protein encoded by gene 30 clone	2004	99
411	AB043953	Mus	HTSEV09. Chat-H	2628	82
412	Y86233	musculus Homo sapiens	Human secreted protein HNTMX29, SEQ ID	1014	92
		Pan	NO:148. MHC class I A	265	71
413	U10542	troglodytes		850	95
414	AF155097	Homo sapiens		88	48
415	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	266	89
416	Y57911	Homo sapiens	Human transmembrane protein HTMPN-35.		60
417	W27651	Homo sapiens	Secreted protein AT205.	481	
418	Y76884	Homo sapiens		3077	87
419	AF255559	Notothenia coriiceps	alpha tubulin	289	68
100			Human secreted protein, SEQ ID NO: 6065.	209	74
420 421	G01984 AL109827	Homo sapiens Homo sapiens	A CD 55 (cienting	1446	96
422	AC008075	Arabidopsis	to rat sperm antigen 4 (SPAG4))) F24J5.4	112	35

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	ì				100
423	AF231705	Homo sapiens	Alu co-repressor I	1090	
124	AF234887	Homo sapiens	FLAMINGO 1	6268	97
25	Y35942	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 191.	1961	99
26	AB009288	Homo sapiens	N-copine	635	98
27	L12392	Homo sapiens	Huntington's Disease protein	16080	99
128	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
	AJ293573	Homo sapiens	zinc finger protein Cezanne	542	87
129 130	Y84441	Homo sapiens	Amino acid sequence of a human RNA- associated protein.	2074	100
	000000	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
131	G02850		Human secreted protein, SEQ ID NO: 8148.	73	42
132	G04067	Homo sapiens	extensin-like protein	613	48
433	AF159296	Lycopersicon esculentum		135	44
134	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	3442	97
435	X73874	Homo sapiens	phosphorylase kinase		
136	AF161426	Homo sapiens	HSPC308	268	74
137	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
438	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	168	56
439	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
440	X02344	Homo sapiens	beta-tubulin	311	95
441	AF168418	Homo sapiens	activating signal cointegrator 1	1882	100
442	L11672	Homo sapiens	zinc finger protein	795	54
442	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
444	A52140	unidentified	HUMAN NDR	2451	100
	X98330	Homo sapiens	rvanodine receptor 2	9356	99
445		Homo sapiens	PRO2738	227	49
446	AF116712		sphingosine kinase type 2 isoform	576	99
447	AF245447	Homo sapiens	membrane-type serine protease 1	2630	94
448	AF133086	Homo sapiens	transmembrane receptor UNC5H1	817	93
449	U87305	Rattus norvegicus			99
450	AF081249	Homo sapiens	JAW1-related protein MRVI1A long isoform	4568	
451	AC005498	Homo sapiens	R31665_1	316	62
452	M60235	Homo sapiens	granule membrane protein-140	464	73
453	AB036706	Homo sapiens	intelectin	730	88
454	G00918	Homo sapiens	Human secreted protein, SEQ ID NO: 4999.	263	81
455	Y22634	Homo sapiens	Human cytokine inducible regulatory protein-1 (CIRP-1).	192	67
456	Y36705	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	106	40
457	N91325	Homo sapiens	DNA encoding human growth hormone receptor.	3282	96
457	M19155	Plasmodium	S-antigen precursor	110	36
470	14117177	falciparum		<u> </u>	
459	Y13377	Homo sapiens	Amino acid sequence of protein PRO257.	509	98
460	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	149	43
461	Y14482	Homo sapiens	clone HTDAD22.  Fragment of human secreted protein encoded by	184	54
462	Y53005	Homo sapiens	gene 17.  Human secreted protein clone pm749_8 protein	135	47
		Triticum	sequence SEQ ID NO:16. low molecular weight glutenin	109	33
463	X84960	aestivum		1781	85
464	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	502	59
465	AF189764	Mus musculus	alpha/beta hydrolase-1		
466	U93569	Homo sapiens	p40	101	30
467	Y41528	Homo sapiens	Fragment of human secreted protein encoded by gene 77.	1172	99
468	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	149	52
469	AJ000008	Homo sapiens	PI3-kinase	5832	97
470	X70922	Mus musculus	neurotoxin homologue	118	47
471	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	75
	1 (dus/9/	I momo sapiens	Fragment of human secreted protein encoded by	72	57

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
D D	No.	1		Score	
40:	ļ		gene 62.		
173	G02313	Homo sapiens	Human secreted protein, SEQ ID NO: 6394.	328	100
74	Y07007	Homo sapiens	Breast cancer associated antigen precursor	1013	97
			sequence.		\ <u></u>
175	W93254	Homo sapiens	Human ESRP1 protein.	943	80
476	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	236	65
477	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	202	60
		<u> </u>	clone HTDAD22.  Human secreted protein, SEQ ID NO: 5951.	267	100
478	G01870	Homo sapiens	FYVE finger-containing phosphoinositide kinase	3427	92
479	AF102777	Mus musculus	FYVE linger-containing phosphomositide knaze	3,2,	
480	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	123	53
481	W87701	Homo sapiens	A human membrane fusion protein designated	221	77
401	1 47 87 701	110me sapieme	SYTAXI.		
482	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
483	AF210651	Homo sapiens	NAG18	124	59
484	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
485	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
486	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	149	73
	1.50	1,711,121,131	Human secreted protein encoded by gene 44.	627	100
487	Y76167	Homo sapiens	stabilin-1	1244	91
488 489	AJ275213 G03798	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
489 490	L12392	Homo sapiens	Huntington's Disease protein	16081	100
490	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	197	66
492	J03799	Homo sapiens	laminin-binding protein	228	70
493	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	128	41
.,,			3	1	1-5-
494	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	197	67
			clone HTDAD22.	889	94
495	AC005175	Homo sapiens	R31449_3	229	61
496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	90	48
497	AB030237	Canis familiaris	D4 doparnine receptor	1 30	"
498	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
498	U70935	Peromyscus	reverse transcriptase	213	52
427	070933	maniculatus	-		
500	U48508	Homo sapiens	skeletal muscle ryanodine receptor	26406	99
501	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
502	AF119851	Homo sapiens	PRO1722	156	62
503	AF113685	Homo sapiens	PRO0974	116	50
504	U79458	Homo sapiens	WW domain binding protein-2	322 608	59
505	W29651	Homo sapiens	Human secreted protein CD124_3.	986	70
506	W85459	Homo sapiens	Secreted protein encoded by clone dh1135_9.  Human secreted protein HUSXE77, SEQ ID	115	33
507	Y86265	Homo sapiens	Human secreted protein HUSXE/7, SEQ ID   NO:180.	11.5	"
600	AT 160176	Homo sapiens	bA243J16.3 (similar to MYLK (myosin, light	184	92
508	AL160175	Tollio sapiens	polypeptide kinase))		1
509	U43360	Peromyscus	reverse transcriptase	97	62
207	043300	maniculatus	•		
510	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	117	63
511	W79092	Homo sapiens	Human secreted protein dn740_3.	1058	100
512	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	205	64
513	AJ133439	Homo sapiens	GRIP1 protein	2151	100
514	AE003456	Drosophila	CG6393 gene product	259	42
		melanogaster		128	40
515	Z17206	Xenopus	p46XIEg22	120	40
		laevis	Land times suppressed 1	1766	94
516	AF104413	Homo sapiens	large tumor suppressor 1 Human secreted protein, SEQ ID NO: 7878.	92	40
517	G03797	Homo sapiens Homo sapiens	HSPC249	444	98
518	AF151083	Homo sapiens	cytochrome c-like polypeptide	318	50
519 520	S80864 X92485	Plasmodium	pval	170	61
220	A3440J	vivax	F	İ	1

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	002700	Ueme conienc	Human secreted protein, SEQ ID NO: 7871.	159	59
521	G03790	Homo sapiens	sorting nexin 7	259	40
522	AF121857	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	82	37
523	G02654	Homo sapiens	Secreted protein encoded by gene 94 clone	253	73
524	W88627	Homo sapiens	HPMBQ32.	İ	
525	AF119851	Homo sapiens	PRO1722	162	57
526	Y27761	Homo sapiens	Human secreted protein encoded by gene No. 47.	154	57
527	G02707	Homo sapiens	Human secreted protein, SEQ ID NO: 6788.	70	45
528	U47924	Homo sapiens	C8	1112	86
529	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	45
530	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	60
531	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	92	65
532	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	75	29
533	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	182	48
534	AF068286	Homo sapiens	HDCMD38P	861	100
535	U07707	Homo sapiens	epidermal growth factor receptor substrate	228	60
536	G01955	Homo sapiens	Human secreted protein, SEQ ID NO: 6036.	484	75
537	AF219232	Gallus gallus	qin-induced kinase	206	53
538	AF135022	Homo sapiens	mediator	128	100
539	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	141	59
540	AF016430	Caenorhabditi s elegans	contains similarity to a BR-C/TTK domain	853	39
541	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	408	66
542	M29487	Homo sapiens	integrin alpha subunit precursor	517	81
543	AF102530	Mus musculus	olfactory receptor F3	327	73
544	Y73431	Homo sapiens	Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.	386	100
545	AE004833	Pseudomonas aeruginosa	probable TonB-dependent receptor	279	42
546	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	264	53
547	Y69192	Homo sapiens	A human monocyte-macrophage apolipoprotein B receptor protein.	1772	67
548	Y91493	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:166.	176	100
640	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
549 550	AF044588	Homo sapiens	protein regulating cytokinesis 1; PRC1	1953	88
550 551	Y29332	Homo sapiens	Human secreted protein clone pe584_2 protein	1224	94
<i>55</i> 1	125552	220110 2-4110	sequence.	İ	
552	X98330	Homo sapiens	ryanodine receptor 2	24621	99
553	Y42782	Homo sapiens	Human UC Band #331 protein.	684	95
554	AB025258	Mus musculus	granuphilin-a	501	41
555	AJ010346	Homo sapiens	RING-H2	1468	100
556	W92388	Homo sapiens	Human TR-interacting protein S239a.	538	92
557	AF119851	Homo sapiens	PRO1722	175	59
558	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	183	32
559	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	319	68
560	D86214	Mus	Ca2+ dependent activator protein for secretion	1010	93
561	AF187325	Canis	melanoma antigen	287	55
	1,700,000	familiaris	OVAIL	2512	99
562	AJ001981	Homo sapiens	OXAIL	338	66
563	Z17238	Rattus norvegicus	glutamate receptor subtype delta-1	Í	
564	W30638	Homo sapiens	Partial human 7-transmembrane receptor HAPO167 protein.	371	100
565	AC005620	Homo sapiens	R33590_1	467	97
566	Y99358	Homo sapiens	Human PRO1772 (UNQ834) amino acid sequence SEQ ID NO:63.	1138	78
567	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1002	58
568	AF151043	Homo sapiens	HSPC209	798	100

SEQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:	_		<u> </u>	231	100
69	AF097518	Homo sapiens	liver-specific transporter	1532	100
70	AB035698	Homo sapiens	Misshapen/NIK-related kinase MINK-1	1064	100
/1	Y07096	Homo sapiens	Colon cancer associated antigen precursor sequence.		
72	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	735	55
73	Y66639	Homo sapiens	Membrane-hound protein PRO290.	254	45
74	AB037108	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
	D43949	Homo sapiens	This gene is novel.	836	100
75		Homo sapiens	Human breast tumour-associated protein 57.	108	50
76	Y48596		Human secreted protein, SEQ ID NO: 4433.	141	75
77	G00352	Homo sapiens	Neural thread protein.	140	65
78	R95913	Homo sapiens	unnamed protein product	201	70
79	AK025116	Homo sapiens	Human gene 52-encoded protein fragment, SEQ	77	70
80	Y86473	Homo sapiens	ID NO:388.	450	100
581	AF196779	Homo sapiens	JM10 protein		98
582	AF188706	Homo sapiens	g20 protein	330	
583	AB030234	Canis familiaris	D4 dopamine receptor	64	56
584	G02621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
585	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	268	85
606	V20810	Homo sapiens	Human secreted protein encoded from gene 9.	235	35
586	Y30819	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	132	56
587	G00357		Human secreted protein, SEQ ID NO: 6953.	182	79
588 589	G02872 AF235017	Homo sapiens Mus	2P1 protein	764	80
590	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	329	81
591	Y30709	Homo sapiens	HPMBQ32.  Amino acid sequence of a human secreted	110	43
592	Y53875	Homo sapiens	protein.  A human seven transmembrane signal transducer	1369	92
593	Y53051	Homo sapiens	polypeptide.  Human secreted protein clone dd119_4 protein	1112	97
			sequence SEQ ID NO:108.  Human secreted protein encoded by gene No. 92.	763	79
594	Y27658	Homo sapiens	Human secreted protein encoded by gene 140. 22.	156	58
595	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	2215	95
596	AF151110	Mus musculus	COP1 protein	157	65
597	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	143	40
598	AF192499	Mus musculus	putative secreted protein ZSIG37		
599	AF119855	Homo sapiens	PRO1847	236	76
600.	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	73
601	Y00295	Homo sapiens	Human secreted protein encoded by gene 38.	567	88
602	AF184971	Homo sapiens		2015	74
602	AF164971 AF061936	Homo sapiens	diacylglycerol kinase jota	773	96
604	AL096828	Homo sapiens		1333	93
105	AD022106	Homo sapiens		3915	100
605	AB033106	Home sapiens		3916	99
606	X75756	Homo sapiens		5758	99
607	D86983	Homo sapiens		1377	99
608	W69341	Homo sapiens		339	82
609	W88627	Homo sapiens	HPMBQ32.	116	62
610	Y27868	Homo sapiens	107.		
611	AF202636	Homo sapiens	angiopoietin-like protein PP1158	2164	100
612	AF090944	Homo sapiens	PRO0663	218	82
613	Y02693	Homo sapiens	1-11	195	59
614	M87053	Rattus norvegicus	lens membrane protein	450	84
014				1	
615	AC004232	Homo sapiens	FPM315	163	37

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO: 1	Y91524	Homo sapiens	Human secreted protein sequence encoded by	821	99
			gene 74 SEQ ID NO:197.	2258	99
518	AJ245621	Homo sapiens	CTL2 protein  Human secreted protein encoded by gene 75.	108	64
519	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	3922	94
520	AF067864	Homo sapiens	transferrin receptor 2 alpha	573	90
521	D90721	Escherichia coli	Transmembrane protein dppC		100
522	W75858	Homo sapiens	Human secretory protein of clone CS752-3.	730	100
623	Y94982	Homo sapiens	Human secreted protein vb12_1, SEQ ID NO:4.	733	
624	AF034745	Mus musculus	LNXp80	637	83
625	U42580	Paramecium	Pro-rich, IPPPNMSLPLS (3x)	94	46
	042360	bursaria Chlorella			
			unknown	194	70
626	U79260	Homo sapiens	Neural thread protein.	99	50
627	R95913	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.	427	100
628	G03450	Homo sapiens	Human secreted protein encoded by gene 58.	590	100
629 630	Y36281 Y02693	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 44	165	76
		<u> </u>	clone HTDAD22.  Human secreted protein, SEQ ID NO: 6220.	268	96
631	G02139	Homo sapiens	Human secreted protein, SEQ 1D NO. 0220.	351	80
632	U16996	Homo sapiens	protein tyrosine posphatase	2019	100
633	AF121857	Homo sapiens	sorting nexin 7	340	77
634	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899		
635	Y07090	Homo sapiens	Renal cancer associated antigen precursor sequence.	277	64
636	AB013382	Homo sapiens	DUSP6	414	76
637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
638	M95762	Rattus norvegicus	GABA transporter	924	89
639	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
640	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	137	79
641	AC008075	Arabidopsis thaliana	F24J5.4	121	33
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96 clone HAOBK61.	615	62
-, 10	4 D 01 5002	Homo sapiens	serine/threonine kinase	485	98
643 644	AB015982 Y25806	Homo sapiens	Human secreted protein fragment encoded from gene 23.	162	46
	A E122004	Homo sapiens	membrane protein DAP10	474	100
645	AF122904	Homo sapiens		200	38
646	AF233323		277.150 1	1203	99
647	W48804	Homo sapiens		1440	98
648	AF257330	Homo sapiens		233	73
649	Y36203	Homo sapiens		173	78
650 651	G02872 Y32199	Homo sapiens Homo sapiens	Human receptor molecule (REC) encoded by	1012	100
652	AB032909	Hylobates	Incyte clone 2022379. dopamine receptor D4	122	32
		agilis	and protein product	186	69
653	AK021848	Homo sapiens		57	37
654	W73411	Homo sapiens	15.	116	34
655	L22455	Rattus norvegicus	mu opioid receptor		45
656	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	110	
657	G02345	Homo sapiens	Human secreted protein, SEQ ID NO: 6426.	459	97
658	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBO32.	291	75
659	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	65
660	Y91423	Homo sapiens		333	96

	Accession No.	Species	Description	Smith- Waterman Score	% Identity
40: L	Ì		SEO ID NO. 7870	168	68
61	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	375	43
62	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.		
(2)	W75771	Homo sapiens	Human GTP binding protein APD08.	629	100
563 564	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	480	55
			KIAA1313 protein	978	96
665	AB037734	Homo sapiens	Human cerebral protein-1.	192	84
666	W82841	Homo sapiens	Human cerebral protein-1.	182	87
667	W82841	Homo sapiens	contains transmembrane (TM) region and ATP	757	68
668	AB030184	Mus musculus	binding region	85	37
669	AB032919	Hylobates muelleri	dopamine receptor D4		-
670	AF107295	Rattus	outer membrane protein	746	81
		norvegicus	leukocyte surface protein	394	93
671	Z33642	Homo sapiens	Secreted protein clone du410_5.	261	91
672	W85608	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
673	G03203	Homo sapiens	Human secreted plotein, SEQ ID 110. 7201.	2388	99
674	AL035587	Homo sapiens	dJ475N16.4 (KIAA0240)	1134	53
675	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	174	74
676 677	G03797 AF026954	Homo sapiens Bos taurus	Human secreted protein, SEQ ID NO: 7878.  pyruvate dehydrogenase phosphatase regulatory	1013	95
678	1.11625	Mus	subunit precursor; PDPr receptor protein-tyrosine kinase	545	96
070	51.025	musculus		715	100
679	AL031427	Homo sapiens	dJ167A19.3 (novel protein)	745	77
680	AJ133430	Mus musculus	olfactory receptor	528	
	000533	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	70
681	G02532	Homo sapiens	Human secreted protein, SEO ID NO: 7870.	336	76
682 683	G03789 Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	118	100
684	U43360	Peromyscus	reverse transcriptase	100	37
		maniculatus	Human secreted protein, SEQ ID NO: 4966.	162	60
685	G00885	Homo sapiens	unnamed protein product	590	100
686	AK001518	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
687	G01982	Homo sapiens	Human cancer associated antigen precursor	2405	99
688	Y92241	Homo sapiens	(MO-REN-46).	423	36
689	AC024792	Caenorhabditi s elegans	contains similarity to TR:P78316		
690	Y27868	Homo sapiens	1 107	183	81
691	Y56514	Homo sapiens	Human Jurkat cell clone P2-15 AIM10 longest	180	88
		17	1 1 1 1 1 1 2 7 0	1539	99
692	Y27795	Homo sapiens		428	98
693	Y36268	Homo sapiens		308	89
694	U12465	Homo sapiens		1517	99
695	Y45272	Homo sapiens		1242	98
696	AF191838	Homo sapiens		275	75
697	Y02693	Homo sapiens	clone HTDAD22.		90
698	Y87280	Homo sapiens	1 57 SEO ID NO:57	576	
699	Y97999	Homo sapiens		729	99
1	+ + + + + + + + + + + + + + + + + + + +	Us-s series	to the second se	610	79
700	AJ006701	Homo sapiens		2357	100
701	AF209198	Homo sapiens	Applied protein	709	45
702	AJ298841	Mus musculus	torsinA protein	622	98
703	AK021729	Homo sapiens	unnamed protein product		51
704	Z46787	Caenorhabditi s elegans	similar to Glutaredoxin, Zinc finger, C3HC4	920	_ }
1	G02882	Homo sapiens		589	98

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
D	No.			Score	
10:		1		125	58
06	G02501		Human secreted protein, SEQ ID NO: 6582.	121	95
07	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain	121	/3
,			ligand (clone 2DD).	125	139
08	G03002	Homo sapiens	Human secreted protein, SEQ ID NO: 7083.		98
09	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	516	1
	M63577	Saccharomyc	SFP1	131	59
10	1/103377	es cerevisiae			<del> </del>
	1000001	Rattus	acetoacetyl-CoA synthetase	467	85
711	AB026291		accidacily i control in a contr		
		norvegicus	protein tyrosine phosphatase (PTP-BAS, type 3)	368	44
712	D21211	Homo sapiens	protein tyrosine phosphatase (* 12 25 25, 97 27	615	83
713	AF044033	Marmota	olfactory receptor		1
		marmota	9FO ID NO. 7642	251	100
714	G03561	Homo sapiens	Human secreted protein, SEQ ID NO: 7642.	1380	100
715	AB033062	Homo sapiens	KIAA1236 protein	80	73
716	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.		99
717	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	835	100
	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	234	
718		Homo sapiens	similar to chicken gamma aminobutyric acid	578	99
719	U47334	TIOINO Sapions	receptor beta4 subunit	l	
	17000500	Home reniere	pentide transporter 3	1096	100
720	AB020598	Homo sapiens	A suppressor of cytokine signalling protein	570	74
721	Y53886	Homo sapiens	designated HSCOP-6.	}	ł
			insulin receptor-related receptor	6787	100
722	J05046	Homo sapiens	insulin receptor-related receptor	111	41
723	AF001958	Ambystoma	electrogenic Na+ bicarbonate cotransporter;	***	
	1	tigrinum	NBC	5253	94
724	AF127084	Mus	semaphorin cytoplasmic domain-associated	3233	1,
		musculus	protein 3A	3114	99
725	X54673	Homo sapiens	GABA transporter		100
726	AF016191	Rattus	potassium channel	370	100
120	Arololyi	norvegicus			
	AB029559	Rattus	BATI	139	35
727	AB029559	norvegicus		l	
	-	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	2186	97
728	Y28503	Homo sapiens	plexin-BI/SEP receptor	729	56
729	AJ011415	Homo sapiens	bK390B3.1 (manic fringe (Drosophila)	142	68
730	Z93096	Homo sapiens			- 1
	1		homolog)  cDNA encoding a human vanilloid receptor	675	99
731	Z10062	Homo sapiens	cDNA encoding a numan variation receptor	1	İ
	\		homologue Vanilrep1.	492	94
732	AF161382	Homo sapiens	HSPC264	3826	99
733	AB029033	Homo sapiens	KIAA1110 protein	592	97
734	AE000493	Escherichia	putative transport protein	392	1 27
,54	1,200,00	coli		12172	99
725	AL033379	Homo sapiens	dJ417O22.2 (novel 7 transmembrane receptor	2173	1 79
735	ورودوس		(rhodonsin family) protein similar to high-	1	
1		ł	affinity lysophosphatidic acid receptor homolog)		<del></del>
<u> </u>	AE122500	Homo sapiens	Cl sisted T lymphocytes-	245	56
736	AF132599	Homo sapiens	1	J	
	1	11		883	99
737	X55019	Homo sapiens		1978	100
738	X91906	Homo sapiens		1444	98
739	AB026116	Homo sapiens	organic anion transporter 4	83	24
740	D00570	Mus	open reading frame (196 AA)	1	-
	1	musculus	- COPPAN	118	40
741	W03626	Homo sapiens		614	100
742	U66059	Homo sapiens	V segment translation product		99
743	AF119815	Homo sapiens	G-protein-coupled receptor	2751	
	X16663	Homo sapiens	haematopoietic lineage cell protein (AA 1-486)	148	93
744		Homo sapiens	- and ad by gene 17	448	95
745	W67838	LOHIO SAPICHS	clone HLTCJ63.		
L				2414	100
746	W57260	Homo sapiens		968	65
747	W21578	Home sapiens	Alzheimer's disease protein encoded by DNA	- 55	
	1		from plasmid pGCS2232.	622	100
748	Y94935	Homo sapiens	Human secreted protein clone yd218_1 protein	022	
, ,,,	1 - 2 - 2 - 2		sequence SEQ ID NO:76.	1214	06
749	AL022238	Homo sapien	d11042K10.5 (novel protein)	314	85
			Human secreted protein, SEQ ID NO: 7970.	391	87

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
IO:	AB025258	Mus	granuphilin-a	773	41
		musculus	. 17003000	900	99
752	Y52386	Homo sapiens	Human transmembrane protein HP02000.	2527	99
753	Y48586	Homo sapiens	Human breast tumour-associated protein 47.	694	100
754	AJ272207	Homo sapiens	putative G protein-coupled receptor 92	979	68
755	M85183	Rattus norvegicus	vasopressin receptor		\
756	AF190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	71
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
	700535	Homo sapiens	AT K-3	439	98
758 759	Z22535 R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	564	97
760	W74902	Homo sapiens	Human secreted protein encoded by gene 175	1217	99
			clone HE8BI92.	223	88
761	G03706	Homo sapiens	Human secreted protein, SEQ ID NO: 7787.	4433	99
762	AB020676	Homo sapiens	KIAA0869 protein	2285	99
763	AK026992	Homo sapiens	unnamed protein product	573	100
764	AF173358	Homo sapiens	glucocorticoid receptor AF-1 coactivator-1	2019	89
765	AF268066	Mus musculus	netrin 4		89
766	Y48585	Homo sapiens	Human breast tumour-associated protein 46.	1169	45
767	AF230378	Mus musculus	interleukin-1 delta	309	
768	AF121975	Mus musculus	odorant receptor S18	268	62
760	AB008515	Homo sapiens	RanBPM	611	57
769 770	Y09945	Rattus	putative integral membrane transport protein	458	50
		norvegicus	AD026	688	99
771 772	AF226731 Y27132	Homo sapiens Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
	<u> </u>		NOV/plexin-A1 protein	1821	98
773	X87832	Homo sapiens		500	41
774	AB025258	Mus musculus	granuphilin-a		
	1 5105101	Homo sapiens	HSPC040 protein	232	93
775	AF125101		Human secreted protein, SEQ ID NO: 6896.	314	95
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	191	68
777	G02493	Homo sapiens	Sequence of pre-human atrial natriuretic peptide.	213	45
778	R03301	Homo sapiens		232	100
779 780	AL357374 AF100346	Homo sapiens Homo sapiens	neuronal voltage gated calcium channel gamma-	1434	89
781	Y19566	Homo sapiens		103	52
	1		Protein.  Human secreted protein encoded by gene 10.	1098	93
782 783	Y36233 AF084464	Homo sapiens Rattus	GTP-binding protein REM2	141	30
784	W49042	norvegicus  Homo sapiens	Human low density lipoprotein binding protein	2693	99
			LBP-3.	1904	91
785	AF238381	Homo sapiens		547	100
786	Y91870	Homo sapiens		1062	94
787	Y71062	Homo sapiens		8684	98
788	AF117754	Homo sapiens	complex component TRAP240		
789	AL049569	Homo sapiens	dJ37C10.3 (novel ATPase)	2848	96
790	AF151848	Homo sapiens	CGI-90 protein	745	96
791	Y08639	Homo sapiens	nuclear orphan receptor ROR-beta	1421	95
	Y41706	Homo sapiens	Human PRO381 protein sequence.	644	99
		Homo sapiens	thyroid hormone receptor-associated protein	1037	100
792 793	AF121228		L complex component i KALYJ		
792 793			complex component TRAP95  Human secreted protein, SEO ID NO: 8153.	124	62
792	G04072 Y69384	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124 119	100

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
ID `	No.	ļ		Score	
NO:	AF258340	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
797	AF159615	Homo sapiens	FGF receptor activating protein 1	461	98
798		Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
799	Y59863	Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
800	W70459	Homo sapiens	renin	1913	93
801	L00073	-	CRI protein.	11963	97
802	P92219	Homo sapiens (human)	•		<u> </u>
803	X15357	Homo sapiens	ANP-A receptor preprotein (AA -32 to 1029)	5199	98
804	W64473	Homo sapiens	Human secreted protein from clone EC172_1.	4018	95
805	AJ243874	Homo sapiens	oligophrenin-4	2067	100
806	G01731	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
807	Z24680	Homo sapiens	gam	1562	83
808	AF171669	Homo sapiens	glycoprotein-associated amino acid transporter LAT2	1364	90
		***	Secreted protein CC198_1.	1154	96
809	W70321	Homo sapiens	Human secreted protein encoded by gene 115	855	99
810	W74843	Homo sapiens	clone HOVBA03.		
011	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
811	AF108831 AF092135	Homo sapiens	PTD014	862	100
812 813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	784	100
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone	358	100
017	C01092	Homo sapiens	Human secreted protein, SEQ ID NO: 5163.	549	100
817	G01082 AF151800	Homo sapiens	CGI-41 protein	1106	95
818		Homo sapiens	low density lipoprotein receptor	3980	100
819	L00352	Homo sapiens	IGF-I receptor	5832	99
820	X04434		Human secreted protein, SEQ ID NO: 7925.	572	100
821	G03844	Homo sapiens	TERA	396	48
822 823	AF212220 Y50125	Homo sapiens Homo sapiens	Human glycophosphatidylinositol-anchored	4897	99
823	130.23	1	protein GPI-122.	2676	98
824	AF156778	Home sapiens	ASB-3 protein	2675	100
825	AF096322	Homo sapiens	neuronal voltage-gated calcium channel gamma- 2 subunit	1105	100
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded from gene 28.	1540	100
827	AB032013	Homo sapiens	potassium channel Kv8.1	2435	95
828	Y13620	Homo sapiens	BCL9	5284	96
829	Y91474	Homo sapiens	Human secreted protein sequence encoded by gene 24 SEQ ID NO:147.	541	98
000	V64000	Homo sapiens	glypican	1625	87
830	X54232	Homo sapiens	071	2540	100
831	X14830	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1002	100
832	Y71262	Homo sapiens	020 ID NO. 7064	638	96
833	G03873	Homo sapiens		1389	93
834	AC003030	Homo sapiens		964	87
835	Y38422			85	36
836	U41557	Caenorhabditi s elegans		998	75
837	AL121889	Homo sapiens	AL023803))	1580	60
838	AJ011415	Homo sapiens		1105	67
839	W80398	Homo sapiens		255	92
840	G00862	Homo sapiens		644	97
841	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.		99
842	AF036717	Homo sapiens	FGFR signalling adaptor SNT-1	2629	100
843	Y73446	Homo sapiens	Human secreted protein clone yc27_1 protein sequence SEO ID NO.114.	1089	
844	G02872	Homo sapiens		357	69
CAA	AF151810	Homo sapiens		1443	88
215					
845 846	X83378	Homo sapiens		1620 655	99

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	L	<del>                                     </del>	A F020040 (DVD) - 2927207)	JUJE	+
			to AF038969 (PID:g2827207)	160	76
348	X99886	Homo sapiens	monocyte chemotactic protein-2	963	98
349	AC005587	Homo sapiens	similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)		
350	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
351	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
852	Y86217	Homo sapiens	Human secreted protein HWHGU54, SEQ ID NO:132.	1189	99
853	AF224741	Homo sapiens	chloride channel protein 7	3748	99
854	X17094	Homo sapiens	furin (AA 1-794)	3550	99
855	W78245	Homo sapiens	Fragment of human secreted protein encoded by gene 19.	1245	99
856	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	1926	100
857	Y41765	Homo sapiens	Human PRO1083 protein sequence.	3211	99
858	AF057306	Homo sapiens	transmembrane proteolipid	481	84
859	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone HLDRM43.	824	100
862	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived protein #375.	96	30
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	211	67
866	X54870	Homo sapiens	Type II integral membrane protein	1201	100
867	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
868	Y07894	Homo sapiens	Human secreted protein fragment encoded from gene 43.	388	88
869	J00123	Homo sapiens	preproenkephalin (	1349	95
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:305.	1048	98
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	237	93
872	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	960	94
873	AF161382	Homo sapiens	HSPC264	1124	99
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573	96
876	M15530	Homo sapiens	B-cell growth factor	171	56
877	W63681	Homo sapiens	Human secreted protein 1.	1652	99
878	L27867	Rattus norvegicus	neurexophilin	1448	
879	Y10835	Homo sapiens	Amino acid sequence of a human secreted protein.	321	100
880	W88991	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
881	AF118670	Homo sapiens	orphan G protein-coupled receptor	1971	100
882	AF208865	Homo sapiens	EDRF	528	100
883	Y18462	Homo sapiens	cathepsin L	209	72
884	Y94950	Homo sapiens	Human secreted protein clone dh1073_12 protein sequence SEQ ID NO:106.	348	100
885	AF070661	Homo sapiens	HSPC005	404	100
886	Y04315	Homo sapiens	Human secreted protein encoded by gene 23.	385	100
887	X92744	Homo sapiens	hBD-1	375	100
888	Y22496	Homo sapiens	Human secreted protein sequence clone cn621_8.	994	94
889	Y41293	Homo sapiens	Human soluble protein ZTMPO-1.	4595	99
890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	63
891	AF208856	Homo sapiens	BM-014	1012	99
892	U29195	Homo sapiens	neuronal pentraxin II	2002	98
893	X68149	Homo sapiens	Burkitt lymphoma receptor 1	1953	100
894	Y94914	Homo sapiens	Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	537	100
895	W61630	Homo sapiens	Clone HNFGW06 of EGFR receptor family.	326	63
896	M24110	Homo sapiens	GOS19-2 peptide precursor	481	100
897	Z68747	Homo sapiens	imogen 38	2018	99
898	AF186112	Homo sapiens	neurokinin B-like protein ZNEUROK1	619	100
J / U	AF225420	Homo sapiens	AD025	734	100

CTO.	Accession	Species	Description	Smith-	%
SEQ ID	No.	<b>Бресте</b>	2.55.7.	Waterman Score	Identity
NO:			Sequence of human lipocortin.	1835	100
900	P60657	Homo sapiens	oncostatin M	1297	99
901	M27288	Homo sapiens Homo sapiens	Polypeptide with transmembrane domain.	749	100
902	W85737	·	Human secreted protein, SEQ ID NO: 5430.	650	99
903	G01349	Homo sapiens	Human secreted protein encoded by gene 4.	1133	99
904	Y00261	Homo sapiens	antigen NY-CO-3	771	99
905	AF039688	Homo sapiens		2544	100
906	AB007836	Homo sapiens	Hic-5	224	100
907	AB017507	Homo sapiens	Apg 12	1537	98
908	AK000056	Homo sapiens	unnamed protein product Human secreted protein HFOXB55, SEQ ID	427	100
909	Y86299	Homo sapiens	NO:214.		100
910	AF231023	Homo sapiens	protocadherin Flamingo 1	7393	99
911	Y14134	Homo sapiens	Vascular endothelial cell growth inhibitor beta	1319	100
			protein sequence.	1950	100
912	Z90420	Homo sapiens	Human GDF-3 (hGDF-3) polypeptide encoding cDNA.		
913	Y19757	Homo sapiens	SEO ID NO 475 from WO9922243.	1361	100
914	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	48
915	U14971	Homo sapiens	ribosomal protein S9	886	90
916	AF172854	Homo sapiens	cardiotrophin-like cytokine CLC	1204	99
917	AC005525	Homo sapiens	F22162_1	1963	100
918	AF166350	Homo sapiens	ST7 protein	4711	99
919	Y87285	Homo sapiens	Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.	430	100
920	Y36131	Homo sapiens	Human secreted protein #3.	465	88
920	AF193766	Homo sapiens	cytokine-like protein C17	724	100
921	Y95013	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.	357	100
923	X75208	Homo sapiens	protein tyrosine kinase-receptor	5256	100
923	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	813	98
925	AB039886	Homo sapiens	down-regulated in gastric cancer	785	78
926	G03368	Homo sapiens	Human secreted protein, SEQ ID NO: 7449.	55	50
927	Y48606	Homo sapiens	Human breast tumour-associated protein 67.	539	100
928	Y36151	Homo sapiens	Human secreted protein #23.	668	100
929	AF110399	Homo sapiens	elongation factor Ts	1666	100
930	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2763	99
931	Y73328	Homo sapiens	HTRM clone 082843 protein sequence.	931	100
932	G01959	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
933	U47924	Homo sapiens	B-cell receptor associated protein	1469	100
934	G03827	Homo sapiens	Human secreted protein, SEQ ID NO: 7908.	529	93
935	AB039371	Homo sapiens	mitochondrial ABC transporter 3	196	63
936	X56385	Canis	rab8	1064	100
930	ASOSOS	familiaris		<u> </u>	1
937	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	117	44
938	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	1064	99
939	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	515	42
940	Y16630	Homo sapiens	Human Putative Adrenomedullin Receptor	1904	99
941	AC005102	Homo sapiens	(PAR). small inducible cytokine subfamily A member	627	99
	<u> </u>		24	1289	81
942	M12886	Homo sapiens	T-cell receptor beta chain	1049	98
943	AF226046	Homo sapiens	· · · · · · · · · · · · · · · · · · ·	667	100
944	Y36078	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 463.	L	
945	M22877	Homo sapiens	cytochrome c	565	93
	W67869	Homo sapiens	clone HHGDB72.	551	
946			1		1 100
	W67859	Homo sapiens	Human secreted protein encoded by gene 53	283	100
946 947	W67859		clone HBMCL41.	789	100
946		Homo sapiens Homo sapiens	clone HBMCL41.  Novel protein (Clone BG33_7).	<u> </u>	

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			and the sales	1314	100
51	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog	402	70
52	Y36111	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 496.		
	10010100	Homo sapiens	APC10	990	100
53	AB012109	Homo sapiens	transmembrane protein BRJ	1405	100
54	AF246221		putative transmembrane GTPase	1883	100
55	AF054986	Homo sapiens	Human secreted protein fg949_3.	1879	100
56	W74726	Homo sapiens	Human viral receptor protein (ACVRP).	1581	100
57	Y27096	Homo sapiens	Human viral receptor protest (110 114)	1920	100
58	AJ222967	Homo sapiens	cystinosin 4000 3 protein	587	100
59	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	283	100
960	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	1214	96
	AF151855	Homo sapiens	CGI-97 protein	250	65
961 962	U26592	Homo sapiens	diabetes mellitus type I autoantigen	1	100
		Homo sapiens	dJ475B7.2 (novel protein)	3796	
963	AL050306	Homo sapiens	PTD004	2089	100
964 965	AF078859 AB020315	Homo sapiens	homologue of mouse dkk-1 gene:Acc# AF030433	1466	100
		<u></u>	precursor polypeptide (AA -22 to 1185)	6580	99
966	X04571	Homo sapiens	hepatocellular carcinoma antigen gene 520	993	99
967	AF146019	Homo sapiens	minK-related peptide 1; MiRP1	632	100
968	AF071002	Homo sapiens	minK-related peptide 1, Mikt 1 membrane-type-5 matrix metalloproteinase	3545	100
969	AB021227	Homo sapiens	membrane-type-5 matrix metanoprotestase	1579	100
970	AF180920	Homo sapiens	cyclin L ania-6a	5621	99
971	AF105365	Homo sapiens	K-Cl cotransporter KCC4	739	100
972	AF083248	Homo sapiens	ribosomal protein L26 homolog	6295	100
973	AJ132429	Homo sapiens	hyperpolarization-activated cyclic nucleotide gated cation channel hHCN4		100
074	W61619	Homo sapiens	Clone HTPFF86 of TM4SF superfamily.	454	100
974	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	99
975	AF133100 AF275948	Homo sapiens	ABCA1	11763	100
976		Homo sapiens	cystine/glutamate transporter	2552	
977 978	AB026891 AF117657	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP80	3348	99
979	AF044201	Rattus	neural membrane protein 35; NMP35	1570	92
		norvegicus	neuroendocrine-specific protein-like protein 1	1170	99
980	AF119297	Homo sapiens	potassium channel modulatory factor	1983	99
981	AF155652	Homo sapiens	Human stomach carcinoma clone HP10412-	1553	99
982	W88499	Homo sapiens	encoded protein.	2012	98
983	7.56281	Homo sapiens	interferon regulatory factor 3	2160	100
984	AB026125	Homo sapiens	ART-4	172	$-\frac{700}{70}$
985	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.		
	AB023888	Homo sapiens	b-chemokine receptor CCR4	1895	100
986		Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
987 988	W27291 AF153450	Manduca	juvenile hormone esterase binding protein	226	32
	<del> </del>	sexta	Human secreted protein, SEQ ID NO: 7778.	194	88
989 990	G03697 AF204159	Homo sapiens Homo sapiens	-tto-se colours-activated	1486	100
1				558	99
991 992	G02061 AL031266	Homo sapiens Caenorhabditi		327	40
332	1,00,1200	s elegans		4730	99
993	Y66749	Homo sapiens	Membrane-bound protein PRO1124.		77
993	G01246	Homo sapiens		141	99
	AF133845	Homo sapiens	corin	5811	
995 996	AF133843 AF117756	Homo sapiens		4999	100
		<b></b>	<del></del>	284	93
997	W62066	Homo sapiens	t in anguing SE() II)	725	100
998	Y87173	Homo sapiens	NO:212.	1654	99
999	Y13379	Homo sapiens	Amino acid sequence of protein PRO263.		47
	Y95008	Homo sapiens	Human secreted protein VI3_1, SEQ ID NO.30.	1747	100
1000		Homo sapiens			

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			GEO FD VIO. 5215	398	96
1002	G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	2150	100
1003	W73420	Homo sapiens	Human secreted protein encoded by Gene No. 24.		100
1004	X12791	Homo sapiens	19kD SRP-protein (AA 1 - 144)	742	
1005	M23323	Homo sapiens	membrane protein	642	100
1006	X63745	Homo sapiens	KDEL receptor	326	98
	Y35997	Homo sapiens	Extended human secreted protein sequence, SEQ	824	99
1007			ID NO. 382. dopamine receptor D4	92	35
1008	AB032918	Hylobates moloch		1372	99
1009	Y91680	Homo sapiens	Human secreted protein sequence encoded by gene 81 SEQ ID NO:353.		98
1010	AL136125	Homo sapiens	dJ304B14.1 (novel protein)	825	
1011	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	379	98
1012	Y17531	Homo sapiens	Human secreted protein clone BL205 14 protein.	818	97
	G00724	Homo sapiens	Human secreted protein, SEQ ID NO: 4805.	462	100
1013 1014	AF288092	Naegleria Naegleria	haem lyase	114	37
	j	gruberi		20/7	99
1015	AB045292	Homo sapiens	M83 protein	3867	100
1016	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	644	
1017	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
1018	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	589	100
1019	X83425	Homo sapiens	Lutheran blood group glycoprotein	3054	99
	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	100
1020	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1021 1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.	768	100
			hADV36S1	573	100
1023	AE000660	Homo sapiens	CGI-31 protein	1550	100
1024	AF132965	Home sapiens	Human TR-interacting protein \$103a.	1466	97
1025 1026	W92380 R66278	Homo sapiens Homo sapiens	Therapeutic polypeptide from glioblastoma cell	830	100
	<u> </u>		line. S100P calcium-binding protein	476	100
1027	X65614	Homo sapiens	Human PRO704 protein sequence.	1323	100
1028	Y41741	Homo sapiens		806	100
1029	AJ001014	Homo sapiens	RAMP1	1354	99
1030	W63682	Homo sapiens	Human secreted protein 2.	766	100
1031	AK023007	Homo sapiens	unnamed protein product	2672	99
1032	W97900	Homo sapiens	Human SR-BI class B scavenger.	639	99
1033	Y82453	Homo sapiens	Human TGC-440 secretory protein SEQ ID NO:1.		
1034	Y73473	Homo sapiens	Human secreted protein clone yd178_1 protein sequence SEQ ID NO:168.	752	93
1035	Y86468	Homo sapiens	Human gene 48-encoded protein fragment, SEQ	96	90
1026	U09813	Homo sapiens	mitochondrial ATP synthase subunit 9 precursor	698	100
1036	AJ242832	Homo sapiens	calpain	3699	99
1037		Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
1038	X66403		polyhomeotic 2	1310	100
1039 1040 -	AJ242730 AF169968	Homo sapiens Mus	DNA binding protein DESRT	1453	80
10-10	76 107700	musculus		1	<del></del>
1041	X52563	Bos taurus	permability increasing protein	383	29
	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	75	50
1042		Homo sapiens	: CEO (D.)(O. ((1))	60	53
1043	G02532	Homo sapiens		1850	100
1044 1045	M94582 AL080239	Homo sapiens	TOPAT C / I like	1704	50
			subunit))	1	100
1046	AF125101	Homo sapiens	HSPC040 protein	580	100
	W74809	Homo sapiens	1 11 01	176	100
1046 1047		i			
1047				2201	100
	AL022238	Homo sapiens Homo sapiens	dJ1042K10.4 (novel protein)	1559	99

	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	W78324	Homo sapiens	Fragment of human secreted protein encoded by	1318	98
1052	Y21851	Homo sapiens	gene 81.  Human signal peptide-contianing protein (SIGP)	1643	95
	AL163815	Arabidopsis	(clone ID 2328134). putative protein	661	62
1053		thaliana	Human secreted protein encoded by gene 77.	262	100
1054	Y76200	Homo sapiens	TC10-like Rho GTPase	1160	100
1055	AJ276567	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
1056	Y27620	Homo sapiens	ribosomal protein	745	100
1057	D14530	Homo sapiens		1132	100
1058 1059	AF132000 AL031778	Homo sapiens Homo sapiens	TADA1 protein dJ34B21.1 (novel BZRP (benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)	920	100
			Isoquinoline-olliding protein) Elect protein	134	33
1060	AF227135	Homo sapiens	candidate taste receptor T2R9  Human secreted protein encoded by gene No. 9.	1392	100
1061	Y27575	Homo sapiens		1088	100
1062	Z11697	Homo sapiens	HB15 putative transmembrane protein	819	100
1063	AF123757	Homo sapiens	novel retinal pigment epithelial cell protein	2932	99
1064	AF155135	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
1065	Y41674	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	2575	100
1066	AJ250042	Homo sapiens	Extended human secreted protein sequence, SEQ	770	85
1067	Y36087	Homo sapiens	ID NO. 472.  Human secreted protein clone mc300_1 protein	301	100
1068	Y94959	Homo sapiens	sequence SEQ ID NO:124.  Human secreted protein clone mc300_1 protein	301	100
1069	Y94959	Homo sapiens	sequence SEQ ID NO:124.  Human leukocyte cell clone HP00804 protein.	2014	99
1070	W64535	Homo sapiens	Human leukocyte celi cione in 00804 protein.	148	50
1071	X03145	Homo sapiens	pot. ORF III dJ889M15.3 (novel protein)	821	91
1072	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	249	62
1073	X82200	Homo sapiens	gpStaf50 Human secreted protein, SEQ ID NO: 7294.	99	47
1074	G03213	Homo sapiens	Human secreted protein encoded by gene 10.	506	55
1075	Y36233	Homo sapiens	Human secreted protein, SEQ ID NO: 7268.	424	98
1076	G03187	Homo sapiens	ribosomal protein L10	332	76
1077 1078	L25899 Y91447	Homo sapiens Homo sapiens	Human secreted protein sequence encoded by	898	97
			gene 48 SEQ ID NO:168.  Human secreted protein, SEQ ID NO: 5943.	290	89
1079	G01862	Homo sapiens	WNT receptor frizzled-3	1376	92
1080	AB039723	Homo sapiens	Na/PO4 cotransporter homolog	269	100
1081	AB020527	Homo sapiens	ribosmal protein small subunit	499	80
1082 1083	L13802 W75098	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 42	143	81
		<del>                                     </del>	clone HSXB125.  Human secreted protein, SEQ ID NO: 7645.	83	51
1084	G03564	Homo sapiens	CEO ID NO. 9144	88	43
1085	G04063	Homo sapiens		124	64
1086	AF090942	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	129	41
1087	G00517	Homo sapiens Homo sapiens		126	36
1088	G04091	Homo sapiens	G-protein coupled receptor 14	364	82
1089	AF140631	Homo sapiens		114	32
1090	G04063	Mus sp.	LMW G-protein	146 .	83
1091 1092	S72304 W88708	Homo sapiens		405	100
1003	1006612	Homo sapiens	Secreted protein clone fh123 5.	4358	97
1093 1094	W85612 Y53012	Homo sapiens	Human secreted protein clone pm514_4 protein	1013	99
1095	Y92345	Homo sapiens	i i i i i i i i i i i i i i i i i i i	409	100
				147	60
1096	AF090942	Homo sapiens		166	58
1097	L24521	Homo sapiens		490	70
1098	X56932	Homo sapiens		83	35
1099	G04063 Y02693	Homo sapiens Homo sapiens	1	149	59

SEQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			2001422	183	72
101	AF119851	Homo sapiens	PRO1722	207	62
102	G04086	Homo sapiens	Human secreted protein, SEQ ID NO: 8167.	91	52
103	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	128	69
104	X74856	Mus musculus	ribosomal protein L28		62
105	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	130	
106	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	48
107	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	69	43
108	AF039942	Homo sapiens	HCF-hinding transcription factor Zhangfei	744	99
109	AF201951	Homo sapiens	high affinity immunoglobulin epsilon receptor	738	94
110	AF111108	Mus musculus	transient receptor potential 2	223	79
			PRO2822	144	59
111	AF119900	Homo sapiens	A protein that interacts with presenilins.	265	39
112	Y16589	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	178	67
113	G02872	Homo sapiens	Fragment of human secreted protein encoded by	164	63
114	Y02999	Homo sapiens	gene 121.	1217	99
115	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	130	40
116	X51394	Xenopus laevis	APEG precursor protein	442	65
117	M27826	Homo sapiens	neutral protease large subunit	72	60
118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	491	97
119	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	244	197
120	Y35906	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 155.		65
121	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	90
122	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	110	
123	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1124	AF212862	Homo sapiens	membrane interacting protein of RGS16	442	88
1125	W64469	Homo sapiens	Human secreted protein from clone CW795_2.	191	53
1126	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	154	100
1127	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
1127	Y84320	Homo sapiens	Human cardiovascular system associated protein	815	99
1100	G02105	Homo sapiens	Human secreted protein, SEQ ID NO: 6186.	88	73
1129 1130	Y32923	Homo sapiens	Transmembrane domain containing protein clone HP01512.	700	100
	3/00017	Homo sapiens	Human synanse related glycoprotein 2.	260	91
1131 1132	Y29817 Y91644	Homo sapiens	Human secreted protein sequence encoded by	525	96
1133	Y91449	Homo sapiens		542	100
	1 101000	Homo sapiens	4F2 light chain	2399	93
1134	AB017908	Homo sapiens		312	55
1135 1136	X51760 Y99426	Homo sapiens		917	72
1125	002700	Homo sapiens		102	50
1137	G03790		NY-REN-36 antigen	768	91
1138 1139	AF155106 AL031055	Homo sapiens Homo sapiens		117	50
	1.501.255	Des tours	regulator of G-protein signaling 7	138	96
1140 1141	AF011359 Y70018	Bos taurus Homo sapiens	The state of the s	623	100
	<del> </del>	172-1	OFO ID NO. 8172	113	38
1142 1143	G04091 AB030235	Homo sapiens Canis	D4 dopamine receptor	89	48
1144	Y94922	familiaris Homo sapiens	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	539	88
				398	96
1145	X99962	Homo sapiens		168	79
1146	G03807	Homo sapiens	CEO ID NO. 7703	512	85
1147	G03712	Homo sapiens		705	76
1148	Y28279	Homo sapiens		247	36
1149	U13642	Caenorhabditi	exon 3 similar to transmembrane domain of 3.		

~ \	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:	į				
			cerevisiae zinc resistance protein	117	62
150	G03438		Human secreted protein, SEQ ID NO: 7519.	181.	80
151	G01003	Homo sapiens	Human secreted protein, SEQ ID NO: 5084.	198	63
1152	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	95	41
153	X88799	Oryza sativa	DNA binding protein	155	96
154	D85245	Homo sapiens	TR3beta	341	87
1155	R74272	Homo sapiens	Tumour suppressor protein, p53.	99	41
1156	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID		
	G02577	Homo sapiens	Human secreted protein, SEQ ID NO: 6658.	263	98
1157	AF104334	Homo sapiens	putative organic anion transporter	185	42
1158	G01393	Homo sapiens	Human secreted protein, SEQ ID NO: 54/4.	173	57
1159		Homo sapiens	Human GTP binding protein APD08.	224	81
1160	W75771	Homo sapiens	M ARC2 protein	410	83
1161	AF216833	Homo sapiens	Human secreted protein encoded by gene 10	1156	100
1162	W67816		clone HCEMU42.	230	70
1163	AF119851	Homo sapiens	PRO1722	113	31
1164	Y87252	Homo sapiens	Human signal peptide containing protein HSPP- 29 SEQ ID NO:29.		92
1175	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	82 64
1165	AF269286	Homo sapiens	IIC6	134	
1166	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	149	51
1168	D90789	Escherichia	Dipeptide transport system permease protein	411	90
	ľ	coli	DppC.	344	90
1169	R63783	Homo sapiens	TG0847 protein.	478	98
1170	Y45274	Homo sapiens	Human secreted protein encoded from gene 18.	347	96
1171	D64154	Homo sapiens	Mr 110,000 antigen	311	67
1172	AB026256	Homo sapiens	organic anion transporter OATP-B	60	52
1173	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438. similar to human GTPase-activating	178	59
1174	D87717	Homo sapiens	protein(A49869)		
	M64716	Homo sapiens	ribosomal protein	391	78 67
1175		Homo sapiens		285	
1176	R08330	Homo sapiens		242	72
1177	L06505	Homo sapiens	organic cation transporter (OCT2)	276	88
1178	AJ251885	Homo sapiens	Human secreted protein, SEO ID NO: 7339.	155	71
1179	G03258	<del></del>	CEO ID NO: 5288	282	90
1180	G01207	Homo sapiens Rattus	tRNA selenocysteine associated protein	249	62
1181	AF181856	norvegicus	IRC 11 Selection y Const		
		Homo sapiens	HSPC176	138	90
1182	AF161524	Homo sapiens	Human secreted protein, SEO ID NO: 7870.	282	66
1183 1184	G03789 Y02671	Homo sapiens		107	71
1_				88	69
1185	G03797	Homo sapiens		118	46
1186	G03564	Homo sapiens	dopamine receptor D4	96	37
1187	AB032905	Hylobates			
L	<u> </u>	concolor	Human secreted protein, SEQ ID NO: 5037.	292	78
1188	G00956	Homo sapiens	CEO ID NO 1349	178	79
1189	G03258	Homo sapiens		324	76
1190 1191	G03361 AF117755	Homo sapiens Homo sapiens	thyroid hormone receptor-associated protein	187	70
		Homo sapiens	complex component TRAP230	202	67
1192	Y70455	1	5).	99	42
1193	G03052	Homo sapien		192	76
1194	G02607	Homo sapien	OTCAS Select secreted profess	2001	98
1195	W29661	Homo sapien	E Homo sapiens C1542 2 clone secreted protein.	239	69
1196	Y14104	Homo sapien	s Human GABAB receptor 1d protein sequence.	149	90
1197	X61972	Homo sapien	s I macronain subunit inta	145	51
1198	G00534	Homo sapien	E. Liuman secreted protein, SEO ID NO. 4013.	1089	89
1199		Homo sapien	S Human secreted protein HELHN47, SEQ ID		
1	G02607	Homo sapien	1	154	57

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
D	No.		1_	Score	<u> </u>
10:		¥\$	Human secreted protein, SEQ ID NO: 4919.	404	50
201	G00838	Homo sapiens	neutral protease large subunit	202	49
202 203	M27826 Y73424	Homo sapiens Homo sapiens	Human secreted protein clone yi4_1 protein sequence SEQ ID NO:70.	265	61
204	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein	625	98
			M160 precursor Human secreted protein #75.	219	59
205	Y36203	Homo sapiens		205	57
206	U78111	Gallus gallus	AQ putative G protein-coupled receptor	416	76
207	AF095448	Homo sapiens	putative G protein-coupled receptor	127	75
208	AF116715	Homo sapiens	PRO2829	475	95
209	AF099137	Homo sapiens	MaxiK channel beta 2 subunit	423	79
210	AF205718	Homo sapiens	hepatocellular carcinoma-related putative tumor suppressor	224	70
1211	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	117	44
1212	G00719	Homo sapiens	Human secreted protein, SEQ ID NO: 4800.	351	73
1213	G01009	Homo sapiens	Human secreted protein, SEQ ID NO: 5090.	124	70
1214	AF090942	Homo sapiens	PRO0657		77
1215	Y14427	Homo sapiens	Human secreted protein encoded by gene 17	99	'
216	G03905	Homo sapiens	Human secreted protein, SEQ ID NO: 7986.	173	57
	Y57897	Homo sapiens	Human transmembrane protein HTMPN-21.	1173	100
1217	J00194	Homo sapiens	hla-dr antigen alpha chain	454	78
1218	Y59709	Homo sapiens	Secreted protein 76-28-3-A12-FL1.	470	92
1219 1220	W81576	Homo sapiens	EBV-induced G-protein coupled receptor (EBI-	725	100
1221	W96745	Homo sapiens	High affinity immunoglobulin E receptor-like	650	98
1222	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	135	31
1223	Y00278	Homo sapiens	Human secreted protein encoded by gene 21.	260	95
	AF161422	Homo sapiens	HSPC304	568	90
1224	U14970	Homo sapiens	ribosomal protein \$5	202	95
1225	G01733	Homo sapiens	Human secreted protein, SEQ ID NO: 5814.	610	100
1226	AF099973	Mus musculus	schlafen2	333	56
1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	155	81
1229	AF217188	Mus musculus	YIP1B	801	63
1020	AF176813	Homo sapiens	soluble adenylyl cyclase	275	100
1230		Homo sapiens	organic cation transporter	1704	100
1231 1232	X98333 W74955	Homo sapiens	Human secreted protein encoded by gene 77	212	53
1233	Y94940	Homo sapiens		526	100
1234	U76618	Mus musculus	N-RAP	482	82
-1005	AF044034	Homo sapiens	hook2 protein	380	97
1235	AF044924	Homo sapiens	CEO ID NO. 5540	417	100
1236	G01459	Homo sapiens	adapter protein	164	84
1237 1238	AF000018 W88633	Homo sapiens	did by some 100 slone	250	90
	11122442	110-0 00-10-0		697	98
1239	W29660	Homo sapiens	peroxisomal Ca-dependent solute carrier	154	52
1240	AF004161	Oryctolagus cuniculus	7-24	709	97
1241	Y92710	Homo sapiens			88
1242 1243	Y95002 Y44905	Homo sapiens	Human potassium channel molecule ERG-LP2	325	100
			partial protein.	511	97
1244 1245	AF284422 Y53629	Homo sapiens Homo sapiens	A bone marrow secreted protein designated	1888	93
	1	<u> </u>	BMS115.	389	97
1246	AB039371	Homo sapiens	mitochondrial ABC transporter 3 Extended human secreted protein sequence, SEQ		39
1247	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	1.00	

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			ID NO. 160.		
248	AF072509	Rattus	glutamate receptor interacting protein 2	559	90
	15045040	norvegicus	tandem pore domain potassium channel TRAAK	661	98
249	AF247042	Homo sapiens Homo sapiens	Human secreted protein sequence encoded by	1087	97
250	B08974	Homo sapiens	gene 27 SEQ ID NO:131.	i	L
1251	L15313	Caenorhabditi	putative	858	59
1252	Y29338	s elegans Homo sapiens	Human secreted protein clone it217_2 alternate	278	75
			reading frame protein.	211	92
1253	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	294	83
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 7155.	253	91
1255	G01818	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	222	54
1256	AF286368	Homo sapiens	eppin-1	87	93
1257	AF220264	Homo sapiens	MOST-1	281	78
1258	G02227	Homo sapiens	Hurnan secreted protein, SEQ ID NO: 6308.	81	94
1259	Y07970	Homo sapiens	Human secreted protein fragment #2 encoded from gene 26.		
1260	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	986	100
10/1	AF140674	Homo sapiens	zinc metalloprotease ADAMTS6	172	36
1261	U28369	Homo sapiens	semaphorin V	237	67
1262 1263	Y07049	Homo sapiens	Renal cancer associated antigen precursor sequence.	288	71
		1	Human secreted protein #25.	187	80
1264 1265	Y36153 Y78114	Homo sapiens Homo sapiens	Human cytokine signal regulator CKSR-2 SEQ	723	93
	<u> </u>	<u> </u>	ID NO:2.  Amino acid sequence of protein PRO334.	191	100
1266	Y13397	Homo sapiens	phosphatidylinositol 5-phosphate 4-kinase	859	95
1267	AF030558	Rattus	gamma		
		norvegicus	candidate tumor suppressor gene LUCA-1	159	96
1268	U73167	Homo sapiens	LMBR2	552	76
1269	AF190664	Mus	LMBR2		1
		musculus	dJ570F3.1 (homolog of the rat synaptic ras	820	98
1270	AL050332	Homo sapiens	GTPage-activating protein p135 SynGAP)	]	
	1 000100	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	131	95
1271	G02126	Homo sapiens	NADH-cytochrome b5 reductase isoform	253	92
1272 1273	AF125533 AL035661	Homo sapiens	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthethase (acetate-coA ligase))	1280	100
1274	AF064748	Mus	S3-12	3523	61
		musculus		377	78
1275	D17554	Homo sapiens	TAXREB107	643	90
1276	Y30715	Homo sapiens	protein.		
1277	AF146760	Homo sapiens	septin 2-like cell division control protein	707	100
1278	Y05069	Homo sapiens	Human PIGR-2 protein sequence.	281	46
1279	X59668	Oryctolagus cuniculus	aorta CNG channel (rACNG)	267	85
1280	G01051	Homo sapiens	Human secreted protein, SEQ ID NO: 5132.	489	98
1280	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	120	43
1282	AF055084	Homo sapiens	very large G-protein coupled receptor-1	1635	100
1282	AF117814	Mus musculus	odd-skipped related 1 protein	357	98
1284	U87318	Xenopus	NaDC-2	535	60
1285	AF061346	Mus Mus	Edp1 protein	452	68
1286	AB030182	musculus Mus	contains transmembrane (TM) region	582	68
1.230		musculus		+,,,-	07
1287	A13595	synthetic construct	immunosuppresive protein PP15	185	97
1288	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1	837	100
1289	AF084205	Rattus	serine/threonine protein kinase TAO1	319	98
				1	

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			membrane associated guanylate kinase 2	523	100
290	AF038563	Homo sapiens Homo sapiens	double-stranded RNA specific adenosine	468	100
291	AF034837	Homo sapiens	deaminase		ļ
292	M15888	Bos taurus	endozenine-related protein precursor	937	87 45
293	AB010692	Arabidopsis	ATP-dependent RNA helicase-like protein	636	45
293	AD010072	thaliana	_1	1570	100
294	AF209923	Homo sapiens	orphan G-protein coupled receptor	504	98
295	W67828	Homo sapiens	Human secreted protein encoded by gene 22	JU <del>1</del>	1
			clone HFEAF41. similar to 45 kDa secretory protein; similar to	648	65
296	AC004832	Homo sapiens	CAA10644 1 (PID):g4164418)	575	70
297	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	223	97
298	G02645	Homo sapiens	Human secreted protein, SEQ ID NO: 6726.	122	32
299	Y59440	Homo sapiens	Human delta3 fragment #4.	459	81
300	W70504	Homo sapiens	Leukocyte seven times membrane-penetrating type receptor protein JEG18.	3916	99
301	Y67315	Homo sapiens	Human secreted protein BL89_13 amino acid sequence.		96
302	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	174 254	69
303	G01331	Homo sapiens	Human secreted protein, SEO ID NO: 5412.	747	99
304	G01491	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	602	98
305	AF148509	Homo sapiens	alpha 1,2-mannosidase	333	98
306	G01658	Homo sapiens	Human secreted protein, SEQ ID NO: 5739.  D1-like dopamine receptor activity modifying	332	98
1307	Y90899	Homo sapiens	protein SEO ID NO:1.	348	52
1308	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	147	66
1309	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	296	90
1310	AF063243	Bos taurus	ribosomal protein L30 arsenite inducible RNA associated protein	688	70
1311	AF224494	Mus musculus	_		100
1312	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	1154	78
1313	Y99419	Homo sapiens	Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.	1145	97
1314	AF116667	Homo sapiens	PP 01777	807	97
1315	W75100	Homo sapiens	Human secreted protein encoded by gene 44 clone HE8CJ26.	789	100
1316	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	2607	98
1317	AB041533	Homo sapiens	sperm antigen	806	92
1318	U19617	Mus musculus	Elf-1	768	100
1319	U82598	Escherichia coli	ferric enterobactin transport protein		
1320	D90892	Escherichia coli	SORBITOL-6-PHOSPHATE 2- DEHYDROGENASE (EC 1.1.1.140) (GLUCITOL-6- PHOSPHATE DEHYDROGENASE) (KETOSEPHOSPHATE REDUCTASE)	709	100
1321	W67847	Homo sapiens	Human secreted protein encoded by gene 41 clone HPBCJ74.	601	92
1322	AJ276101	Homo sapiens	GPRC5B protein	466	93
1323	AJ276101	Homo sapiens	GPRC5B protein	504	100
1324	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1584	89
1325	U91561	Rattus norvegicus	pyridoxine 5'-phosphate oxidase		100
1326	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1606	90
1327	Y32206	Homo sapiens	1 - 1 - (DEC) encoded by	1531	
1220	AF151048	Homo sapiens		657	85
1328 1329	Y10530	Homo sapiens	olfactory receptor	1645	100
1329	AF180681	Homo sapiens	guanine nucleotide exchange factor	4314	99
1331	AF111856	Homo sapiens	sodium dependent phosphate transporter isoform NaPi-3b	1	99
1332	Y13583	Homo sapiens		2171	100
111/	1 112202	Homo sapiens		1395	100

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
ID `	No.			Score	lachary
NO:		<u> </u>	Human secreted protein encoded from gene 45.	1380	96
1334	Y25755	Homo sapiens	Human secreted protein encoded now gone	4742	99
1335	AF152325	Homo sapiens	protocadherin gamma A5	639	81
1336	X74070	Homo sapiens	transcription factor BTF3	1931	95
1337	AF095927	Rattus	protein phosphatase 2C	1,75.	1
	1	norvegicus	9FO ID NO. 7058	621	100
1338	G03877	Homo sapiens	Human secreted protein, SEQ ID NO: 7958.	626	100
1339	AL008582	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	5820	99
1340	X61615	Homo sapiens	leukemia inhibitory factor receptor	7528	97
1341	Y01519	Homo sapiens	A carcinogenesis-inhibiting protein.	2372	100
1342	AF207600	Homo sapiens	ethanolamine kinase		97
1343	U54807	Rattus	GTP-binding protein	1167	37
		norvegicus		1 2222	51
1344	AC020579	Arabidopsis	putative phosphoribosylformylglycinamidine	3283	31
	}	thaliana	synthase; 25509-29950	944	100
1345	Y28576	Homo sapiens	Secreted peptide clone pe503_1.	1171	100
1346	W74787	Homo sapiens	Human secreted protein encoded by gene 58	11/1	100
			clone HHFHN61.	2636	87
1347	M55542	Homo sapiens	guanylate binding protein isoform l	1329	100
1348	AF183428	Homo sapiens	28.4 kDa protein	167	24
1349	U70669	Homo sapiens	Fas-ligand associated factor 3	562	99
1350	AF295530	Homo sapiens	cardiac voltage gated potassium channel modulatory subunit	302	

## TABLE 3

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  TPSLIHQAPTPCPAGLWG/PPNGHYHGS*PGC
1	1351	A	2	337	1	HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAGRLPGPAWSWHASGAAPA
2	1352	A	27	100	366	IRNSSIRPMKERETKLSAKHMITCSASYDIRGL QIETT\YHHTPIRMAKIQKT/GHHQC**ECGAT GTLIHGWWGCKVVEPLGKTVWQIPK HASAHASVVLKDNSELEQQLGATGAYRARA
3	1353	A	40	3	314	LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVVDTH\RTPI*R SCNYTI ALILFI.
4	1354	A	74	2	292	TASALFSCPDGGSLAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQQARQSPG*RTNPE/ALQWVLPVSDGWH VLPLP
5	1355	A .	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRISAHPP NAGGEVSNGPKRKLTLMLNFSLPSSGLNAGA FYALSTLLNRMVIWHYPGEEVNAGRIGLTIVI AGMLGAVISGIWLDRSKTYKETTLVVYIMDT GGAWWCYTFYLGTGDTCG*CFITAGVIMGFF MTGYLPLGFEFAVEL\SYPESEGISSGLLNISA QVFGIIFTISQGQIIDNYGTKPGNIFLCVFLTLG AALTAFIKADLRRQKANKETLEN
6	1356	A	81	97	376	EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A YLRVPFIRILLNAR*IRKAYKRMSLEIKLLI/RE *CLFQEMGLSLQWLYSARGDFFRATSRL
7	1357	A	93	2	872	TLSSACLIGDAWKELTIVAGAVSNQLLVWYP ATALADNKPVAPDRRISGHVGIIFSMSYLESK GLLATASEDRSVRIWKGGDLRVPGGRVQNIG HCFGHSARVWQVKLLENYLISAGEDCVCLV

		-37.	CEO I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D=A enartic Acid. E=Glutamic Acid.
NO: of	NO: of	noa	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			/ / /	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	i	peptide	} -	/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
	<del></del>	<del> </del>	<del> </del>			WSHEGEILQAFRGHQGRGIRAIAAHERQAWV
	ļ	Ì				ITGGDDSGIRLWHLVGRGYRGLG/DLGSLLQ
		1		1		VP**ARYTQGCDSGWLLATAGSD*YRGPVSL
	1	1		1		*RRGQVLGAAARG*TFPVLLPAGGSSWSRGL
	1	1		1	ĺ	RIVCYGQWGRSCQGCPHQHSNCCCGPDPVS
		1				WEGAQLELGPAWL
8	1358	Ā	106	3	350	FSSLLSGRISTLRDETGAILIDGDPAACAPIIKF
						LLTEELHLRGVSIYVLRHEAQIYGITPL\VCAL
						LI/CRRL*SDSCMRAALNDRGLYQVLILDGLV
	ĺ	[	<b>\</b>		<u></u>	QCLGFVDSDSRKMVSTLT QAWAJFKGKYKEGDTGGPAVWKTRLRCALN
9	1359	A	115	49	186	KSSEFNEGPERERMDV
		1				KGCRTQEKVDRTEVIRTCINPVYSKLFTVDFY
10	1360	A	123	2	1249	FEEVQRLRFEVHDISSNHNGLKEADFLGGME
		1	Ì			CTLGQIVSQRKLSKSLLKHGNTAGKSSITVIA
ł	Ì	1	1			EELSGNDDYVELAFNARKLDDKDFFSKSDPF
i		1		ļ	\	LEIFRMNDDATQQLVHRTEVVMNNLSPAWK
1		}	}	}		SFKVSVNSLCSGDPDRRLKCIVWDWDSNGK
	1	1				HDFIGEFTSTFKEMRGAMEGKOVOWECINPK
			}	j	1	VKAKKNYKNSGTVILNLCKIHKMHSFLDYI
	<b>\</b>	1		j	ł	MGGCOIOFTVAIDFTASNGDPRNSCSLHYIHP
		Ì				VOPNEYLKALVAVGEICODYDSDKMFPAFGF
İ		1				GARIPPEYTDSHDFAINFNEDNPECAGIQGVV
	1					EAYQSCF\PKAPTFTGPTNICPHSSRKVAKFRR
					1	SEGN*HQGRAFAIIFILVDPGQVGVYSQDMGP
		ĺ	Ì			DNPGGHFV
11	1361	A	147	614	9	ACARKQLLGRTVFIWFVGQLLGGELKGYSKT NTTSSRPASSRG\TLSSSSSSSSSLTKDALPSSL
1.	1		1			KSDSTTITSGLVFPFRSLCVNPAKSSVSESVSSI
					-	KILLSSVKYLE*KRTSCCFPDSSESKLSQLSS
1	}	1		ł	ı	DERVSMGTSSRKPTNSSSSLGALKMSATS\*G
	1	-		1		SGSESPTPFFLTGLQSPPSTRPREPGLTTARNS
		-		<b>\</b>		TTLTRDC
					416	LIPSEPALDSLVDPRVRSRKQPFVIYPVYDTAI
12	1362	Α	177	12	410	DTKIHFSLLDGNVGEPDMSAGFCPNHKAAM
		Į.		]		VLFLDRVYGIEVQDFLLHLLEGGFLPDLRAA
		1	-		-	ASLDT/AEIGAMDFLLS*LFTLCLMMFFFIYPFI
		- 1	İ			NI I TMNVY
			240	535	105	WTFHRHLSPAPLIVCDQGTCVVSYYPQNIVQ
13	1363	Α	249	ددر	1.05	MPDTOMEOGLN/HLFLDGNA*PHSVECYCPS
		1			1	TFEIAIKITSFVLYFHRYRAPEVLLRSSVYSSPI
1	-{	ł				DVWAVGSIMAELYMLRPLFPGTSEVDEIFKIC
		1	-			OVI.GTPKKVSTLVPKLL
14	1364	A	254	572	201	VILTXIGNLMMLLVINADSCLRTXM*FFLGH
14	1304	\^	237	""	1	FFFLDICYSSVTAODAAEFPVS*KPILVWGYIT
1			)	1		*SFFFIFSWGTNGCLLSAITYACYAAICHPLLS
				- [		TMVMNRPLCTATVNATNKMGFLNSQVN
15	1365	A	257	425	68	THAKFLNKKFNIPKLVILPKLVYIVKAIPTKM
13	1303	1				AIEFLLECDQNITVKLICENT*KNIAKNI*KRRV
1		1		· ·		TFTPIET*HPVKQMIKWQ*LTAWLRNRGYKKI
		1				KOTPNSETAPSVCRNLVFDKCG
16	1366	A	263	104	481	FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK
10	1300	11	-3-			SKDVFSKPVNIFWALEESVLGVKARQPKPFFA
		- 1		{		AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV
	1	1		1		GDLSSPNETKYIISLDQDSVVKLENWTDASRV
17	1367	A	298	68	208	RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW
1	-					VSSLAMKEMLTKTTM LVVGITGTRHHARVIFIFLVETGFPHVGQAGL
18	1368	A	300	904	1	ELLTSGDPPALASQSAGITGMSHCARPKGHFG

	CCO ID	Met	SEQ	Predicted	Predicted end	Arnino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
O: of ucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
q-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
ence	Genee	ļ	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
CHCC	Į			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	{	ł		residue of	sequence	/=possible nucleotide deletion, \=possible
	}		}	peptide		/=possible nucleotide deterion, /-possible
			ì	sequence		nucleotide insertion  IHLK*MFYTMSQKMP*PTINLILLLIIPGNLNIF
	<del> </del>	<del></del>	1			KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR
		<b>\</b>	1			KPNMGWLGPK I AFV * KDE V LSOH I MECKEL
	{	i			1	WK*DY*C/LQEVTDPIMEKGKKKKRTASFFK
	}	1	ì			GQPHQSTNALLRRCVR*RYHLS\TVETAGLP* KNTGHIPGQPFLFKLVFKC*NVICI**QYKW*Q
	}	1		ł		NIGVKNKSFCPH*SSSPSL*FIGHHSRNF/CSFK
	1	j	1		}	NIGVKNKSFCPH-555F5L MOITHSIGHT COLUMN ACCOUNTS OF C
		1			ļ	TEPHSVVQAGGQWRNLSSLQAPPPGLMPLSR
		1				ISLMSSWDYRRPPQ
19	1369	A	302	3	445	NSPSRWAKIQMFEHTFCG*GCG/ER/NVHIHCS
19	1307	1.,	1		l	WICRLRPLLWRAVREYLSKLKNAELSFDPGV
	}		j	]	1	SLLRIYAIDMPTSI*DEKEALLFAFLAFHE*HC
	1	Ì	1		KSRIWAVIQ/CIHLWDWLRKL*CFHRMKFYA	
		1	1	1		AV*NKPRHILLSHIWKDVQNILLK
-	1370	A	304	1	1339	FFFCGKEVPLFEQNKHPGPRATTSPGA/HARA
20	13/0	1 .,		1	1	LLSAGEFTAGVGLSP*AIHSFVWLCTFIQHGA
		ľ		1		GGPCHQPGGSPGPWMHTTQAGHLWEGAYPC
	Ì	1		}	}	GSSTWHQVPGQLGGSWGPRERSLLGSFIKCSI
	ł	1			Ì	CPHPPGFRLWMSPNQKPPTENPGVMGRVWR
	1	ł		1		LMPGESPLIWEAEGKEDHLSPEGQGHSE/PVA
	1	•				PLHSSLGNTVKP*PKNQKPKQNRSRHGQ\GF
			1		MAGQGQSRPAAR*PPCPALTPASHSAGTWPP	
	1		]		RICRTVPGGPCPSPSGFRSCRR*GFSA*TRSWF	
						DAEPPSTPDTAPRCCTQSDTSSQGPQ*S*WRR
	1	ì		ì		CRALPGRICSAPAAGLRRARPRISESRRGNSI
	}	1	}	}	Ì	PASPAAASARCPSWGPSCPARPPSRPAAGTEF
	ļ	1	}	}		AAPSRCTAWLRGEREPGPRPPGRRPRSGRGP
		1	1			VSFAPEVLSLPAVRQTKSWRWRNEEEITRPW
		Ì		}		ALVRSRGG
21	1371	A	326	799	1587	GSQVLPPPPSQDSATLPQDA*GPRAAPGQPVC
21	13/1	1	320			E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCL
		ļ				HLSFSPRQGAAPDTEPSAWGPAPTGATGPGL
						LRHVRLFSAGAPRGAATPCPPALLHGPAWPF
	ļ					ARPMFRGHPPVRPLGPWGKVAAGPRALCLA
	-	ł				GVPAVQGECATKPSG*GL*PAHLRGPPGPEV
			1			QWHWQLSAGRDPVPAEDPPL*EGPLGPGGP.
		1		}		AAQAEPGADPEPEDKDQAAESRPAGAMSLS
	1	1				QGSGPVGGQGLR
	1372	A	327	146	652	PHLENPHPEHSFPGAPLT*STLSWSILSPREPS
22	13/2	^	1 32'	1		GAPCYPGHPHLENPHLEHLLTWRTVTWSTL
				1	-	PGAPCYPEHPHLEHPLTWSTPHLEHPSPGEPI
ı		1		1	!	SCRTPTRSILHRDHPLP*CLSTEESPI*GWGSL
i	1		ł			APPSTPLVLDVAPPGPQPASSCPGRDSCYSVI
	1	1				GTVVSP
	1000		348	397	2	CIVSSCOGTRKPCHLEDANKINKQSPTLEKIE
23	1373	Α	340	1 37'		LQESL*VKQ*LIVAEKYVQILHPRKKYFQRP
				1	1	- I NEEDDWMWERKEEKKKCRERMOKKSKWE
		1				EEKKE*RREE\EERKKEKEDRKERRKETSPRO
1		-				CDDIIRD
			262	170	352	GRAIDTAAGSPVOTAHGLPSDALAPLDDSN
24	1374	A	362	170		UPGOTTAOWSI HRKRHLARTLLVSKVKUP
				373	128	VI ITTI ETGYI WKNRHSDO*KRTENPERDO
25	1375	Α	384	3/3	1 20	KYPKVDFCKSNSMKNRLCNKWHWTNWIFI
1						VVINI NI KPHTKI TPNIKKN
r .					165	EVENTNPETESGTNI.TIWIRSI*RKSDEINQKI
1	1376	Α	397	383	1 103	*MEKYSISLDRRLNTVKMSFLPNLIYKFNTIS
26	1 .5.0	1	1	Ì	1	
26	1.570	į		- 1	1	I KIPANE
26					200	KIPANF  KSKATGYMYNI*KLIVFLYANDEQLEIEMN
26	1377	A	406	103	380	KIPANF KSKATGYMVNI*KLIV\FLYANDEQLEIEMN IVP\FNGSKNKIAFTNLTKYQNIQNRHAENY

00010	CCCOTO	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	]	1	} /17	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	\	i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide	304	/=possible nucleotide deletion, \=possible
	}	i		sequence	]	pucleotide insertion
	<u> </u>	<del> </del>	400	14	427	TICTNKFNNLDEIK/FLERHKLSKLTQEEVENL
28	1378	A	408	14	721	ITI KTSRETELVINK*VIPHKEKPGPDSFTGEF
1	ł		l		VOTEKEELJIJILHKLFOTIKYGRILPNSVYETSI	
	1	ł	1			TLKPKPEKDL\KENYRPLPLSNIDAK\LNKTLA
	1		1	)		NRI++HIR
			<u> </u>	1	120	TVSKMCMERORI NN*ILKKNKVRGIAVPDVK
29 1379	Α	434	395	128	VYYKPTVIK/TSWIL*KDSHIVEWNRLENLEID	
ļ		1	<b>{</b>	1	PN/IKRLILDKGAEATEWRKDSFFRQWQ	
	1	1	ļ	l		FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS
30	1380	A	455	2	228	SWDYRYAPPRP\ANF\*FLVETGFYYVAQAGL
30	1.555	{	j	}		SWDYRYAPPRPAINT TEVER OF THE TOTAL SWDYRYAPPRPAINT TO THE TOTAL SWDYRY TO
	[		1	<b>\</b>		KLLSPGDLPALAS
1	1381	+A	462	393	2	QLMFDKGVKNIH\WGWTPPFTK*YWKNWISI
31 1381	} ^	1 .02			CRRMNLNPYLSRYIKINSR\KDLTVRPEPIKLV	
			}	1		EENTGKTIQDTGLGK*FIAKTSKAQSTKTNK*
	l l		- 1		1	KRQTRYIKLK\KKSTASKENNRVKRQPLE*EK
		1	1	l .		IEAN
			174	125	471	VKPYEIAVFLVKPIEYK*HLLSDPAIPLSGI*LK
32	1382	A	474	123	17/1	FIK AVT/RRICTPMFAAPVSVIA/RN*KQSK/CQ
	ļ					KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT
	1	Ĭ	į	1		II PETDRIHKTTYDVISLI
	<b>-</b>	l		<del> </del>	<del></del>	KSACSFICSEEQPASPSPLKPGTYASET\RPRDP
33	1383	A	488	1825	2	LIAAGPREDSSEAETRRPRGA/DGSGTVVKG1
	1	1	1	}	PGSPAPPCSWGHGG\ETEGAG*CPAAPGTDLR	
	1		{		ł	APGGSAGS*\GLPSAGGSRGRKGWRAAGRQP
ļ	ļ		ì			STR*GRPGRHGGRGE*AGHPEPRQSALQSAG
i	1			· I	1	L/ASSPEPMGAALAEDGSGDSRGAGPRPQE*P
	1	1	ł			PSVLSRS\GS*G*G*AASGTASSPRSHSSRLGPP
	į	- 1	1			SAGFHGLRCGQPPFAAAPPGPWPGTGRPAGG
1		- {	l	1		SAGFHGLRCGOPPFAAAFGI WIGIGIGIG
1	- 1	1	ļ.	Ì		AGSPPAAAGTAPPATRGAQSRRQNRTAGRNA
	ł	-	}		1	SPQTAAGAGSPVQWALSRATG*TGETGSWC
ţ	1	ì	1			AGGTHQATHLTAAWVCPPTWSVRPGGSGPA
		1	ŀ	1		AGLGR*GRHPAQSPPLPVPRG*PAWPQEAPSP
	1	Ì	1	1	ļ	SPASSEVALSSGSCWPDQAPGPARGSPPAPLA
ł		. [	- (	1		PAWPAAGRGRQR*GRQSAHPPPRR*STAVSL
	Į	1	i		1	SGTS*WRRSP*AGTRTQQC*SPWLVPACSSRP
)	•	ļ	1	1	l	I *RGTRRPSTOOSPOTTGTPGRSAGPGHPRS*
ļ	ŀ	- 1	l			GGRSPAGTGHLGAOTVASPH*GHWPTALSCL
1	į	ļ				WASASPPGPEAPPOTGACIGTNCRYRAASAK
1	1	- 1	ſ			RSSVAPACA*GWQ*AGSPPAVLRGPP*RVREF
1	l l	1	į		1	CALTURERAPDE
]				126	<del></del>	APGASVGRAOAAEG*RGGPTGRPPSALGVS/E
34	1384	A	497	422	2	AGRAGRAGEGRPVPPAYPLCKSAQTSGPPKA
1		1		Į.		RLS\PPLASCGGRGPPGGAACATCAPPAGPAR
	1	- [	1	*	1	SSRCRRSPPE*GPR*PSRPARPSPGSAASRRQ
	1	Ì	-	[	1	22KCKKK2LLE.OLK.L2KG VIG 21 CONTRIGKS
	1	- 1		1		KLTPCRCQFRGLCA
25	1385	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN
35	1303	1 ^	307			LTELVVAVTDENIVGLFAALLAERRVLLTAS
1		1	1			KLSTLTSCDHAFCALLYPMRWEHVLIPTLPPH
1			1	[		LLDYC*CPPLPRT
				$\frac{1}{3}$	1631	FFFSFVCHLYCVSPTPGPHGRLATWL/PGLLA
36	1386	A	512	٥	1031	FI GI AAGGOTLCPAGELPGHARAQASGAPGS
		1				VI TAVPGRRRVHTCGPGPAAPSTRGECPPPAL
1				ļ		CHTRPARPRPV\PFAPAVPOEPGGQGHGAA/P
1		Ì				PATGHSAPRGCPPARAAPTGSATPAPPPAACA
1		1		1		AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT
	1	1		1		PGQHLLDRPGAPPAQGSGPAPAPPPRLAGPA
	1	}	}			PGQHLLDKPGAPPAQUSUPAPAPPPACAGEA
1		- 1		Ì		GPAAPPPGPPAASWHSSLSKSSSSL\GWSPPLF
	ì	l l				
	]					VGPGSLQ*TPPPQGPHLSGSCGGTSSWRGQR
						VGPGSLQ*TPPPQGPHLSGSCGGTSSWRGQR AAVARRLRSWNACGLSRVAGRSSASYPGRE

					Deadistad and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	l			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	1	residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ	Ì		peptide		nucleotide insertion
	Ì	ļ		sequence		GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD
	+	· · · · ·	1			GRPSQSQ*PAGPPGMRGCCLRGW 1333G0D
	1	ļ	ì		ì	GPGPHPASTWLRAGKTGPSPPACGCA*LPPPS
•	1		1			VSAAPQSPRTRCPRGCAAAAGLCVLAAAGAS
	l	ì	1			HGA\GLPGVRVHTQRVHIH*GAG\GCQTPRPR
	}	l				LRSLPVLGLPAPRCPVSAHPWHRRSGSSCHA
	}	1	1			ARLVPRHPAPGCP**TG*\PLITGFPEP*A*GLP
	1	1		ļ	j	NHQAVGLEASGALQAGHRDELPTMVQLLDH
	l		1			CDDVDI KGRPHAP
		1	<del></del>	1000	1	FRI PLAAGA/RGAAEPRVAVSMAPDPSAKIH
37	1387	Α	620	828	1	WEASPEMOSKCHOKGKNNOTECFNHVRFLQ
	ĺ	}	1			DINSTHI VACGTHAFOPLCAAIDAEAFILPIS
	ì			1		FEEGKEKCPYDPARGFTGLIIDGGLYTATRYE
		1	)	1		FRSIPDIRRSRHPHSLRTEETPMHWLNG*EDE
						AQDDGG*GTISSFLLPWPADHPTPKSPGEPVH
	]			1		SIPVCCQVRGQPQSGGKESPACLKSLSNCLTH
	Ì	1	}			\DAEFVFSVLVRESKASAVGDDDKVYYFFTE
	1	1	İ	ł		RATEKESGSFTQSRSSHRVARGIPPL
	1	}	1			FRAMVSSTLKLGISILNGGNAEVQ/QGNRGKG
38	1388	A	739	1	427	TSEEGKEG*EVPV*LPVSPPLPRPLQKMLDYL
30	1300	1		İ	İ	TSEEGKEG*EVPV*LPVSPPLFKI LQKVILD ID
	1	1,		}		KDKKEVGFFQSIQALMQTC\GEKVMADDEFT
	1		ľ			QDLFRFLQLLCEGHNNDFQNYLRTQTGNTTT
İ	1		· ·	l	İ	INIIICTVDYLLRLQESI
-	1389	A	767	1	1030	TLDLTGPLLLGGVPNVPKDFRGRNRQFGGCM
39	1389	^	'0'	1		RNLSVDGKNVDMAGFIANNGTREGCAARRN
			1			FCDGRRRQNGGTCVNRWNMYLCECPLRFGG
	1		1			KNCEQGEWPASSIPPVTAAWEALLLDVPGTT
	1		- [	]		VPCI HIOVROPI VVYAAFTVDSHRPLQETVL
	ļ	-	l l	}		PRAPAPASGVPSPSGVGWDR*AGPAEPSPSTP
}	ł	1	1			ATVIISVPWYLGLMFRTR\KEDSVLMEATSGG
ļ	1		}	}		PTSFRI OVTGAPCHOGTC*VGARGRDPMLSG
}			Į.			I DVTDGEWHHLLIELKNVKEDSEMKHLVIM
			į.	ĺ		TI DYGMDOVSWHLHLLWG*TLPPAQGKTGA
ļ	1		Ì	}		SEDKVSVRRGFRGCMQVRGGCGGRGEACPS
	1	}	- 1	Ì	Į.	OA APRI
	1				200	IHKIIIHKEDLNKWKYILCSGMERLSTVMIPVV
40	1390	A	801	69	399	POITYKENA*O\VILKETW*E*GAKITILRKNKL
	İ	1	1		ì	RGLVLVPLSTC*VKYLLDKVLPHIKTYYEAR
	1		1			VNKSVVLVQVTIM
		1	1	1		SMLKERKVFQFPSCLFFQYITWLGPPYHVLFD
41	1391	A	835	7	195	SSVTNFSIGAK*DILQSVMNCLYAKRIPCVT
1 7		-	1	1		221 ULZINAL DIFOZAMINE LAGUI CAL
42	1392	A	841	1	415	GSTHASGYDKTPDFILQVPVAVEGHIIHWIES
72	1372	( **	"			KASFGDECSHHAYLHDQFWSYWNSLKHRTW
1					-	QGIGTVASNLSQL*TLNAPFPELLLFRSLARTG
1	- }				1	FVLT*\RFGPGLVIYWYGFIQELDCNRERGILL
1	1			ļ	}	KACEPTNIVTL
			0/5	358	92	DAT SPADVPOKKGSPLPLDPCLGPSSWLLSVG
43	1393	A	845	338	1	LGWPRL*PRRGPGDPGSLPATPPLLTPPHTLLP
	1		1			ORPMI PPSHAGLARPPPPEPISVP
				<del></del>	<del></del>	LPOYCEFPRI SPKSKLVKHSAL**PSALKPPIK
44	1394	A	853	452	1	SPRCIPRTSLYFTICC/PPALQL/SPIEDPPAIYRS
1						PPTHMLRSASQPLNQAPTLVKGHPPSRFLQG
		İ		1		OVSCPPOPTLPREKPLPLHLRPPPRPAOPPLPR
1			Į	1		GA2CLACLITURED PIPER I LIGHT I
						PLTFSTRRNVDPEIPERFR
45	1395	A	894	379	162	GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG
رب ا	1373	^		1		QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT
1		1	}			WLSMSMGK
<u> </u>			900	<del>-                                     </del>	366	TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL
46	1396	Α	900	1	1.333	FIOKYMRT/DO*CVTHDISLYIVTKLALIFLIPR
1			1	1	1	TO THE PERSON OF THE CAR
	ļ	- 1	l	1	<b>{</b>	VFLFHQLNIT**CLHFFTMTTFIAIPFSFLFLGR

		- <del></del>	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D-A courtic Acid E=Glutamic Acid,
O: of	NO: of	noa	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ıci-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
q-	uence	)	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
nce			717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ĺ	ļ	peptide	304	/=possible nucleotide deletion, \=possible
		1		sequence	Ì	nucleotide insertion
			<del> </del>	sequence		DAKSLAMI PRI VSNSWPOVILPP
			<del> </del>	162	2	OLONI ASRGCL*SOLLRRLRRENRLNPGGGG
7	1397	A	944	162	12	CSFIAPACTPAWVTORDFFRKKK
	<u> </u>			<del> </del> _	1300	HFTPDRIAIVKNTRDSHCWRGC*EEGAPARC
3	1398	A	963	216	308	PRKRESWWGERLP/PRGFPPAAEDAPAPGWK
•	1399	A	967	466	1	GRKHASRTARAHVFHPIRQSIRSPVRGRPGDP
	1	1	[	١.		RAAHTRSAGTRLQCKASRGG*GKGPAPTR*E
		\	1		l .	GGPGSAPAPLPASSGCSLFPDSSPWTPPPPAPC
	1		]	1	1	AAAAQP**TPRCPAALRAGAHIGRVGRPY
	1		1	İ		EKCIQALDVFVFCYIDHSSHCLMSCD*E/DQA
0	1400	A	973	45	421	EKCIQALDVFVFC TIDHSSRCLMISCD EDQ.
J	1400	1 ' `	1		1	LNFMPLEMEPKMSKLAFGCQRSSTSDDDSGC
	1	1	1			ALEEYAWVPPGLRPEQIQLYFACLPEEKVPY
	1		1	1		VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLS
		• ]	1	1		E
	1		992	2095	194	IRIRHEAARSCLGCAAGHVPAPGLRLLPTVRO
1	1401	A	992	2093	1.	PPGRRGPAAPGCVCY*SGESTFVSHVPQRMA
	ļ		1	j	)	WPGSAPPRGFHPLQSQTSPSDTVSSPQLSKEE
			1			DCPGWEHPLSSSL*SLGOAGGNH*QPEELAG
		1	1	l	ĺ	WEPR GPPSLAPSSPT/TMWTALVLIWIFSLSLS
	1		1	1		FSHAASNDPRNFVPNKMWKGLVKRNASVE
	1	}	1	1		VDNKTSEDVTMAAASPVTLTKGTSAAHLNS
	}	1	ì	i .		MEVITEDISRIDVSEPATSGVAADGVISLAP
	ļ	ì	1	1		AVASSTTAASITTAASSMTVASSAPTTAASST
	1		1	1		TVASIAPTTAASSMTAASSTPMTLALPAPTST
	İ		- 1			- Letartestatatalesi.STALAOVPKSSALPKI
	- {	1	Į.			ATLATLATRAQTVATTANTSSPMSTRPSPSK
	i	1	1			MPSDTAASPVPPMRPQAQGPISQVSVDQPVV
	- {	Ì	1	-		NITNKSTPMPSNTTPEPAPTPTVVTTTKAQA
	Į.					EPTASPVPVPHTSPIPEMEAMSPTTQPSPMPY
		1	1			QRAAGPGTSQAPEQVETEATPGTDSTGPTPR
	Ĭ	1	1	1		SGGTKMPATDSCQPSTQGQYMV/DHH*APH
	į.		l			SGGTKMPATDSCQF51QQQTMVDIIIT ILLI
	- [		- 1			GRGRQNSPSGGAVTRGDPFHHSLGFVCPAG
	ł	l	1			*ELQEEGLHPGGLLNQRDVCGLRNVRGAGA
	l l	-	l l			WREAWPLPRPFLLPLRPNQVLPNSFGAIEEIG
	1		1			QMLKHI
	<del>-   </del>	<del></del>	994	<del>    1                                 </del>	462	ESGEFLVSFTLKKPTNVFHHINGMKFFNK/L
52	1402	A	774	1 *	1.52	*SHTDIAFYKIOHPFMLKALTKWA*EGT*PD
	1	1	1	1		RVI H*SLRLNGEOLKTFPLRSGMR*G/CAILI
		1				VINAMLSIVPAVVPAGKTRHEKEITCPLIGQ
	1	1	1	1		FK*FS*FVGDMNTCVENKKESKKLLE
					(30)	PEVIOOSAYDSKADIWSLGITAIELAKGEPPI
53	1403	A	1011	1	630	TO A STATE OF THE PROPERTY OF THE STATE OF T
				1		*LMLA*TKDPSI\RPTAKELLKHKFIVKNSKK
		1		1		SYLTELIDRFKRWKAEGHSDDESDSEGSDSI
	1		-	1		TSRENNTHPEWSFTTVRKKPDPKKVQNGAI
	1	}	1		1	DLVQTLSCLSMITPAFAELKQQDENNASRY
	1			1		DLVQTLSCLSMITTATAELAQQUEINIASA
		l				AIEELEKSIAVAEAAGPG
	1404	- A	1016	1	222	ISIDA*KAFDKIQH/CFMITTLKKLGIDGKYL
54	1404	^	1010	\ -		TIKAIDDRHTVSTILNVEKLKAFL*RSGTRQI
				İ		PISGSGARI
					366	UASVDGDEGSDDVYYYYYTPAILRELQALN.
55	1405	A	1033	3	300	EAAFHRPEEDRMI SEDPWRPAHMIKGYMP
	1	-	İ			LINIPHTEVIDVTGLNOSHLYOHLNKGIPMK
	1	1		Ţ		QKRAALYTWHVLEQLEILRQINQQSHGPG
	1					SVLTLQTRSPSKPLS\RKLMDWEVVSRNSIS
56	1406	T A	1044	5	429	DRLETQSRASRSPPVTPNQSQETPVDGKPL
20	1400	''	1	1		DRLETQSKASKSPPV1PNQSQETPVLOKFL
	ļ	1				PPNQSQKNIRYHIHYLHLQYYLDRHISATLI
				1		SSSGIPTPIAVITDALTDLVELILGQPCSEESC
					1	APGTLFLLAL

		77-4	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,	
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D-Accordic Acid E=Glutamic Acid,	
NO: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,	
nucl-	peptide	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,	
otide	seq- uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,	
eq-	uence	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,	
ence		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,	
	1	{		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,	
		ĺ		peptide		/=possible nucleotide deletion, \=possible	
		ĺ	į.	sequence		nucleotide insertion GAYAFETNGFPIMLVLTTDKIEGDVGIAGLYD	
57	1407	A	1050	11	430	MHVISLPMAFLLRTLVRCTSYIIPVTHVLSTPV	
,	110,			Ì		TCLRRREKDGVIVDVLSDTASNHNGFPVEEH	
	1		1	1		ADDTHPARLQGPTLRSQPMGPLKHKAFEERA	
					ł		ADDITHPARLQGPILRSQFMOI ERGING ESSECTION
						NLGLVQRRLRLED LKHRDTPVVGANNRALSCTPLTSLTLCALCPL	
58	1408	A	1058	258	419	PCLGCPTXATCRLYQTTVAVVF	
50	1.00	1	ŀ			KAFSFITSLIGHQRMHTGERPYKCKECGKTF	
59	1409	A	1064	3	425	KAFSFI I SLIGHQRWH I GERL I KECGRAFSQC KGSSSLNNHQRIHTGEKPYKCNECGRAFSQC	
	1107			1		SSLIQHHRIHTGEKPYECTQCGKAFTSISRLSR	
		Ì	1	1	,	HHRIHTGEKPFHCNECGKVFSYHSALIIHQRIH	
	l	1	Ì			HHKIHIGENFIICNECOKVISTIISIASIA	
	1		İ	_		TGEKPYACKDVGK GGPPGPFLAHTHAGLQAPGPLLAPAGDEGDL	
60	1410	A	1065	204	419	LILAVQQSCLADHLLTASWGGK/DPIPTKALO	
	}	l	i		LLLAVQQSCLADHLLIASWOODDID III		
	i	1			<u> </u>	EGQEGLPLTV RHSRAHLCQPFHLVMRDLLQLGQDIPQGCHY	
61	1411	A	1079	3	383	LEENHLIHRDIAARNCLLSCAAPTRAATIGDF	
0.	1					GMARYIYRTRYYQLGDRAL/LPRKWMPPEAI	
	1	i	1			LEGIFTYNTDSWTFGVLLWEIFSLGYMPYPGH	
		l	(		I control of the cont		
			1			TN VVEFLWSRRPSGSSDPRPRRPASKCOMMEER	
62	1412	A	1080	1	859	ANLMHMMKLSIKVLLQSALSLGRSLDADHA	
OL.						PLQQFFVVMEHCLKHGLKVKKSFIGQNKSFF	
		-	1		İ	GPLELVEKLCPEASDIATSVRNLPELKTAVGR	
	1	1	1			GRAWLYLALMQKKLADYLKVLIDNKHLLSE	
	•	1		1		FYEPEALMMEEEGMVIVGLLVGLNVLDANL	
	l	į	1	1		CLKGEDLDSQVGVIDFSLYLKDVQDLDGGKI	
	)		Į	}		HERITOVLDQKNYVEELNRHLSCTVGDLQTK	
		1	ì	1		IDGLEKTNSKLQERVSAATDRICSLQEEQQQI	
	1	- {	ŀ	{		DEONEL IR	
1						SSFAKHKRIHTGEKPFICLECGKAFTSSTTLTE	
63	1413	A	1083	2	615	HRRIHTGEKPYTCEECGKAFRQSAILYVHRRI	
	- 1			}	1	HTGEKPYTCGECGKTFRQSANLYAHKKIHTC	
ļ	1		ļ		İ	EKPYTCGDCGKTFRQSANLYAHKKIHTG\EK	
	ì	Ì	ļ	ļ	1	VKCKECGK AFKSYYSILKHKRTHTRGMSYE	
	1	1		}	1	DEC/QRSLN/RSSILSNHKIIHNEEK/PLKCEKC	
ļ					1	L MARKILITSICCRHKKN	
	}	}				KKQDLSSSLTDDSKNAQAPLALTESHLATLA	
64	1414	A	1084	946	1	SSSQSPEAIKQLLDSGLPSLLVRSLASFCFSHI	
1				1		SSESIAQSIDISQDKLRRHHVPQQCNKMPITA	
		1	}	ł	1	LVAPILRFLTEVGNSHIMKDWLGGSEVNPLV	
}		Į			1	TALLELL CHSGSTSGS\HNLG\AQQDQCKISES	
	1	ł	ì	- 1	1	FESTI TTGL TTOORTAIE\NATVAFF\LQC\\SC	
1		- 1	ĺ	1		HPNNQKLMAQVLCELFQTSPQRGNLPTSGN	
1	1		1		•	S\GFIR\RLFLQLMLEDEK\TMFLQSPCPLYK	
		1	1	1	•	RINATSHVIQHP\MYGAGHKFRTLHLPVSTTI	
		1	1	1		SDVLDRVSDTPSITAKLISKQKDDKKKK	
	ļ			_L		PRAFEFVHTEMIVG/RVQNIHLFTLQVLEDRA	
65	1415	A	1087	103	324	LFTMSVGSSLWSTYLIHVMALP/DRELLKPN	
""						SVALHKLSNALV	
1		1				HETCSVTHIVSFSLPFLNPSHPASTPGHTENE	
66	1416	A	1095	3	493	PSLVWFDRGKFYLTFEGSSRGPSPLTMGAQI	
"	*			1		TLPVAAAFTETVNAYFKGADPSKCIVKITGE	
1						MVLSFPAGITRHFANNPSPAALTFRVINFSRI	
		1	- 1			MVLSFPAULIKHFANNFSFAALLI KYINI SIG	
		1	1			HVLPNPQLLCCDNTQNDANTK\EFWVNMPN	
				1		MTHLK	
67	1417	A	1098	57	356	LKLTSLGFIIGVSVVGNLLISILLVKDKTLHR	
0/	1-71/	1 7	1.070		1	PYYFLLDLCCSDILRSAICFPFVFNSVKNGST	
	l l	ł	<b>I</b>		)	WTYGTLTCKVIAFLGVLSCFHTAFMLFCISV	

	1 000 10	1 3 6 - 4	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ			to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	иепсе	ĺ	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	1	}	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		j	ľ	residue of	sequence	/=possible nucleotide deletion, \=possible
İ			1	peptide	1	nucleotide insertion
		1	l l	sequence	l	
	<del>                                     </del>	<b>†</b>				RYL
68	1418	A	1106	1	1326	MGKISATGINMGTKCSWALVWHLESYDPKH
00	1410	1	1		1	YEREGMQDWKTASGQSEEATQQSSQKPQPH
		1	1	Í		YTTYOSSSFLKYSSESHLLAWRENSSEGSFQF
	1	1	-			PGRSRARPPRTRQQRRGAAAGPGRGAVRLG
		}	i		j	HPOSAAOPOLRAAARIPESPAAFPAQPRPGSA
i	1		ł			RNSDASGPASLSRTLGRASSPRPPQAPDVTAP
}	1		ì	1		SPAALAPRAARGGSRAAALAGAEAEEPLRTL
1	1	1	ì			APRPTRAAAPPPPPPPPPPPPPPPPPVRCVSR
}	Ì		1		1	RARAPPWR/PAATGPPP\RPVAPSRKLGSARAP
	,	1				APALQIRKGTSSGLPGRGGGSGPGNNLSSVA
1		(	ł			APALQIRAGISSGLI GRAGGOSGI GINESSI A
ļ	1	1	1		1	GNWRGSSFAVERPGMAKYQGEVQSLKLDDD
		1	ļ	ļ		SVIEGVSDQVLVAVVVSFALIATLVYALFRNV
	l-		1			HONIHPENQELVRVLREQLQTEQDAPAATRQ
1	1		i			QFYTDMYCPICLHQASFPVETNCGHLFCGSLT
	1	Î	ĺ		1	PNSIW
69	1419	A	1107	2	466	FDTARLHEFGTSITQIFAVDNREDLQKWMEA
69	1417	1	1107	] ~	1	FWQHFFDLSQWKHCCEELMKIEIMSPRKPPLF
1	1	(	1	}		1.TKEATSVYHDMSIDSPMKLESLTDIIQKKIEE
	i	1	İ	•		TNGQFLIGQREESLP/SS/CGPHSLMVTIKWSS
1		ļ	1	1		RKRY/SYPASEPLHDEKGKKRQAPLPPSDK
			<del></del> _		23	ALRRLHYVRATKV\FLSFRRPFWREEHIEGGH
70	70 1420	A	1111	698	23	SNTDRPSRMIFYPPPREGALLLASYTWSDAAA
ļ		1	ì			AFAGLSREEALRLALDDVAALHGPVVRQLW
1	ļ	}	<b> </b>	1		DGTGVVKRWAEDQHSQGGFVVQPPALWQT
1	1		}	1		EKDDWTVPYGRIYFAGEHTAYPHGWVETAV
	į	1	ļ			KSALRAAIKINSRKGPASDTASPEGHASDMEG
1		1	١	1		KSALKAAIKINSKKUPASDI ASI EUHASDIVEO
	- {		1		•	QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL
1	1	Į	1			QNTTHTRTSH
71	1421	A	1119	2	385	QKQTLQNGYLDSSMDILYLGSLPPELQVSSDE
1 ''	.   * 122	••	1		ļ	PPGPPEQAGLSQFHLEPETQNPETTEEIQSS/LQ
}	1	1	1			QEAAAQLPQLPEVVELSSTKA\EAPALPSQSL
1		ŀ	ŀ	ľ		EGVHSSTEOKAPAQQLPAFEEILAPLLIHHE
	+,,,,,,	A	1127	+1	906	HAOYVGPYRLEKTLGKGOTGLVKLGVHCIT
72	1422	A	112/	} 1	1 300	GQKVAIKIVNREKLSESVLMKVEREIAIL\RLI
-		1		ł	1	EHPHVLKLHGVYENKKYFPPDELTSGPSMLA
ł				[	1	QVSPHGKLSARRSWDLLSGFPRYLVLEHVSG
ì	ì		i	1		GELFDYLVKKGRLTPKEARKFFRQIVSALDFC
		1		1	}	HSYSICHROLKPENLLLDEKNNIRIADFGMAS
					1	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR
		-	1	1	1	RADMWSCGVILFALLVGALPFDDDNLRQLLE
					1	KADM ASCAAITLATT AQUELLODDIATE ACTOR OF THE
1			}	1		KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR
[		1		1		LSLEQIQKHPWYLGGNFIS
73	1423	A	1128	1	802	LRNALDVLHREVPRVLVNLVDFLNPTIMRQV
1 "	. , ,				1	FLGNPDKCPVQQAMLEPLGSKTETLDLRAE
1				]		MPITCPTONEPFLRTPRNSNYTYPIKPAIENWG
		1		1		SDFLCTEWKASNSVPTSVHQLRPADIKVVAA
1				1		LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG
1	1	-		l l		GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG
		1		1	1	TAGLNVAAEGARARDMPAQAWDLVERMKN
		ļ		İ		SPDINLEKDWKLVTLFIGGNDLCHYCENPEA
				1	İ	HLATEYVQHIQQALDILSE
		-			<u> </u>	PREDOLITING DIODI DE ACUT AN ADDICI MOT
74	1424	A	1139	60	480	FREPCLLVPGDHQPLREASWLA/LPPIGLWGT
1				1		DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG
	1	1		1		VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE
		- 1		1		EQPAADAAVAKGEF/QGEQIAPVPAVIAAHPE
		}		1		AADPAPVHTTAHPKGA
76	1425	-+-	1147	2	413	PFPHOHPOEP\KGSCWPQSALRGQCPGPVLGV
75	1425	A	114/	1	1	TTTSDLCSLQVPVSSHRNPLLDLAAYDQEGR
L						

	L OPO ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide	seq-	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	dence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	<b>\</b>		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		]	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	_	/-possible nucleotide deletion, \-possible
		1	ļ	sequence	ļ	nucleotide insertion
	<del> </del>	<del> </del>	<del>                                     </del>			RFDNFSSLSIQWESTRPVLASIEPELPMQLVSQ
		l .		1		DDESGQKKLHGLQAILVHEASGTTAITATAT
	}	1	}			GYQESHLSSAR
76	1426	A	1155	38	410	PIISAPAQDDPILLSFIHCLHANLLCVWRRDVK
, ,			l .			PDCKEIWIFWWGDEPNLVVQYIMNCMLWK
		1		1		KDSGKMAFPMNVGRC/FFKEIHNLLERCLMD
				1		KNFVLIGKWFVRPYYKDEKPVNKSEHLSCAF
		1				T CONTROL OF CHARLES O
77	1427	A	1162	526	350	RFPQGLEDVSTYPVLIEELLSRGWSEEELQGV
	1	1			<u> </u>	LRGNLLRVFRQVEKVQEENKWQSPLED
78	1428	A	1171	I	1293	MAESASPPSSSAAAPAAEPGVTTEQPGPRSPP
	1	1				SSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQT TSPRNWCIKMVCNPWFECVSMLVILLNCVTL
		1	1	1		GMYQPCDDMDCLSDRCKILQVFDDFIFIFA
			-	1		MEMVLKMVALGIFGKKCYLGDTWNRLDFFI
	1			1		VMAGMVEYSLDLQNINLSAIRTVRVLRPLKA
						INRVPSMRILVNLLLDTLPMLGNVLLLCFFVF
	1	1		1		FIFGIIGVQLWAGLLRNRCFLEENFTIQGDVAL
ŀ		1	ļ	1		PP/YYQPEEDDEMPFICSLSGDNGIMGCHEIPP
ł	-	i i	1	1		LKEQGRECCLSKDDVYDFGAERQDLNASGL
ł	{	1: "		1		CVNWNRYYNVCRTGSANPHKGAINFDNIGY
		1	ļ .	1		AWIVIFOVITLEGWVEIMYYVMDAHSFYNFI
	1	}	1		1	YFILLIIVSVREPGLLGGSFSTAQSPKCQGDSFP
İ						GVAAESLLLRGWVLWLPGGG
-	1429	A	1175	1	405	PNDFFKDMFPDLPGGPLGPIKAENDYGAYLN
79	1429	^	1175	1.		FLSATHLGGLFPPWPLVEERKLKPKASQQCPI
}	1				}	CHKVIMGAGKLPRHMRTHTGEKPYMCTICE
		1				VRFTRQDKLKIHMRKHTGERPYLCIHCNAKF
		-		ļ		VHNYDLKNHMR
80	1430	A	1182	25	198	EMNELSQQLSQQGGRGASQCPSPPAPTLPNPT
"						PLCQLQLQRVNTGLPTPPCHPGAGAA
81	1431	A	1186	254	583	KTVLDVGAGTGILSIFCAQAGARRVYAVEAS AIWQQAREVVRFNGLEDRVHVLPGPVETVEL
	}		1	1		PEQVDAIVSEWMGYGLLHESMLSSVLHARTK
	Ì	1		•		VVKDGGFFLPXSSELFM
						DFVDAARNLPLESTKSPAEPSKSVPSLE\DPRA
82	1432	A	1187	2	716	SSQGLPSQGPVQNQGRRGEQRPKKF/TVIQHT
1		1				SSFEKSDSLEOPSGLEGEDKPLAQFPSPPFAFA
1		}		1		GRSAHSLOPKLVRQPNIQVPEILVTEEPDRPD
1	1			1		TEPEPPPKEPEKTEEFOWPOGSQTLAQFPVEK
1		1				L PPKKKRLGLAKMAOSSGESSFESSVPLFRSP
İ	1		1			SOESNVSLSGSSRSALFERDDHGKAEAPSPSF
						DMGPKPLGTHMLTV
02	1422	A	1188	517	804	ESPGLSKVLRTGAFAYPFLFDNLPLFYRLGLC
83	1433	A	1,100	} ~~~		WGRGHGCGOEALSTSHGYHLFCALLTGFLFA
				1		SHLPERLAPGRFDYIGHSHQLFHICAVLGTHF
1	}		}	1	1	Q
84	1434	A	1192	45	476	LGDVGFWVERTPVHEAAQRGESLQLQQLIES
04	1434	^	1172	'		GACVNQVTVDSITPLHAASLQGQARCVQLLL
İ				1	1	AAGAQVDARNIDGSTPLCECLRLGQHRVCEA
[	- {	-		1		LAVLRGQGQPSPVHSVPPARGLHXREFRMC*
		1				GFLFDVGXNLEAHEFHFGEP
85	1435	A	1194	69	410	KRSEEASAPPFPLGGTGAAPTRASLPEQILLPR
55	1,133	1	1			SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ
				1	!	HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT
	1	1	1			GRSPCPSLPGTTRTNSLL
	1436	A	1215	3	405	LPSHTCGNPGRLPNGIQQGSTFNLGDKVRYSC
86	1430	,				
86	1436			1	i	NLGFFLEGHAVLTCHAGSENSATWDFPLPSC RADDACGGTLRG/AEWHHLQPPLPLG/ATKN

			1.000	<b>5</b> 1.63	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SÉQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	i	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	]	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		ļ	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ	ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		(		peptide	554	/=possible nucleotide deletion, \=possible
	1	1		sequence	1	nucleotide insertion
	ļ.——-	<del> </del>	<del> </del>	Sequence	<del> </del>	NADCTWTILAELGDTIALVFIDFQLEDGYDFL
	1	}		l		EVTGTEGSSLW
87	1437	A -	1216	226	964	GTARFGPMVGFGANRRAGRLPSLVLGVLLV
87	1437	1	1210	120	,	VIVVLAFNYWSISSRHVLLQEEVAELQGQVQ
		1		ļ	j	RTEVARGRIEKRNSDLFAVVGHAQETDRPEG
		1	Į		1	GRLRPPQQPAAGQRGPREEMEDDKVKLQNN
						ISYQMADIHHLKEQLAELRQEFLRQEDQLQD
		ł	1	1		YRKNNTYLVKRLEYESFQCGQQMKELRAQH
	1	1				EENIKKLADQFLEEQKQETQKIQSNDGKELDI
	}	1		}	1	NNQVVPKNIPKVAENVADKNEEPSSNHIPHG
88	1438	A	1218	1	534	PEFGTTISCGYLMATDVSRRPSVHKAVEIEQE
00	1430	1		1		RVKSAGAWIIHPYSDFRFYWDLIMLLLMVGN
		1				LIVLPVGITFFKEENSP\PWIVFNVLSDTFFLLD
ł	1					LVLNFRTGIVVEEGAEILLAPRAIRTRYLRTW
		1	1			FLVDLISSIPVDYIFLVVELEPRLDAEVYKTAR
				1		ALRIVRFTKILSLLRL
89	1439	A	1223	1	743	MGFDEVFMINLRRRQDRRERMLRALQAQEIE
"		1	-		1	CRLVEAVDGKVGMLTRSNAAPGRHLAMLET
	1		]	ļ	ļ	LVVVAPRFVDADNLILNPDTLSLLIAENKTVV
1			1			APMLDSRAAYSNFWCGMTSQGYYKRTPAYI
				}		PIRKRDRRGCFAVPMVHSTFLIDLRKAASRNL \AFYPPHPDYTWSFDDIIVFAFSCKQ\AEVQMY
1	}	1	1	į.	ļ	VCNKEEYGFLPVPLRAHSTLQDEAESFMHVQ
ł		1		Ĭ	İ	LEVMVPSSPSSAQSMAVVSADHIGLVISYL
İ		1		J		NKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGF
90	1440	Α	1227	2	349	GPWDFKFILCRYTSVLFYANMDTSIVVLGLIT/
		1				YDRY/WKVVRHL/WDSWMTGI/SFTRVYLLG
		1	1		j	LGARLVWFGKLILAKGGHGGISWL
			1	<del> </del>	1937	LGSSDVRAPQRSELGAESPSRMVASQAYNLT
91	1441	A	1245	3	1937	SALTPILTRSRVLNEEPLTLAGF\SRAPANLSD
		-				VVQLIFLVDSNPFPFGYISNYTVSTKVASMAF
1		1	1			OTOAGAOIPIERLASERAITVKVPNNSDWAAR
	1					GHRSSANSV\VOPQAFVGAVVTLDSSNPAAV
	)	}				LHLOLNYTLLDGRYLSEEPEPYLAVYLHSEPR
	ļ	1	}			PNEHNCSASRRIRPESLQGADHRPYTFFISPGT
	1	-				RDPVGSYRLNLSSHFRWSALEVSVGLYTSLC
		]				QYFSEEDVVWRTEGLLPLEETSPRQAVCLTR
	[					HLTAFGTSLFVPPSHIRFVFPEPTADVNYIVML
				l l	•	TCAVCLVTYMVMAAILHKLDQLDASRGRAIP
1	}	1				FCGQRGRFKYEILVKTGWGRGSGTTAHVGIM
	{			ĺ		LYGVDSRSGHRHLDGDRAFHRNSLDIFQLATP
1						HSLGSMWKIRVWHDNKGLSPAWFLQHIIVRD
1	1	-		1		LQTARSTFFLVNDWLSVETEANGGLVEKEVL
		ļ		1		AASKASFRVPTPS\AALLRFRRLLVAELQRGF
			1	1	i	FDKHIWLSIWDRPPRSCFTRIQRATCCVLLICL
1			-	[		FLGANAVWYGAVGDSAYSTGRVSRLNPLSV
		ſ	ţ.			DTVAVGLVSSVVVYPVYLAILFLFRMSRSKV
	-	-				GWGWGPGSTGNGAWASAPCPEPPLSSAAAR
1						GKGVHQRLLGKGQHT  VFDEENILNELNDPLREEIVNFNCRKLVATMP
92	1442	A	1246	5	562	LFANADPNFVTAMLSKLRFEVFQPGDYIIREG
			]	Į.		AVGKKMYFIQHGVAGVITKSSKEMKLTDGS
		}				YFGEICLLTKGRRTASVRADTYCRLYSLSVD
						NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN
						SILLQKFQKDLNTGVFNNQENEILKQIVKH
					1	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL
			1249	180	901	I ALLLA CALLA LA LA LA LA LA LA LA LA LA LA LA LA
93	1443	Α	1249	1	i	DODY ACCOMA COCODOL DD/CODAT/CCAUNIDA
93	1443	A	1249		İ	PGRKASCSTAGSGSRGLPP\SSPMVSSAHNPN
93	1443	A	1249		ļ	PGRKASCSTAGSGSRGLPP\SSPMVSSAH\PN KAEIPERRKDSTSTP\N\LPPSM\MTRR\NT\Y\CT ERPGAER\PS\LP\GKE\NS\GTPR\VPPAS\PS\S\HS\

CT 0.73	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
nucl-	peptide	,,,,,,	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	dence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uciac		1	'	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		į.	}	peptide		/=possible nucleotide deletion, \=possible
	1	1		sequence		nucleotide insertion
	<del> </del>	† <del></del>	<b>†</b>			LAPPSGERSRLARGSTIRSTFHGGQVRDRRAG
	1	1				GGGGGVQNGPPASPTLAHEAAPLPAGRPRP TTNLFTKLTSKLTRRVADEPERIGGPEVTRRP
		1				TINLFIKLISKLIKRVADEPERIOOFEVING
		1				RQEDHLSPGGRGCSEL KFSQWGLTKPKLSNASP/WISLVKKLMKKWS
94	1444	A	1261	3	385	VTQNLTFREQLEAGIRYFDLRVSSKPGDADQ
,	}		j		1	EIYFIHGLFGIKVWDGLMEIDSFLTQHPQEIIFL
		1	1		)	DFNHFYAMDETHHKCLVLRIQEAFGNKLCPA
			1	1		1
	-		1	L		CR GPRDNPG\EDPRFEIVEHFGIAWFTFELVARFA
95	1445	Α	1282	2	550	VAPDFLKFFKNALNLIDLMSIVPFYITLVVNL
		1			}	VAPDFLKFFKNALNLIDEMSIVTITIE
		1			1	STGLRSLGATLKYSYKEVGLLLLYLSVGISIFS
	1	1	{			VVAYTIEKEENEGLATIPACWWWATVSMTT
		}	1	Ì		VGYGDVVPGTTAGKLTASACILA
				1	1156	OLLPPSNRENAGLLVGRCLCSAALRPVGDLIT
96	1446	A	1294	1	1456	SSGQVAVRNAPQAGSAKAGKGKFQDNFEFIQ
!					Ì	YFKKFFDANCNEKDYNPVAAGQGQETEVAP
			1		İ	SIVAPVLNKPNQCPEGYICVKAGRNPNYGYT
	)	]	1	i	1	SFDTFSWAFLSLFRLMTQDYWENLYQLTLRA
			j	1		AETTYMIF/LV/LVILLGSLYLVTLILAV/VAMA
		1				VEEONOATLEEAEOKEAEFQQMLEQLKKQQ
		-			l	EAAOOAATATASEHSREPSAAGRLSDSSSEAS
	1				1	KLSSKSAKERRNRRKKRKOKEOSGGEEKDED
	1		j		}	EFOKSESEDSIRRKGFRFSIEGNRLTYEKRYSS
			<b>\</b>		1	PHOSLLSIRGSLFSPRRNSRTSLFSFRGRAKDV
			1			GSENDFADDEHSTFEDNESRRDSLFVPRRHGE
				Ì		RRNSNLSOTSRSSRMLAVFPANGKMHSTVDC
	}				ł	NGVVSLVGGPSVPTSPVGQLLPEVIIDKPATD
						DNGTTTETEMRKRRSSSFHVSMDFLEDPSQR
1	}	-				ORAMSIASILTNTVE
- <del></del>	1442	A	1295	2	2057	IOTOL PTKSSOOLRKGGNCVRCKMQMNFIAE
97	1447	Α.	1293	1	2001	EVILKYRITFYNNNKGPNMLYIEIKAFVHFMI
		]				NRYL SYGSGPKRFPLVDVLQYALEFASSKPV
	1	]				CTSPVDDIDASSPPSGSIPSQTLPSTTEQQGALS
		- 1	į	{		SELPSTSPSSVAAISSRSVIHKPFTQSRIPPDLP
			ì	Ì		MHPAPRHITEEELSVLESCLHRWRTEIENDTR
			j		ļ	DLQESISRIHRTIELMYSDKSMIQVPYRLHAV
	'		1		ļ	LVHEGQANAGHYWAYIFDHRESRWMKYNDI
		1				AVTKSSWEELVRDSFGGYRNASAYCLMYIN
					ļ	DKAQFLIQE\DLIKTGQPLVGIETLPPDLRDFV
	j	- )		ì	1	EEDNQRFEKELEEWDAQLAQKALQEKLLAS
	<b>!</b>	ļ				QKLRESETSVTTAQAAGDPKYLEQPSRSDFSK
		1			j	HLKEETIQIITKASHEHEDKSPETVLQSAIKLE
	Ì	}			1	YARLVKLAQEDTPPETDYRLHHVVVYFIQNQ
	1				1	APKKIIEKTLLEQFGDRNLSFDERCHNIMKVA
				1	}	QAKLEMIKPEEVNLEEYEEWHQDYRKFRETT
	{				1	MYLIIGLENFQRESYIDSLLFLICAYQNNKELL
}	1			1	[	SKGLYRGHDEELISHYRRECLLKLNEQAAELF
			}	1		ESGEDREVNNGLIIMNEFIVPFLPLLLVDEMEE
		}		1		KDILAVEDMRNRWCSYLGQEMEPHLQEKLT
		Ì		1		DFLPKLLDCSMEIKSFHEPPKLPSYSTHELCER
						FARIMLSLSRTPADGR
Co	1448	A	1304	118	453	SGPSSRAIYLHRKEYSQNLTSEPTLLQHRVEH
98	1448	^	1304	1		LMTCKQGSQRVQGPEDALQKLFEMDAHGRV
	1	1	1			WSQDLILQVRDGWLQLLDIETKEELDSYRLD
Ì		1	1	1		SIOAMNVALNTCSYNSILS
00	1440	+-	1306	3	1660	CGYECHTTCAPOAPPCPVPPDLLRTALGVHPE
99	1449	A	1300			TGTGTAYEGFLSVPRPSGVRRGWQRVFAALS
L						

			I CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
10: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence	ì	l	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i	1	1	amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Ì	Į	1	residue of	sequence	possible nucleotide deletion, possible
		{	ì	peptide		nucleotide insertion
	1	Į.		sequence		DSRLLLFDAPDLRLSPPSGALLQVLDLRDPQF
	1	†				SATPVLASDVIHAQSRDLPRIFRVTTSQLAVPP
		1	}	ļ		TTCTVLLLAESEGERERWLQVLGELQRLLLD
	ļ	Ĭ	1	1	1	TICTVLLLAESEGERER WLQVLGELQIADEDD
	1	1	ł	}	1	ARPRPRPVYTLKEAYDNGLPLLPHTLCAAILD
		1				QDRLALGTEEGLFVIHLRSNDIFQVGECRRVQ
	1	1	}	1	Į.	QLTLSPSAGLLVVLCGRGPSVRLFALAELENI
	İ	1	1	1		EVEVPKIPESRGCQVLAAGSILQARTPVLCVA
		1	Į.			VKRQVLCYQLGPGPGPWQRRIRELQAPATVQ
	1	1	i			SIGLI GORL CVGAAGGFALYPLLNEAAPLAL
	ŀ	l	1	į		GAGLVPEELPPSRGGLGEALGAVELSLSEFLL
		1	1	ì	l .	1 FTTAGIYVDGAGRKSRGHELLWPAAPMGW
	1	1	į	}	ľ	GVAAPYI TVESENSIDVFDVRRAEWVQTVPL
	1	1		ì	}	KKVRPLNPEGSLFLYGTEKVRLTYLRNQLAE
	ì	1	ļ	1		KDEFDIPDLTDNSRRQLFRTKSKRRFFFRVSE
		Į.	Į.	1		EQQKQQRREMLKDPFVRSKLISPPTNFNHLV
	Ì	ĺ	1	1		HVGPANGRPGARDKSP
	ļ	l				SLCVPGPVDTGTFAVMSVMVGSVTESLAPQA
100	1450	A	1318	918	190	LNDSMINETARDAARVQVASTLSVLVGLFQV
,00	1			1	)	GLGLIHFGFVVTYLSEPLVRGYTTAAAVQVF
	1	1		1	1	VSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKL
	Į.		i i	1		PQSKVGTVVTAAVAGVVLVVVKLLNDKLQQ
	1	ļ	}	1		POSKVGTVVTAAVAGVVLVVVKLLINDREQQ
	}	)	1	}	ŀ	QLPMPIPGELLTLIGATGISYGMGLKHRFEAG\
	ł		l l	1		PPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGK
	1		1	1		IFALRHGYRVDSNQVWVMRDV
	1451	$+_{\overline{A}}$	1353	220	445	DWPDLFTYPLIGSPKCFQSARPE\RMYRRTVR
101	1451	A .	1333	220		SSHGNHALQEVLPRSGHGTEFTKQKHLEAAD
		Ì	1			UCUPPARMSIFSR
			1363	542	2	AHLLMLNLAL\TDLL\YLTSLPFLIHYYASGEN
102	1452	A	1303	342	1 -	WIEGDEMCKFIRESFHENLYSSILFLTCFSIERY
	Ì	(	<b>\</b>	ĺ	ļ	CVIIHPMSCFSIHKTRCAVVACAVVWIISLVA
	ì	1	1	l		VIDATELITSTNRTNRSACLDLTSSDELNIIKW
	ļ		l	İ		YNLILTAYLLCLPLVIVTLCYTTIIHTLTHGHAN
İ	l	1	Ì	1		ADSCLKOKARRITILLL
1					110	CHSTESSSDFILPGDYLLGGLCPLHSGCLQV\C
103	1453	A	1371	2	410	SFNEHGYHLFQAMRLAVEEINNSTALLPNITL
		ì				GYQLYDVCSDSANVYATLRVLSLPGQHHIEL
İ	1		j			QGDLLHYSPTVLAVIGPDSTNRAATTAALLSH
		ļ	ł	l		CODEMISTATION
	1					FLVPMLLEQ NSRVEDRS/NMSLWTQNITVCPVRNVTRDGG
104	1454	A	1376	3	432	NSKAEDKSININOT A I GUIT ACLAVIA I ICOGO
104	1,454	1	1			FGPWSPWQPCEHLDGDNSGSCLCRARSCDSF
1			ļ	}	1	RPRCGGLDCLGPAIHIANCSRNGAWTPWSSW
Ì		1	ł	1	<b>f</b>	ALCSTSCGIGFQVRQRSCSNPAPRHGGRICVG
				1	1	KSREERFCNENTPCPVPIF
L			1379	2	396	GLGLL YLTEAAVEGVMRVIGGSNHLAVVLDL
105	1455	A	13/9	1 2	370	TIT AVIDSTEVWEIEISLAOTMKTLRLRKNIVK
1	[	1				CLUBURKNITHEAVLASIVEMGWITKIFKIAK
		Ì		1		COSDWMERWVDDAFWSFLF\SLILIVIMFLW
1	İ	- (		1		RPSA
		L			422	EDGHGGWSSRCLVDHAEEGHREPWKRLCIW
106	1456	A	1383	1	432	OPCCHETREAFYFPGHPLLSPQICLAPETPPRO
			Ì			CPPVSSLHFISLQ/RLPRDCQELFQVGERQSGI
						FEIQPQGSPPFLVNCKMTSGTFWTCRTDSRV
		1	1	1	1	PERCENCIA A HEREODETE
				1		QNANPSNAAHSEDQPTP
100	1457	-	1386	719	558	FFFVTRSHSVAQAECSGVFTAHRSLDLVGSS
107	1457	A	1,500	1		YPALSLQSSWDHRHTWLIFAFL
		-+-	1397	631	12	DVAISLI CAAIFISFMVOSAGKRWPTGVMLM
		Α	139/	1 69 1	-	VVVLFAFLYSWPIOALLPTYLKTDLAYNPH1
108	1458					
108	1458				1	VANVLSESGEGAAVGCCV/GGFLGDWLGTR
108	1458					VANVLSFSGFGAAVGCCV/GGFLGDWLGTR AYVCSLLASQLLIIPVFAIGGANVWVLGLLLI

				D. Park	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	иелсе		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	}		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide		/=possible nucleotide deletion, \=possible
	1	i		sequence	1	nucleotide insertion
	<del> </del>		<del> </del>	soquence		FQQMLGQGIAGILPKLIGGYFDTDQRAAGLG
	li .	ļ				FTYNVGALGGALAPIIGALIAQRLDLGTALAS
	1		}	ļ		LSFSLTFVVILRNRRPGKSLVR
100	1459	A	1402	15	387	VLVALPDT\VTSETVVTEVLGHRVTLPCLYSS
109	1439	Α	1402			WSHNSNSMCWGKDQCPYSGCKEALIRTDGM
		ļ		}	1	RVTSRKSAKYRLQGTIPRGDVSLTILNPSESDS
	1	ļ	}	Ì	_	GVYCCRIEVPGWFNDVKINVRLNLQRASTT
110	1460	A	1421	3	350	HEDLSSLLTRGSGNQERERQLKKLISLRDWM
110	1400	Α	1		1	LAELAFPVGVLATCA*SLLSC*YCVILFPCSCF
	1				1	FFHSPDALFSLLLLSCYFPSYCFFYYLFFSSSPL
	1	}	1			CLLLASSPFPLFILLASL
111	1461	A	1426	2	344	FTSTMTKPFEKESEQPA*ATLAFGAQTSTTAD
111	1401	1	1			QCALKPDLSYLNNSSSSSSTPATSAGGGIFGSS
			}			TSSSNPPVATFVFGQSSDPVSSYGFVNTAESST
						SDSLLFSQDSKLATTS
112	1462	A	1434	46	372	TTSWTTSCTRSCT*SGASSGPGWTPRTTWWR
112	1402			1		SRRSSQRTCSRACSGAWSRTW*RSS*TSSSSC STSCSSSSSRSCGRPGGPLGARGVHITSCLNSC
		1		ļ		STSCSSSSRSCGRPGGFLGARGVIIIISCERVO
		1	i	Ì		MSSSTTSSTTSTF HEDIMTHYDRLVDE*ALNAGKQRYEKMISG
113	1463	A	1439	3	292	MYLGEIVRNILIDFTKKGFLLRGQISEMLKTR
1		}		1		GIFLTFLLSNFLIVCVLLFYVSFYLFQSCINFVL
	į					KQQAVPEPHSSTTTPQEQEQNWYGQDLLNLQ
114	1464	A	1463	1	396	QRTKVHLPGHKTGPAVAKDTPEPVKKEFTVP
		1	1			ATSQGP*SPFSEEPPLPPSNEEVPPTLPP*EPQS
	i	1		}		EDP*KNA*LKQMHAATTHWQQHQQHQVGC
İ		-				OVEGIMO
	J				2	ACSYPSMYWSCHWGVTOKRRAL*VYSFEEG
115	1465	A	1464	291	2	GRRKCGOYWPLEKDSRIRFGFLTVSNLGVEN
		ļ		Į.		MNHYKKSTLEILNPEVNPGFFFLTLWKQGEN
1		1	}	1		NVCN
	<del></del>		1465	667	337	LPPQRPA*TDSYSTCNVSSGFLAGQSHNIHLQ
116	1466	A	1405	1007		YWTKYQVWEWLQHFLDTNQLDANCIPFQEF
ļ	j	-				DINGEHLCSMSLQEFTRAAGTAGQLLYSNLQ
		1		ı		HLKWNGDSLFLCLSLPC
117	1467	A	1479	1	381	GTSGGPKRVLVTERFPWQNPLPVNRGQAQR
117	1407	1				VLGPSNSFQRVPLQAQKLVSSHKPGQNQKHK
}	- 1	-				QLQATSVPHPVCMPLNNTQKSKQPLPSAPEN NPEEELASDPNNEESL*RPWALEDFEIGRPLG
1	Ì			[		l e e e e e e e e e e e e e e e e e e e
				L		KGK TYLWL*GNPPFYEKNDGGLFELILRAKDEFNS
118	1468	A	1485	3	385	TYLWL*GNPPFYEKNDGGLFELLKARDLTNS PYWDDMSDSAKHFIRPLTGRDP*KPFPCDQPL
1	1	-		l		QHPWIEGHTCLDNNIHQAASEPINNNFAESKR
	1		1			NLAFLATGVVRHMRKLFMGANLEGPGPTVS
		1				
			1			H GTTSKHH*LARSLIRGPFDHDLKPNAATRDQL
119	1469	Α	1486	1	398	NIIVSYPPTKQLTYEEQDLGWKFRYYLTNQE
1		- 1				KALTKFLKWVNWDLPQEAKQALELLGKWK
				Į.	1	PMDVKDSLELLSSHYTNPTVRRYAVARLRQA
	Ì	- 1				DDEDLLMYL
					000	MGESPAV*GYEVI.AGMNSAGLSFGGGAGKY
120	1470	A	1497	3	999	LAEWMVHGYPSENVWELDLKRFGALQSSKT
		)			į	FIRHRUMEVMPLMYDLKVPHWDFQTGRQL
}		1				PTCPL VDRLDAOGARWMEKHGFERPKYFVP
1				İ		PDKDLLALEOSKTFYKPDWFDIVESEVKCCK
İ		1	1		1	FAUCVIDMSSFTEFEITSTGDOALEVLQYLFS
	1	1	1			
						NDI DVPVGHIVHTGMLNEGGGYENDCSIAKL
						NDLDVPVGHIVHTGMLNEGGGYENDCSIAKL NKRSFFMISPTDOOVHCWAWLKKHMPKDSN
						NDLDVPVGHIVHTGMLNEGGGYENDCSIARL NKRSFFMISPTDQQVHCWAWLKKHMPKDSN LLLEDVTWKYTALNLIGPRAVDVLSELSYAP

_					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del> </del> -		<del> </del>	1		MTPDHFPSLFCKEMSVGYANGIRVMSMTHT
						GEPGFMLYIPIEYRWGFTMLSTLVSNS
121	1471	A	1498	3	306	AQFLLVGWDHIL*LIVL*TNLTELGRTTCDQN
121	1		1		Į.	WPNSPDVLNHGCFYMQCLSKDCTIGYVSRE
		l				MLVAHTHTVEEHTGTHLQYVSWPDHSVPDD
		1	1			SSDFVEFEN LGLFSFVWTEVLEEPKDFSCETEDFKTLHCT
122	1472	A	1533	121	329	WDPGTDTALGWSKQPSQSYTLFES*VGSGYII
		ł	1	1		
					<u> </u>	DNFFLA DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE
123	1473	A	1547	111	408	RGHVEMIEKLTFLNLHTSEKDKGGNTALHLA
	}					AKHGHSPAVQVLLAQWQDINEMNEKQQTPL
	1	ļ	ŀ			HVAADRG
	1	1			1746	MITEDDDDKNTYGVALVWKKFOTOSLRLSDL
124	1474	A	1555	1	745	HRKSHI WRGIVSITLIEGRDLKAMDSNGLSDP
		1	1	1	1	VVKERI CHOKYKSKIMPKTLNPOWREQFDF
		ļ	1	1		HLYEERGGVIDITAWDKDAGKRDDFIGRCQV
	i	}				DLSALSREQTHKLELQLEEGEGHLVLLVTLT
	1	1				ASATVSISDLSVNSLEDOKEREEILKRYSPLKI
		ł				FHNLKDVGFLOVKVIRAEGLMAADVTGKSD
	1	ì				PECVVELNNDRLLTHTVYKNLNPEWNKVFIL
	1		ļ			*VAI VWKKFOTOSLRLSDLHRKSHLWRGIVS
		}				ITI IEGRDI KAMDSNGLSDPYVKFRLGHQKY
			Ì			KSKIMPKTLNPOWREQFDFHLYEERGGVIDIT
	1		1		1	AWDKDAGKRDDFIGRCOVDLSALSREQTHK
		1		1		LELOLEEGEGHLVLLVTLTASATVSISDLSVN
				Ì		SUFDOKEREEILKRYSPLRIFHNLKDVGFLQV
	]		1	}		KVIRAEGLMAADVTGKSDPFCVVELNNDRLL
1	-					THTVYKNLNPEWNKVFTL
125	1475	A	1556	57	509	GGPAPNSRYAEP*KNSLAMT*AHADCENYVA
123	14/3	1 11	1,000	1		CGGLDNICSIYNLKTREGNVRVSRELPGHTGY
	l	1				LSCCRFLDDSQIVTSSGDTTCALWDIETAQQT
İ				ĺ		TTFTGHSGDVMSLSLSPDMRTFVSGACDASS
	}		1	}		KLWDIRDGMCRQSFTGHVSDINAVS
126	1476	A	1592	3	178	KSEKSCVSSLAHFGTSCQRDYDAMVKLVETL
1.2						EMLPTCDLADQHNIKFHYAFALNR*ER
127	1477	A	1612	1	497	TESPLLVRPYLPYITKSELHAIMTAGFSTIAGS VLGAYISFGVPSSHLLTASVMSAPASLAAAKL
	1					FWPETEKPKITLKNAMKMESGDSGNLL*AAT
		1	1			QGASSSISLVANIAVNLIAFLALLSFMNSALA
		l				WVGNMFDYPQLSFELICSYIFMPFSFMMGVE
1				- [		WPDSFM
		l_			102	CCMNSKAQESVFKNVLCNPPALSEMPDVKA
128	1478	A	1619	286	486	EDEVDFRASSISEEVAVGSIAATLKMKQGPM
	-	1	ļ			TQAINR
1	1					PTRGALRYWIFGRFLCNIWAAVDVRCCTATI
129	1479	A	1627	1	395	MGLCIISIDRYVGVSYPLRYPTIVTQRRGLMA
1		-	1			LLCVWALSLVIYIGPLLGWRHPAPEDETICQI
					ŀ	NEEPGYVLFSTPGSFYLPLAIMLVMN*RVYRV
		į	1	}		AKTE
1				<u> </u>	166	DPRVRTKIVNRKTTIYEIQDKTGSMAVVGKG
130	1480	A	1638	2	466	ECHNIPCEKGDKLRLFCFRLRKRENMSKLMS
1		-		1		EMHSFIQIQKNTNQRSHDSRSMALPQEQSQHI
		į		1		KPSEASTTLPESHLKTPQMPPTTPSSSSFTKVT
		1				KDKDIK*LLFNLYSSVEILPEVLHLKT
						LAEGGDVFDCVLNGGPLPESRAKALFRQMVE
	1481	A	1651	607	3	AIRYCHGCGVAHRDLKCENALLQGFNLKLTD
131			1	1	1	- MKICHOCO AMIROPICONARDO COLINDED IO
131			1		i	ECEARIA DE SHREI SOTECGSTAYAAPEVLO
131						FGFAKVLPKSHRELSQTFCGSTAYAAPEVLQ GIPHDSKKGDVWSMGVVLYVMLCASLPFDD

SEQ ID SEQ ID With SEQ	
	id sequence (A=Alanine C=Cysteine, ic Acid, E=Glutamic Acid,
NO: 01 NO. 01 Inou IB NO. Degrames	alanine, G=Glycine, H=Histidine,
nucl. peptide   m	ine, K=Lysine, L=Leucine,
POHOE 1 SCU- 1 00011 1 100-1011	onine, N=Asparagine, P=Proline,
Seq- Renec	nine, R=Arginine, S=Serine,
lience	nine, V=Valine, W=Tryptophan,
minio della filipia	ne, X=Unknown, *=Stop codon,
	e nucleotide deletion, \=possible
popular	e insertion
sequence nucleotide	LWQQKGVSFPTHLSISADCQDLLK
PILEDU	MILRPSIEEVSWHPWLAST**KQWQV
I SNK VO	GGESKPKKKK
IVAKSI	LYCGCLFFLLQLAKNVGNNSFNDIM
132 1482 A 1656 150 48 LVAKSL	PSPKPTPSSDM*VFLIY*TYFGAWHV
VDAQ	0114 1155211
DYNIVI	LIQKLSDVP*ECQNNQL*KLTEICEKE
133 1483 A 1660 3 406 RKHIKL	KMDDQRPEKITEA*SKDKSPMEEEK
TEMIRS	YIQEVGRYIKRLEEAQSKRLEKLREK
HKEIRO	PILDEKPKGEGSSSFLSETCHEDTSWF
PNFTP	
DCSTUA	SARITIY*L*IILSNATEVDNNFSKPPP
FFPAGA	PPASSSSSSSSSSPPTVSTAPPLIPPPGF
PPPPGA	PPPSLIPTIESGHSSGYDSRSARAFPYG
NVAFPE	ILPGSAPSWPSLVDTSKQWDYYARSS
l l ssssss	SSSSSSPRDRDRER*RTREREREDHS
PTPSVF	NSDEERYRYREYAERGYERHRASRE
KEERHI	RERRHREKEETRHKSSRSNSRRRHESE
EGDSHI	RRHKHKKSKRSKEGKEAGSEPAPEQE
STEATP	PAE
135 1485 A 1673 1 417 PTRPVN	ISSQAFALVYYTLGALGGNLIAHMGL
GYRYW	AGIGVLQSCESALTHYRLVANHVAS
DISLTG	GSVVQRIRLPDEVENPGMNSGMLQE
DLIQYY	/QFLAEKGDVQAQVGLGQLHLHGGR
GV*QN	HQRAFDYFNLAA
136 1486 A 1678 525 9 ANTSLS	SSAAVSAVSPPPCRTSTATTLPPPMPSF
T FCVFPS	SPSMSPSPSEFLSCIASVSRVHSLSSSSS
GSSSTA	ASSLNFSAIMGSSSATASWVLSTASTPP
CPSALF	PSSPAQES*SLAASSSAWPVAGISPSGA GSASGAAKAPSPSWRCPSFRALFSLLD
SSSLSL	IQRKFDALRNSCTVITDLEEQLNQLTE
137 1487 A 1680 1 2999 AHRDE	NNQNFYLSKQLDEASGANDEIVQLRS
EVDUI	RREITEREMQLTSQKQTMEALKTTCT
MI FFO	VMDLEALNDELLEKERQWEAWRSVL
GDEKS	QFECRVRELQRMLDTEKQSRARADQ
RITESR	QVVELAVKEHKAEILALQQALKEQK
IKAESI	LSDKLNDLEKKHAMLEMNARSLQQK
I FTERF	ELKORLLEEOAKLOOOMDLQKNHIFR
LTOGL	QEALDRADLLKTERSDLEYQLENIQV
IVSHE	KVKMEGTISOOTKLIDFLOAKMDQPA
	PLOYNELKLALEKEKARCAELEEALQ
KTRIEI	RSAREEAAHRKATDHPHPSTPATARQ
OIAMS.	AIVRSPEHOPSAMSLLAPPSSRRKESST
PEFESR	RLKERMHHNIPHRFNVGLNMRATKC
AVCLD	TVHFGROASKCLECQVMCHPKCSTC
LPATC	GLPAEYVTHFTEAFCRDKMNSPGLQT
KEPSSS	SLHLEGWMKVPRNNKRGQQGWDRK
YTVLEC	GSKVLIYDNEAREAGQRPVEEFELCLP
DGDVS	SIHGAVGASELANTAKADVPYILKMES
HPHTT	CWPGRTLYLLAPSFPDKQRWVTALES
VVAGC	GRVSREKAEADAKLLGNSLLKLEGDD
	NCTLPFSDOVVLVGTEEGLYALNVLK
	THE PARTY OF THE P
NSLTH	VPGIGAVFQIYIIKDLEKLLMIAGEERA
NSLTH LCLVD	VKKVKOSLAQSHLPAQPDISPNIFEAV
NSLTH LCLVD KGCHL	VKKVKQSLAQSHLPAQPDISPNIFEAV .FGAGKIENGLCICAAMPSKVVILRYN
NSLTH LCLVD KGCHL ENLSK	VKKVKQSLAQSHLPAQPDISPNIFEAV FGAGKIENGLCICAAMPSKVVILRYN YCIRKEIETSEPCSCIHFTNYSILIGTNK
NSLTH LCLVD KGCHL ENLSK FYEID	VKKVKQSLAQSHLPAQPDISPNIFEAV .FGAGKIENGLCICAAMPSKVVILRYN

	00010	) (at	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	,			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	}	1	Ì	sequence		nucleotide insertion
	<del> </del>					YGRRSRTDDLKWSRLPLAFAYREPYLFVTHF
			}			NSLEVIEIQARSSAGTPARAYLDIPNPRYLGPA
	İ		1		j	ISSGAIYLASSYQDKLRVICCKGNLVKESGTE
	İ	ĺ		ĺ		HHRGPSTSRR*PASPLPQYQGQRAFLQGRRK
138	1488	A	1686	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV
		1 .				PLCCLGGAAGRL*ARSGKSGLRRRRAHAGPP PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS
	1	l .			1	CWTRGCQTTARTAAAAAAPGPAGRRPPGGA
			ļ	ļ	1	PONGSCAASASQEAAAPPPMCPPGRRWAVAS
		1	1			PONGSCAASASQEAAAFTIWCTI GIGGWYTTIG
			1			PPETRCPAAPGTRCRRLEAA  LPSMSNCTSCFRLQSRTES*IRQAGHLLGRNE
139	1489	A	1693	3	376	FIETKALGCAWFSLCYYLVLYFESSHKVDFVF
	1	1	1	{	1	IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR
	Ì					RWAGIAKGVGTQKIIGRVHLGEQKALGL
		1		<u> </u>		ERTNKFIKELIMDGKNLIAATKSLSVAQRKFA
140	1490	A	1704	3	376	HSLRDFKFEFIGDAVTDDERCIDASLREFSNFL
	ł					KNLEEQREIMVS*EGCKLISQLSRGKKIWIWK
	į	1	Ì		1	LVLVEVVKHLSLGTVVHCNGKMRFPEP
		İ			100	LITNKVFVARELSCLDVHLDSTGSTAVVADQ
141	1491	A	1743	1	362	DKLELELVLKGSYEDTQTSFLGTASAFRFHY
	1		1		Ì	MAAL*TELSGRLRSSKSNGWNGDNSTGYLTV
		}			l	PLRPLTIVKEVTMDVPAPNVRGLNWMG
		<u> </u>			406	NNPSTLPRGS*PMSPRTTMGRRRQRRREHKSS
142	1492	Α	1769	1	406	LSLASSTVGPGGQIVHTETTEVVLCGDPLSGF
			-			GLQLQGGIFATETLSSPPLVCFIEPDSPAERCG
	1		ļ	1	}	LLQVGDRVLSINGIATEDGTMEEANQLLRDA
		1		Ì	,	AT AHKVV
		<del></del>	1700	<del>-   1</del>	447	OMLRNGGDONTVPDYHFADRIRELL*PTEDQ
143	1493	Α	1789	1 1	447	KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA
	-{	1		1		NELCEVNRKGCTSGDPCLPYFCVQGCKLGQA
	Į.					SDFIAROGTLIQVPSSAGEVECYKICSCGQSGL
		Ì				LENCMEMHCMDLPTDTSALVR
	104		1814	<del>                                      </del>	404	PGRRERPRI SOAGTDSGS*VFPDSFPSAPAEPL
144	1494	A	1014	[ *	[ ,* .	PVFLOEPODAYIVKNKPVELRCRAFPATQIYF
İ	Ì	- }	į			KCNGEWVSONDHVTOEGLDEATGLRVREVH
	1	İ				IEVSRQQVEELFGLEDYWCQCVAWSSAGTTK
		ļ	İ			SRRAYVRI
145	1495	A	1827	26	448	XVEEKHADTWRSXCLSDFFFHAAKXLCXE*N
145	1493	1	102	"		CGDAISLSVGDHFGKGNGLTWAEKFQCEGSE
	1		Ì			THLALCPIVQHPEDTCIHSREVGVVCSRYTDV
		1		ł	İ	RLVNGKSQCDGQVEINVLGHWGSLCDTHWD
				1		PEDARVLCRQLNCGTAL
146	1496	A	1828	574	333	QHEGGDLRRRQLGEIQLTVRYVCLRAASAC*
140	1470	1	1020			SMAAET*HHVPASGADPYVRVYLLPERKWA
				1	1	CRKKTSVKRKTLEPLFDET
147	1497	A	1855	1	372	ERLVLTSEHCLVLTLFWPSWTYHTLLLSRQH
14/	1431	^	1.055	1		VRRLPKLTHAEHDHLASIMNKLLTNYDNLFE
						TSVTYSMG*HGAPTGSEAGANWNH**LHAH
	İ					YYPPLLRSDTVRKFMVGSQMLAQAQRDLTPE
1		1				Q
148	1498	-A	1879	568	7	LLSALDDKGGTQPSASFSNAPTIVCVTACPAG
140	1470	1	13//	1		IAHTYMAAEYLEKAGRKLGVNVYVEKQGAN
ì		- 1				GIEGRLTADQLNSATACIFAAEVAIKESERFN
						GIPALSVPVAEPIRHAEALMQQALTLKRSDET
	1			1		RTVQQDTQPVKSVKTELKQALLSGISFAVPLI
İ						VAGGTQVA*AV*RQGISSLHDVQVRTWNS
149	1499	$\frac{1}{A}$	1880	611	24	GLNSENALSNEAMERGWOCLRLFAERLQDIP
	」」はマフフ	1.0	1.555	1	1	PSQIRVVATATLRLAVNAGDFIAKAQEILGCP
149					i	VQVISGEEEARLIYQGVAHTTGGADQRLVVD

			- ara	D. distant	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
IO: of	NO: of	hod	1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence			ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
елсе	İ	ĺ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	!		į		sequence	/=possible nucleotide deletion, \=possible
	Į	1	1	peptide		nucleotide insertion
			<u> </u>	sequence	ļ	IGGASTEL VTGTGAOTT*LFSLSMGCVTWLER
					}	YFADRNLGQENFDAAQKAAREVLRPVADEL
	1	Ì			ì	RYHSWKEVRGASVTVQALQEIMMAQGMDE
	1	}	1			RITMEIWPVD
	1		<u></u>		1.50	GRVDFFHTDYRPLIRDSNNYVLDEQTQQAPH
150	1500	Α	1894	2	750	LMPPPFLVDVDGNPHPTKYQRLVPGRENSAD
			1	İ		EHLIPQLGYVATSDGEVIEQIISLQTNDNDERS
	1	1				PESSILDGMIRQLQQQQDQRMGADQDTIPRG
	}					LSNGEETPRRGFRRLSLDIQSPPNIGLRRSGQV
	1			1		EGVRQMHQNAPRSQIATERDLQAWKRRVVV
	1	1	ľ	1	{	PEVPLGIFRKLEDFRLEKGEEERNLYIIGRKRK
						TLQLSHKSDSVGLVSQSRPRTCRRKYP
			}		<u> </u>	GKTIQIQTTMQNKYKTVQKQYKTIPKNKKA
151	1501	A	1900	141	785	MEMQIKKQFQDTCKVQTKQYKALKNHQLEV
	1337	ļ		1		TPKNEHKTILKTLKDEQTRKLAILAEQYEQSI
	i	1				NEMMASQALRLDEAQEAECQALRLQLQQEM
	1	1	1			NEMMASQALRIDEAQEAECQALKIQEQQUIN ELLNAYQSKIKMQTEAQHERELQKLEQRVSL
		1	1		j	ELLNAYQSKIKMQ1EAQHERELQRELQRVID
		- {				RRAHLEQKIEEELAALQKERSERIKNLLERQE
		1				REIETFDMESLRMGFGNLVTLDFPKEDYR
152	1502	A	1915	2	377	LVRLLDTQRDGLQNYEALLGLTNLSGRSDKL
132	1302	1.				ROKIFKERALPDIENYMFENHDQLRQAATEC
		ì	1	i .	[	MCNMVLHKEVQERFLADGNDRLKLVVLLCG
						EDDDKVQNAAAGALAMLTAAHKKLCLKMT
	į.	]		ł		QVTT
153	1503	A	1921	1	237	AYQSLRLEYLQIPPVSRAYTTACVLTSAAVQI
153	1303	1	1,72.	\ -		ELITPFQLYFIPELIFKHFQIWRLITNFLFFVPFG
			ĺ			FNFLLYMIFLYT
154	1504	A	1928	2	354	EMVEGGEGKMCINTEWGGFGDNGCIDDIRTE
154	1304	1 ^	1,720	-		YDTEVDEGSLNPGKQRYEKMTSGMYLGEIV
	ĺ	[	-	1		RQILIDLTKQGLLFRGQISERLRTRGIFETKFLS
		ļ				QIESDRLALLQVRRILQQLGLD
	1505	A	1929	2	369	TEIAKIKMEAKKKYEKELTMFQNDFEKACQA
155	1505	Α.	1,72,	-	İ	KSEALVLREKSTLERIHKHQEIETKEIYAQRQ
				ļ	{	LLLKDMDLLRGREAELKQRVEAFESYQLELK
	Ì		ļ	Į.		DDYIIRTYRLIEDDRINIQISGHWQESP
	1506	A	1935	1	270	VTRKLPIFIVDAFTARAFRGSPAADCLLENEL
156	1506	A	1933	1	1 270	DEDMHOKIAREMNI SETAFIRKLHPIDNFAQ
					1	RSCEGI IWETPTTDLOILTSSILPSIL
		<del></del>	1036	584	305	T ESKVNINFKFRTKSPKPAESPOSATKOLDOP17
157	1507	A	1936	304	1 303	AVEVYDAGNHWCKDCNTICGTMFDFFTHML
1			1	1		NKKHTOGOFOKSSDFOKEELQQTFLPPERQG
L		_			423	TTHRI NVTAEPPCTSMPTYWMPDVPHRCTTA
158	1508	A	1939	1	423	NTCPVDI TDYCAONGFYCLVYGFLPYGSLEL
ł			ł			PI HOOTOACPPLSWPORLDILLGTARAIQFLE
		1			ļ	QDSPSLIHGDIKSSNVLLDERLTPKLGDFGLA
		- 1	ì		1	RFSRFAGSSPIQSSM
	1					HTSTARLLLHRGAGKEAVTSDGYTALHLAA
159	1509	A	1974	3	401	NGHLATVKLLVEEKADVLARGPLNQTALHL
				1		AAAHGHSEVVEELVSADVIDLFDEQGLSALH
1			Ì			LAAQGRHAQTVETLLRHGAHINLQSLKFQGG
1				]		
1						HGPAATLLR KFLKDLEKQYNKEEPHLSEIGSCFLQNQEGFA
160	1510	$\overline{A}$	1982	2	417	KELKDLEKU I NKEETALJEIUSCELUNGEUT
100	1310	' '	1	1		IYSEYCNNHPGACLELANLMKQGKYRHFFE
	ļ					CRLLQQMIDIAIDGFLLTPVQKICKYPLQLAE
ı		1		l		LKYTTQEHGDYSNIKAAYEAMKNVACLINE
1	1			1		KRKLESIDKIA
	1		1	I		T COLOR CDCCL EC A ESVAVISDIT VSSPDVK
	<u> </u>		1001	4	770	RETGSVSLSPSGLEGAESYAVSPILYSSPDVK
161	1511	A	1984	4	770	LWLETLQGQRHSHTGVKSTPGQSAAILMKLI SSHNASKTLNANNMETLIECQSEGDIKEHPLI

			1.000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:		location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	]=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutarnine, R=Arginine, S=Serine,
uence	j	}	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	İ	<b>!</b>	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		residue of	sequence	/=possible nucleotide deletion, \=possible
	Į.	i	İ	peptide		/=possible nucleotide detention, /-possible
	1	1	\	sequence		nucleotide insertion
	1		1			ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS
	1		1			PASDFSGALETDLKASLFDQPLSIICGDSDTLP
		· ·	ì		1	RPIQDILTILCLKGPSTEGIFRRAANEKARKEL
		í	1		ļ	KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP
		1	1		İ	RKLLSSDLFEEWMGALEMQDEEDRIEALK
162	1512	A	1986	864	501	LLNSGLFSAPDGSNLEMRLTRGGNMCSGRIEI
162	1312	1 ^	1700	00.		KFOGRWGTVCDDNFNIDHASVICRQLECGSA
		1		]		VSFSGSSNFGEGSGPIWFDDLICNGNESALWN
	1		[	ļ	}	CKHQGWGKHNCDHAEDAGVICSSKD
		ļ.,	<del> </del>	1	187	AVDLSIDESSLTGETTPCSKVTAPQPAATNGD
163	1513	Α	2001	419	107	LASRSNIAFMGTLVRCGKAKGVVIGTGENSE
}			i			FGDIINLSTFVVHS
1	i .					SLLCLFPGTSTVVCKPIVIETQLYVIVAQLFGG
164	1514	A	2012	284	597	SHIYKRDSFANKFIKIQAIEILKIRKPNDIETFKI
1	1		1			SHIYKKUSFANKFIKIQAIEILKIKKI INDILITIKI
ŀ		1	}			ENNWYFVVADSSKAGFTTIYKWERETGFYSH
	1	1		•		QSFTR
165	1515	A	2013	2	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY
103	1	'	1			NVDLPFMYSITYAAFAIIATLLMLNLLIAMMG
į	1	1	1	1		DTHWRVAHERDELWRAQIVATTVMLERKLP
			ŀ	i	}	RCLWPRSGICGREYGLGDRWILRVEDRQDLN
1	1		[			RQRIQRYA
166	1516	1 A	2019	2	927	CCQREGLGLKAVVQILLSHGRNGLPGEPASS
166	1310	1 ^	2017	1-	1	QGLSAASSTPVFHLALQIDSAPDNIDWVEMLF
		ì	1	1		NKNMVTERLONVMVLEQCFSDSSSLYRFLTY
1	1		)	ļ	1	SYLLAFNVWLLLAPVTLCYDWQVGSIPLVETI
	{		j	1		WDMRNLATIFLAVVMALLSLHCLAAFKRLE
	i		1			HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER
	l l	1	1	1		VLYMPSMGYCILFVHGLSKLCTWLNRCGATT
ł	ì		1	Ţ	İ	LIVSTVLLLLLFSWKTVKQNEIWLSRESLFRS
	,	1		1		GVQTLPHNAKVHYNYANFLKDQGRNKEAIY
	1		}	Į.		HYRTALNNKAWDYLCWRFRKTLTDLP
	<u> </u>	1			<u> </u>	AAASAASSLTVTLGRLASACSHSILRPSGPGA
167	1517	Α	2025	696	71	ASLWSASRFNSQSTSYLPGYVPKTSLSSPPW
	1		{			PEVVLPDPVEETRHHAEVVKKVNEMIVTGQY
	1		İ	l	Į.	PEAATEMENT OF ORKITEEDIN ICHELDIA
1		1	ł	ļ		GRLFAVVHFASRQWKVTSEDLILIGNELDLA
· I		1	1	1		CGERIRLEKVLLVGADNFTLLGKPLLGKDLV
1	ļ	j	j	1		RVEATVIEKTESWPRIIMRFRKRKNFKKKRIV
ļ			1	1	l	TTPQTVLRINSIEIAPCLL
168	1518	A	2046	2	366	HLQVAARVFMPLQAVDSAPKPLKGQAQAPQ
100	1.5.0	1	1	1	1	RLQGAARVFMPLQAQVKAKASKPLQMQIKA
				1		PPRLRRAARVLMPLQAQVRAPRLLQVQSQVS
1			1	ł		KKQQAQTQTSEPQDLDQVPEEFQGQDQVLR
1.00	1510	<del> </del>	2049	+	945	ONLEDREVLNGVOTELLTSPRTKDTLSDMTR
169	1519	Α	2049	1 '	1 - 3	TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI
				J	}	EDNSRSKREGLFHENECIVKINNVDLVDKTFA
		{	1	1		QAQDVFRQAMKSPSVLLHVLPPQNREQYEKS
		-		1	1	VIGSLNIFGNNDGVLKTKVPPPVHGKSGLKTA
		1		1	1	NLTGTDSPETDASASLQQNKSPRVPRLGGKPS
1		İ				SPSLSPLMGFGSNKNAKKIKIDLKKGPEGLGF
				1		TVVTRDSSIHGPGPIFVKNILPKGAAIKDGRLQ
İ				1	1	1 A A L KONOTION DALCOLOGIE A VA VILO GLA COLOGIA
						SGDRILEVNGRDVTGRTQEELVAMLRSTKQG
				1		ETASLVIARQEGHFLPRELVMFRSQSH
170	1520	A	2050	363	1	PVATHLTKILNSDEHAVVISSAKTLCETVKDF
1.0	1320	1.,		}	1	VAKVEKTYDKTLENAVVADAVASKCSVLNE
1						KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV
1		- 1	ļ			ESSSEESLGESKEQLGDDVTKPSSQKA
	1	1	j			IPSRPWLGRITGLDPAGPLFNGKPHQDRLDPS
	<del>-  </del> -	<del></del>	2000	120	1 675	I I SKI W LOKI OLDI AGI LI NGIG 11QDI GDI
171	1521	A	2055	139	675	DAOFVDVIHSDTDALGYKEPLGNIDFYPNGG
171	1521	A	2055	139	675	DAQFYDVIHSDTDALGYKEPLGNIDFYPNGG LDQPGCPKTILGGFQYFKCDHQRSVYLYLSSL

			000	Deediated	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
æq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	1		914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
		Ì		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	]		İ	peptide	}	nucleotide insertion
	1		1	sequence		RESCTITAYPCDSYQDYRNGKCVSCGTSQKE
	<del>                                     </del>				1	SCPLLGYYADNWKDHLRGKDPPMTKAFFDT
		ŀ		ļ		SCPLLGY YADNWADHLAGADEF WITH THE TOTAL
	ļ		}	ļ		AEESPFCMYHYFVDIITWNKNVR
172	1522	A	2056	3	361	LIQHKSAVEYAQSHLSLVSMCKESHKCSEPK
1/2	1322	^*	2000		1	MEWKVKIRSDGTRYITKRPVRDRILKERALKI
		}	1			KEERSGLTTDDDTMSEMKMGRYWSKEERKQ
	}	1		1		HLVRGKEQRRRREFMMRIRLKCLKES
	<del></del>	<del> </del>	2000	1	387	GTRIL SMOIPFYGFOPIRTSEHMAAAGVFALL
173	1523	A	2060	1 1	307	OAYAFLOYLRDRLTKOEFQTLFFLGVSLAAG
	ļ	ļ	!			AVELSVIYLTYTGYLAPWSGRFYSLWDTGYA
		1	1		1	KIHIPIIASVSEHQPTTWVSFFFDLHILGCTFPA
	ł.	1			į	l c
		Ì				LLMGPKAKKSGSKKKKVTKAERLKLLQEEEE
174	1524	A	2071	74	443	RRLKEEEEARLKYEKEEMERLEIQRIEKEKW
		1		1	Į	HRLEAKDLERRNEELEELYLLERCFPEAEKLK
	ļ		1			QETKLLSQWKHYIQCDGSPDPSVAQEMNT
	1		1	1		QETALLSQWAFFTQCDOSTDF3VAQEMAT
175	1525	A	2083	139	486	AALTWSQPQEFWPMEMQPIVTDMVTVHWV
173	1525	1	1			AESSTVGWLCALFRVTHVGVGATGHGVVCG
		1				RRVLCGLPLPSPAPMPIMSLPEGESRKEREVQ
		1	ì		ł	RLQFPYLEPGHELPATTLLAFLAAV
	1526	A	2092	3	587	EGSVNFKFGVLFAKDGQLTDDEMFSNEIGSEF
176	1526	A	2092	1 3	""	FORFLNLLGDTITLKGWTGYRGGLDTKNDTT
		{		-		GIHSVYTVYQGHEIMFHVSTMLPYSKENKQQ
		}	Ì	i	į.	VERKRHIGNDIVTIVFOEGEESSPAFKPSMIRS
ŀ			- 1			HETHIEALVRYNOONDNYRLKIFSEESVPLFG
	ļ	1	1	1	1	PPLPTPPVFTDHQEFRDFLLVKLINGEKATLET
	}				1	PCI
	_l				427	GKGOVSLEGRPHRGPLCLGSWWPGSRVPGC
177	1527	Α	2103	44	427	CDGAWLAWACWVFGNDFPSPASAACSALLG
	1	1	Ì	İ		CSVSTACLCVPLCSGSPLAPFRRTAALQEGLR
1		1	\ \	}		RAVSVPLTLAETVASLWPALQELARCGNLAC
1	1	İ	1	<b>\</b>		
1	1		1			RSDLQ ALQSTLGAVWLGLLLNSLWKVAESKDQVFQ
178	1528	Ā	2104	12	409	PSTAASSEGAVVEIFCNHSVSNAYNFFWYLHI
176	1520	1	1	1		PSTAASSEGAVVEIFCNHSVSNATNET WIDIN
1	1	1	4			PGCAPRLLVKGSKPSQQGRYNMTYERFSSSL
1	l	- !			ļ.	LILQVREADAAVYYCAVEVPNTDKLIFGTGT
		)	1	1		RLQVFPNIQNPD
			2111	+1	312	PTRSSTRPPSLFVHASAKGGEKEEGDDGHYL
179	1529	Α	2111	1.	<del>-</del>	MRTESHTGLKKGGNANLVFMLKRNTEPKKG
1		ľ			1	SYHFDLERLRAAHILFEREQEHLAPGGISMPL
	1	1				PPPI PLPACLG
					1266	TSIKRAJETTDVTRSFGWDSSEAWQQHDVQE
180	1530	A	2116	3	366	LCRVMFDALEQKWKQTEQADLINELYQGKL
				1		KDYVRSLECGYEGWRIDTYLDIPLVIRPYGSS
		1		Į.		QAFASVVCTFHLTACVSLHRIHNSTVV
1		1				YGLGAHFGRLFIQAGINENDFYDGAWCAGR
181	1531	A	2117	2	386	YGLGAHFGKLFIQAGINENDF IDOA WCAGK
101	1 ,,,,,	1	1	- L -		NDLQQWIEVDARRLTRFTGVITQGRNSLWLS
ì	1	l				DWVTSYKVMVSNDSHTWVTGKNGSGDMIF
						GNSEKEIPVLNELPVPMVARYIRINPQSWFDN
ļ	1	l				GSICI
			2122	$\frac{1}{1}$	493	RTKTDVYILNLAVADLLLLFTLPFWAVNAVI
182	1532	A	2123	1	773	GWVI GKIMCKITSALYTLNFVSGMQFLACIS
		[				DRYVAVTKVPSOSGVGKPCWIICFCVWMAA
						I I SIPOL VEYTVNDNARCIPIFPRYLGTSMKA
						IQMLEICIGFVVPFLIMGVCYFITARTLMKMP
1	-	ļ				
		ĺ		1	<u> </u>	NIKIS NIKIS AFRAMENTUICCI LAFCIGI IFVO
L	1522	$\overline{A}$	2140	3	561	RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF
182				1		
183	1533		l			VYGIDKFMEDLKDMLGFAPSRYYYYMWKY

					Ch. Parkers	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-A coartic Acid E=Glutamic Acid,
iO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide location	corresponding	IzIsoleucine K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq- }	uence	ĺ	09/496	ng to first	acid residue	O=Chitamine, R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T=Threonine V=Valine W=Tryptophan,
1				residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
					Sequence	/=possible nucleotide deletion, \=possible
	ı İ		\	peptide		avalentide insertion
				sequence		CPL MI I SI LIASVVNMGLSPPGYNAWIEDKAS
				ĺ	<b>\</b>	FEET SYPTWGLAVCASLDVFAILPYPVAFIGK
			ļ		1	PEST IDDGAGPECSAAYTTTGCRTPYL
				<u> </u>	538	LUCI TVA A ADRGOPPOSSVVPVTVTVLDVND
184	1534	A	2145	3	230	NIDDVETDASYRVTVPEDTPVGAELLHVEASU
	į		İ	ł		ADDCDHGI VRFTVSSGDPSGLFELDESSGILK
	ļ	ŀ		ł		I AUAI DOFTOARHOLVVOAADPAGAHFALA
		}		i		PVTIEVQDVNDHGPAFPLNLLSTSVAENQPPG
	ļ	1			1	TI VITTI HAIDGDAGAFGRLRYHL
					<u> </u>	I DE LE DEMENYNIENE YILKOVAATYIKLUW
185	1535	A	2151	2	671	PKNNFNGSLVQASYQHEELRREVIMLACSFG
	"	l	1		1	NEUCHOOASTI ISDWISSNRNRIPLNVRDIV I
						CTCVGLI DEDVWEFTWMKFHSTTAVSEKKIL
		l			1	I EAT TOSDDRNI LNRLLNLSLNSEV VLUQUAL
	1	1		ĺ		DVIIHVARNPHGRDLAWKFFRDKWKILNTRI
	}			[		ROKTLEFDFAEPLILAFPIILYTAIDNPPLVREH
	1	1	1	1	l	
	ļ	!				GPMCDKHSAFAEKFHAGFIDYIVHPLWETWA
186	1536	A	2153	2	400	THE AT BO A ODIT VIT FONROWVDSMIPQSPSPP
100	1.020	1		1		LDEQNRDWQGLLENLHVELTLDEEDSEGPEK
	1	1 .		1	1	EGEGQTYFTSSKTLCGIVPQNTDSLGETGIHIC
	1	1	Ì	1		
	1					AHDKSP FNCFRVASDSFLENSSLLIMILFLRNATQEFIIR FNCFRVASDSFLENSSLLIMILFLRNATQEFIIR
187	1537	A	2158	227	442	PGAVAYTCNPSTLGGWGGWITRSGVRDQPG
107	133.	1	1	(		OUCCEPS
						QHGGTPS AHLGGAWLTQRSLGSWAAPGPARAAKEVVA
188	1538	A	2167	3	486	CIPQNQKMNIWRMKTSKHLQLLSFVLGAVSP
100	1330	1		ł		AVVVPYMMVLQENGYGVEEGIPTLLMAASS
	1	ţ	· ·			MDDILAITGFNTCLSIVFSSGCARSSGSRNSKS
	1	1	- }			LRTPLGTICEGCDDSSIFSHLDHSSKWSSTYG
<u> </u>	İ	ŀ		İ	l	
		1				HSGA EFLSSNQITQLPNTTFRPMPNLRSVDLSYNKL
189	1539	A	2168	2	412	QALAPDLFHGLRKLTTLHMRANAIQFVPVRII
107	1333			1		QDCRSLKFLDIGYNQLKSLARNSFAGLFKLTI
İ	ì	1	ļ	i i		LHLEHNDLVKVNFAHFPRLISLHSLCLRRNK
	ı	1	-	l l		AIVVSSLDW
		l	-			MRLNQNTLLLESFGXXRPYTSEHAPTYHQW  MRLNQNTLLLESFGXXRPYTSEHAPTYHQW
190	1540	A	2179	64	399	MKADELLRWTTSEPLTLEHEYAMQRTWLED
190	1540	1			İ	AYECTFIVLDAEKRHAQPGATEESCMVGDVI
	}		į.	1		AYECTFIVEDAERRIAQI GATEBOOTA
ļ		-		1		LFLTDLEDLTLGEIEVLIAEP CLDRAAGIRHERNVIYINETHTRHRGWLARR
101	1541	A	2190	1	469	CLDRAAGIRHERNVIYINEI HI KAKO WLAIG LSYVLFIQERDVHKGMFATNVTENVLNSSRV
191	1.541	''				LSYVLFIQEKD Y DROCK A OOOK A VNK VK KK
1		-				QEAIAEVAAELNPDGSAQQQSKAVNKVKKK
	1					AKRILQEMVATVSPAMIRLTGWVLLKLFNSF
1		1	-			FWNIQIHKGQLEMVKAATETNLPLLFLPVHR
1	1	1	1	ļ		SH COLORESCE ALARI COLOR
L	1.5.5	<del>-  </del>	2197	26	157	PSKXGGIRLLLTGTQLYGRFGSAIAPLGDLDI
192	1542	A	219/	120	1	DOVNGEGREEPY
			2226	- 2	383	EVERNSIWRSI FSTMDLGDIGFYTYKILQALS
193	1543	Α	2236	1 2	700	VTUCK CIMHR DVKPLNILCNSPRNK VILAU W
1	1	1				CLAFFVHPMRKYSVHVATRYYKSPEILLDY
		1				YYDYSLDIWAVGVILLELLTLKLHVFEGGD!
İ		j	]			FO
į					400	PKGVGK MPTSEGRPGOERSDWVTSYKVMG
194	1544	A	2241	105	409	NOCHTWYTYKNGSGDMIFEGNSEKEIPVLNI
	Ì	- 1		Į		LPVPMGARYIRINPQSWFDNGSICMRMEILG
	{	- 1		1		DI POPNNY
į						MGVASDWTKRIEYOPGSGSMPLFPSIHLETC
	1545	A	2245	-11	672	GAVSSLQIVTELQTNYIGKGCDRETYSEKSL
195	1545	1.7		1		CAVEST OIVITE OF NATIONAL TREESE

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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	~ - \	Met	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
U	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
icl-	peptide		in		corresponding	1=Isoleucine K=Lysine, L=Leucine,
tide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
q-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
nce	ļ		914	ng to first	,	T-Threonine, V=Valine, W=Tryptophan,
1				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
}			<b>)</b>	residue of	sequence	/=possible nucleotide deletion, \=possible
{	i		<b>i</b>	peptide		nucleotide insertion
1			1	sequence		KLCGASSGIIDLLPSPSAATNWTAGLLVDSSE
						MIFKFDGRQGAKIPDGIVPKNLTDQFTITMW
1			İ	}	İ	MKHGPSPGVRAEKETILCYSDKTEMNRHHY
ľ	1				1	MKHGPSPGVKAEKETILCTSDKTEINTIGHT
ì		}	,	1		ALYVHNCRLVFLLRKDFDQADTFRPAEFHW
1		ļ	1			KLDQQALAKVDGQPGKSITRQLQEMPVTIQG
1		ļ	1			ISLKPS
		ļ	2256	i	396	FRGTPVSGLTNRDTLAVIRHFREPIRLKTVKP
96	1546	Α	2230	1 *	370	CKANKDI BHALSTOLOKOSIDHKTAGATKD
	ļ	1	ł			NI VI RTIPCTTRAPRDGEVPGVDYNFISVEUR
	1	}	1			KALEESGALLESGTYDGNFYGTPKPPAEPSPF
	1	-	-	1		OPOPV
	ļ		1			OLAJEIGVRALLEGVEVETEFLDPFORVIQPEE
97	1547	A	2259	43	594	DIT VENDI GOSDNIPTRLMFAISFLIPLAVICY
-		1	1			VKIIRRTDKTEIKEAFLAVSLALALNGVCTNT
		1				KLIVGRPRPDFFYRCFPDGVMNSEMHCTGDP
		l	1			DLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKI
	1	1	1			HCFTESGRGKSWRLCAAILPL
	1			Ì		TCTTVVVIPRMLVDFLSESKTISLPECATQMF
198	1548	A	2275	3	404	TCTTVVVIPRMLVDPLSESKTISLI BOTTQIA
170	1340	1				FLGFASNNCFIMAAMSYDRYTAIHNPLQYHT
	l	1		1		LMTRKICLQMMMASWMVGFLFSLCIIVTVF
	1	ì	]			LSLCDLNTIQHYFCDISPVVSLACNYTFYHEN
	1	1	Ì			AIFVLSA
	- <del></del>	<del></del>	2315	$+_{i}$	375	LTQMFFIHALSAIESTILLAMAFDRYVAICHP
199	1549	A	2313	\	1 3 / 3	RHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLI
	ĺ	1			1	KRI AFCHSNVLSHSYCVHQDVMKLAYADII
	ļ					PNIVVYGLTAILLVMGXDRMFISLSYFLII
		1			409	DRIVEROORKMSFFFKTELGEKLVTKFLFETD
200	1550	Α	2334	2	409	COODING DODOLKKKAPFTNKKLKAHQIPV.
	1	1	Ļ			THE VOVATION ASMOVOAYNGGNANPREANN.
•	Į.	1	l l			EEEDEEDEYDYDYESLSDDNILEDRPENKSC
			{	}		DOI OFFYKEEM
		-	l		_	ISWEAQIAEIIQWVSDEKDARGYLQALASKM
201	1551	A	2350	3	512	TEELEALRSSSLGSRTLDPLWKVRRSQKLDM
20.	1	1	}	į.		SARLELQSALEAEIRAKQLVQEELRKVKDAN
	<b>\</b>		١	1		LTLESKLKDSEAKNRELLEEMEILKKKMEER
	1		ł			FRADTGKLMLCDSALFEYKYFSNECFYFLFI
	}	- }	- 1	İ		FRADIGKLMICOSALIE IKII BIYOO II 21 -
	1		ļ.			LIVTLEAPTEFQIQY
200	1662	A	2351	1	1003	PSSYSSDELSPGEPLTSPPWAPLGAPERPEHL
202	1552	1	1233.	1		NRVLERLAGGATRDSAASDILLDDIVLTHSL
	1		1			LPTEKFLQELHQYFVRAGGMEGPEGLGRKQ
	}		1			CLAMLLHFLDTYQGLLQEEEGAGHIIKDLYI
	1		ł			T TANK DEST VOGT REDTT REHOLVET VELKIR
	1		ļ			ENOPPSKOVKPLFRHFRRIDSCLQTRVAFRO
		}	1	}		DETECTOVIMPHISYVTIRSKLSASVULLUS
			1			TEVI OVSEFPAGREDSLILVAVSSSGEKVLL
		1		1		DTEDCVETALGINSHLEACTRUSYEALVELE
		!		}		EIQVSPGDTEIHRVEPEDVANHLTAFHWELI
[		1			i I	CVHELEEVDYVEHGE
1		-				NNLNCAEPLFEQNNSLNVNFNTQKKTVWL
203	1553	A	2361	2	403	GYRPVGSIPLWLQNFVRILLNEEDMNVIVVI
		İ	1	1	İ	WSRGATTFIYNRAVKNTRKVAVSLSVHIKN
1		ĺ		I		WSKGATITITINKAYKITIKAYA 1555 TITU
1		1				LKHGASLDNFHFIGGSLGAHISGFVGKIFHG
1		1			ļ	LGRITGLDP
- 300	1554	-	2390	280	476	SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSP
204	1554	A	2370	200		AGSRLGAMRRCAREMDATPMPPAPSCPSEI
1	1		1	1	:	ĺΤ
]		1	1	)		AAVALRDISWQQPYPMDFYAGSSLGPWTV
				E 42	745	AAVALKDIS WQQI II WIBI I II GOODOO
205	1555	A	2400	543	745	HGQDRRPHAPGRPARGKVQEGSARPPSAV

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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spertic Acid, E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	ļ	in	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-	1	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496 914	ng to first	acid residue	O=Ghitamine R=Arginine, S=Serine,
enœ		1	914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
		}		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
		ì	Ì	peptide	,	/=possible nucleotide deletion, \=possible
	}	1		sequence		nucleotide insertion
	1556	A	2406	122	485	DLSPDSREDHPQGHRRLLPKRPVRGSLMPGH
206	1226	^	2400			THHPCPVSSTTNDTPDQIWVSVGSLRMGTGG
		1	}	İ	İ	MGANASTSPRCWDLSSGNKKWIIQVPILASIV
	1	1		1		ESRGGLLATGVGGMCACVPRNQPLTGT
202	1557	A	2409	289	418	LWTLYRHKQQVQHNHSNRLSCRPSQEDRAT
207	1337	] ^	2407	1	l	HTIMVLDKENTLS
200	1558	+A	2413	64	492	VQGTGXXFIAFTEAMTHFPASPVWAGMFFL
208	1336	1 ^	2.,,	1		MLINLGLGSMIGTMAGITTPIIDTFKVPKEMFT
		1	Ì			GGCCVFAFLVGLLFVQRSGNYFVTMFDDYSA
			1		l	TLPLTLIVILENIAVAWIYGTKKFMQELTEML
	1	1		i		GFRPYRFYFYMWKFVSP
209	1559	A	2417	3	877	EKERLLDEWFTLDEVPKGKLHLRLEWLTLMP
207	1225	1"	1		1	NASNLDKVLTDIKADKDQANDGLSSALLILY LDSARNLPIRYKTNEPVWEENFTFFIHNPKRQ
						LDSARNLPIRYKTNEPY WEENFIFTHING INCOME.
	ļ	}				DLEVEVRDEQHQCPLGNLKVPLSQLLTSEDM TVSQRFQLGNSGPNSTIKMKIALRVLHLEKRE
	1	l	{	1		RPPDHQHSAQVKRPSVSKEGRKTSIKSHMSG
		- [	1	1		SPGPGGSNTAPSTPVIGGSDKPGMEEKAQPPE
		į				AGPQGLHDLGRSSSSLLASPGHISVKEPTPSIA
		ł	1		<b> </b>	SDISLPIATQELRQRLRQLENGTTLGQSPLGQI
						QLTIP
	1	Ì				REFAASDLEPFIPTDQPISPEAITQPSCIKRQRA
210	1560	A	2422	35	456	AGNPGSLAATIDHKPCSAPLEPKIQASRNQRV
			١,			GAVRAAESLTDIAEPASPQVHETPIDASQTQK
			Ì		l	VEPASKSRFTPELQAKVSHSRERALSTMDATI
				l l		UHAOPORGEG
					764	RRYSOKLIOHTACOLLRTYPAATRIUSSNPNP
211	1561	Α	2431	1	/04	I MEWLHGIOLVALNYOTDDLPLHLNAAMFE
	1	-	1	}	1	ANGGCGYVLKPPVLWDKNCPMYQKFSPLEK
	ĺ	[	ĺ	1		DI DOMDPAVYSLTIVSGONVCPSNSMGSPCII
	1		1		1	VDVI GMPLDSCHFRTKPIHRNTLNPMWNEQ
		-		- {		LEHVHEEDLVFLRFAVVENNSSAVTAQKIIPL
ı	}	- (		1		KAI KRGYRHI OLRNLHNEVLEISSLFINSKKA
			1	İ		EENSSGNTMSASSMFNTEERKCLQTHRVTVI
		- 1		- 1		CVPG
			2436		411	GIRGTTGHLGCPINDDPSLTLTVSWVMEDKP
212	1562	Α	2430	1 *	1	VICNICTEREDDSLITEAVAKRDHVSDTCGAC
	1	Ì	1			TOI DHNI DKGYLTVLGEOATPINKLUALEN
	1		{			RANRTRDLELTYLAERIVRLTWIPGDANNA
Į		1		1	}	TDYDCOIEEHO
			2445	<del>-   1</del>	1294	MSSIGCI WVSRSSOIDGLTAEKSGPEKPHGT
213	1563	Α	2443	1.	} === .	WI MOET HOKEOTI ELL VI EOFLSILPEEL QIW
1		1		1	1	OOHNPESGEESVTLLEDLEREFDDPGQQVPA
1					1	POGPAVPWKDLTCLRASOESTDIHLQPLKIQ
1				}		LKSWKPCLSPKSDCENSETATKEGISEEKSQ
		İ	{		1.	I DOEDSERGISEHESNLVWKOGSATGEKERS
			}	- [		SOCGSESOVIETNKSLGKRULYDEAERCLIL
			- [		1	TOSIMOOK VPPEERPYRCDVCGHSLKQHSSL
						OHORIHTGEKPYKCNOCGKAFSLRSYLIIHQ
				}	1	TUSCER AVECSECGRAFNOSSALIRHRRIHIT
1					\	EK A CK CNECGK AFSOSSYLIIHQRIHI GERP
1						FCMECGKTESOSSKLIRHORIHIGERPYEUNI
-	1	1		1		CGKAFRQSSELITHQRIHSGEKPYECSECGK
		1	{		1	FSI SSNI JRHORIHSG
			2461	$-\frac{1}{1}$	615	GIPGSTISSSRNIFLEDDLAWQSLIHPDSSNIP
	1564	A	2401	1		STRI VSVOEDAGKSPARNRSASITNLSLDRS
214	1			1	1	I more more inno AND TVV/PTCTTEDERKI
214	}		ì			SPMVPSYETSVSPQANKTTVKTETTEDEIGG
214						SPMVPSYETSVSPQANRTYVRTETTEDERKI LDSVQLKDLWKKICHHSSGMEFQDHRYWL THPNCIVGKELVNWLIRNGHIATRAQAIAIG

TO ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID IO: of	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
iucl-	peptide	Lou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			l	amino acid	of peptide	V=Tyrosine X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		musleatide insertion
		<u> </u>		sequence		AMVDGRWLDCVSHHDQLFRDEYALYRPLQV
						I PRIVICOLECSKLIL
		<u> </u>	2464	1 3	2932	GPGVRSSODGMADVFVHLRTAWPRCSFISGQ
215	1565	A	2464	3	2732	UCPGRHGRRVCSSODSMADVFVHLKTAWP1
						CSLISCOHGPGESVSYEDDDIPAPASLLHVNA
	1		1			A ADAI TNPTAPVI CTAPNNTAOKEK VPSGMK
	1					QRPAGVRISSRTPDLTCAVSTHSTVPGVRISSC
		1		1		TPDLTCAVSIHSTVPSVCISSCTPDLTCAVSTH
				1		STVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
		1	1			TPDLTCAVSIHATVPGVRISSCTPDLTCAVSIH
	}	ł	ł	1		ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR TPDLTCAVSIHSTVPGVRISSCTPDLTCAVSIH
				}		ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
		1				TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
			İ	{		ATVPGVRISSCTPDLTCAVSIHATVPGVRISSC
		1		1		TPDI TCAVSIHATVPGVRISSRTPDLTCAVSIH
		I				ATVPGVRISSCTPDLTCAVSTHSTVPGVKISSK
		-	-	}		TPDI TCAVSIHATVPGVRISSCTPDLTCAVSTI
						STUPGURISSRTPDLTCAUSIHATUPGUHISSC
		}	]			TPDLTCAVSTHSTVPGVRISSRTPDLTCAVSIH
		1				STVPGVCISSRTPDLTCAVSIHSTVPSVHISSCI
	1			į		PDI TCAVSIHSTVPGVRISSRTPDLTCAVSTHS
		1	-	]		TVPGVHISSCTTDLTCAVSIHATVPGVHISSCT
t				1		PDLTCAVSTHTTVPGVRISSRTPDLTCAVSIHS
		-				TVPGVRISSCTPDLTCAVSTHSTVPGVRISSRT
ł		1			Í	PDLTCAVSTHLTVPGVRISSRTPDLTCAVSIHATVPGVRISSRT
						PDLTCAVSIHATVPGVHISSCTPDLTCAVSTH
}						TVPGVRISSRTPDLTCAVSIHSTVPGVHISSCT
l	ĺ	1		Ì		PDLTCAVSTHSTVPGVHISSCTPDLTCAVSTH
	İ					STVPGVHISSRTPDLTCAVSIHATVPSVHISSC
ŀ		}				TPDI TCAVSIHSTVPGLLTSVSQTSTG
					114	ERTKSYRKGSYRCIVSEWIAEQGNWQEIQEK
216	1566	A	2477	1	414	AVEVATOVIOPTVLRAAVPKNVSVAEGKELI
		1	}			I TONTTOR ADDVRPEVTWSFSRMPDSTLPG
		l	\	1		RVLARLDRDFLVHSSPHVALSHVDARSYHLI
ŀ	-					VDDVSKENSGYYY
			2480	2	460	CRILCEGPORFEEYEYLGYKAGLYEAIADHY
217	1567	A	2480	-	1.55	MOVE VCOHECVRELATRPGRLSPLENFLPLH
1	1	1		1		DVI OF A YYRVGEY VKALECAKAYLLCHPDL
		Í		1		FDVLDNVDYYESLLDDSIDPASIEAREDLIM
			1			VKRHKLESELIKSAAEGLGXSYTEPNYW
219	1568	A	2483	140	383	AFSSPHPSPAPQFPECGFYGLYDKILLFKHDP
218	1308	^	1 2,03			SANLLQLVRSSGDIQEGDLVEVVLSASATFE
1						LQIRPHALTVHSYRAP
219	1569	A	2489	3	428	SSRLVLLAGAAALASGSQGDREPVYRDCVL
219	1309	'`	-			CEEQNCSGGALNHFRSRQPIYMSLAGWTCR DCKYECMWVTVGLYLQEGHKVPQFHGKW
1	1	}				FSRFLFFQEPASAVASFLNGLASLVMLCRYR
}						FYPASSPMYHTCVAFAWVS
						MDGEAVRFCTDNQCVSLHPQEVDSVAMAP
220	1570	A	2498	1	1297	APKIPRLVQATPAFMAVTLVFSLVTLFVVDF
						HHFGREAEMRELIQTFKGHMENSSAWVVEI
					!	MLKCRVDNVNSQLQVLGDHLGNTNADIQM
					j	KGVLKDATTLSLQTQMLRSSLEGTNAEIQRI
1		1	1			KEDLEKADALTFQTLNFLKSSLENTSIELHV
		1				CDCI ENANSFIOMLNASLETANTOAQLANS
						IKNANAEIYVLRGHLDSVNDLRTQNQVLRI
1	1	1	1	1	1	LAND THE PROPERTY OF THE PROPE
İ	)	l l	1			LEGANAEIQGLKENLQNTNALNSQTQAFIKS

PCT/US01/03800

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in i	nucleotide	location	I=Isoloucine K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	\		914	ng to first		T=Threoning, V=Valine, W=Tryptophan,
	} .		-	amino acid	of peptide	V=Tyrosine, X=Unknown, *=Stop codon,
	1			residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
	ļ	_		sequence		FDNTSAEIQFLRGHLERAGDEIHVLKRDLKM
	<u> </u>		1			VTA OTOK ANGRI DOTDTOIOVFK SEMENVN
	1	l		1	1	TI NACIOVI NGHMKNASREIOTLKOGMKNA
	Į.	)			ł	SALTSOTOMI DSNI OKASAEIORLRGDLENI
	l .	l	}	ļ	i e	I V AT TAKETOOFOSRI KTLHVVITSOEQLQKIQ
	1	ļ				RVRLNNDGLSPLMMAAKTGKIGIFQHIIRREV
221	1571	A	2501	3	500	TDEDTRHLSRKFKDWAYGPVYSSLYDLSSLD
	{	1				TCGEEASVLEILVYNSKIENRHEMLAVEPINE
	ļ	1		1		I I DDK WRKEGAVSFYINVVSYLCAMVIFILI }
	1	ì		1		AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFT
		1				GVLFFFTN
	j	}		l		DAHCQRKLAMQEFMEINERLTELHTQKQKL
222	1572	A	2508	3	395	ADLIVEDKEFEVDLVMOKVESLROELKKILK
				1		AVVELEVHTEALAAEASKDRKLREQSEHYSK
	ļ	)		ļ		QLENELEGLKQKQISYSPGVCSIEHQQEITKL
1		1	1			VITOLEKKS
	1	1			<u> </u>	NDPAIISNFSAAVVHTIVNETLESMTSLEVTK
223	1573	A	2544	2	412	MVDERTDYLTKSLKEKTPPFSHCDQAVLQCS
	(	1				EASSNKDMFADRLSKSIIKHSIDKSKSVIPNID
1	}	}	Ì			KNAVYKESLPVSGEESQLTPEKSPKFPDSQNQ
ł		1	Ì			I TUCCI SAA
l	1	1				CAST CEIST AFT VI TELIDS CRES YPER PHELSM
224	1574	A	2552	401	1	CYNIYSIAYIVRLTVGRERISCDFEEAAEPVLI
	'			1		QEGLKNTGCAIIFLLMYFFGMASSIWWVILTL
	1					TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA
İ	1	}		]		W
1	-	Ì				MCADKERREKGEEEGEGEKDGDEDEKEEEKE
225	1575	A	2563	724	1	GI GEFFEKEAGKKKKKOEEKEKEKGAVYSK
		,				VADICKNINGGSORVLEKHWISFLKARLNU
						L CVDCDSFFVFDVI OSITDIIOINGIPI VVGVFII
1	1	}			i	OI NOTING A VICA FSMDDIEK VFK GREKEUK I P
	1	1	}			DSVWTAVPEDKVPKPRPGCCAKHGLALAYK
	l l	1		1		TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFT
	ŀ	-	1	1	İ	VTDVRVRI TAISVDHSAGPYH
	} _	l		<del>                                     </del>	3	FCVL EVYGNYVGDVMNFEMAAEMAQEVAIP
226	1576	A	2571	449	,	TRIVITIDDISSSPIEDRDGRRGVAGNIFILA
j		1	1	1		A GAACDROMST FACEAVTRKANKKI Y IMG
						VALEPCSLPOTRRHNFEIGAEEMEIGMGINGE
	1	1		1		DGVIDEKMMPADAIVDHIMDKIFS
			<del></del>		1197	VI SDI CI FYYRDEKEEGILGSILLPSFQIALLIS
227	1577	A	2575	3	117/	EDUINBRYAFKAAHPNMRTYYFCIDIGKEM
		1				EL WAK AMI DAAL VOTEPVKRVDKITSENAP
		1	Į.	]		TVETANIPAIUR VI IKPEIONNOKNKEMSKIEE
	]	1	- 1	l.		
İ				l		LVVALEAEKVGFOKDGODRPLTKINSVKLNSL
ļ						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL BSEVESGSACPAOTVHYRPINLSSSENKIVNVS
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEOWIKIOKGRGHEEETRGVISYOTLPRNMPS
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS LPA OIMARYPEGYRTLPRNSKTRPESICSVTP
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI
						KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK
778	1578	A	2583	3	330	KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK LPFLGLGSVLPQGMVMASPEMNPTICSVFEA
228	1578	A	2583	3	330	KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK LPFLGLGSVLPQGMVMASPEMNPTICSVFEA
228	1578	A	2583	3	330	KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK  LPFLGLGSVLPQGMVMASPEMNPTICSVFEA HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
228	1578	A	2583	3		KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK  LPFLGLGSVLPQGMVMASPEMNPTICSVFEA HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
			2583	3	330	KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK LPFLGLGSVLPQGMVMASPEMNPTICSVFEA HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD PTMGIKPHLWWVAA
228	1578	A				KKALEAEKYGFQKDGQDRPLTKINSVKLNSL PSEYESGSACPAQTVHYRPINLSSSENKIVNVS LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS HRAQIMARYPEGYRTLPRNSKTRPESICSVTP STHDKTLGPGAEEKRRSMRDDTMWQLYEW QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI QRGDVTIDRRHRAHHPKVK  LPFLGLGSVLPQGMVMASPEMNPTICSVFEA HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Sequence	/=possible nucleotide deletion, \=possible
		l		sequence	1	nucleotide insertion
		<b></b> _	<del> </del> -	sequence	<del> </del>	GGTCLAGNLCTCPYGFVGPRCETMVCNRHC
	ļ					ENGGOCLTPDICOCKPGWYGPTCSTA
	1500	<del> </del>	2593	2	138	AVTFSVVFAYVADITQEHERSMAYGLVCMFI
230	1580	Α	2393	1 2	130	LYLLYLLRNAFFLR
	1581	<del> </del>	2595	185	2	SGPYTDFTPWPTEEQKLLEQALKTYPVNPPER
231	1381	A	2393	103	-	WEKIAEAVPGRTKKACIKRYKVADLRISK
222	1582	A	2596	1	391	STVTGOPRRII DTAGHOOPFLELKIRANEPGA
232	1382	^	2390	1 *		GRARRTPTCEPATPLCCRRDHYVNFQELGW
					1	RDWILLPEGYQLNYCSGQCPTHLAGSPGIAAS
	}	1			}	FHSAVFSLLKANNPWPGRTSWCVPTARRPLS
		1				LLYL
233	1583	A	2601	184	403	LLFSDEIIMAAPLRIADVTSGLIGGEDGRVYV
233	1565	1^	2001	1		YNGKETTLGDMTGKCKSWITPCPEEKVNVLQ
		l				NSIPYWERIT
	1584	A	2614	178	335	PLTLCLPENNKPPQADAVPDKELTLPVDSTTL
234	1584	1	2014	1 ***		DGSKSSDDQKIISYLWEKTQ
025	1585	A	2616	2	896	DVLEVYGTGVASTRHEMGTLDKHKELEDLV
235	1383	Α.	2010	1		AKFLNVEAAMVFGMGFATNSMNIPALVGKG
		1				CLILRDEVNHTSLVLGARLLGATIGIFKHNYA
		1				QSLEKLLRDAVIYGQPRTRRAWKKILILVEGV
		- [				YSMEGSIVHLPQIIALKKKYKAYLYIDEAHSI
		Ì		İ		GAVGPTGRGVTEFFGLDPHEVDVLMGTFTKS
	1	1				FGASGGYIAGRKARILSPPACLVPNTGSHSLH
	1	ł				RLTRDLQMNEAMVALVTDRLQGWNSGEGN
	1	1				WDRADKFGDLVDYLRVHSHSAVYASSMSPPI
ı		-				AEQIIRSLKLIMGLDGTTQ
236	1586	A	2621	+1	392	NTSSFPAQPSSPARPSLPHLSQHPSNPLLPLAS
230	1300	1	2021	1		ADHPQCGRFLPLHEPEPLCPSPSLSYPTLVSS
		]				WSSPFSSHHGCPPGLYPFPTSPKTIQPPGLAQL
						KMLCIPPGRQQLRGAQSMPGHGALSPLLLPP
		Ì				A CORPAL
237	1587	A	2628	398	1	DLVCKISGFGRGPRDRSEAVYTTMSGRSPAL
231	1307	11		ļ		WAAPETLQFGHFSSASDVWSFGIIMWEVMAF
i	İ		1			GERPYWDMSGQDVIKAVEDGFRLPPPRNCPN
1		ļ		}		LMHRLMLDCWQKDPGERPRFSQIHSILSKMV
			1			QDPEPPNV
238	1588	H <sub>A</sub>	2631	1	1104	WSPCSLTCGVGLQTRDVFCSHLLSREMNETV
ەت ا	1,500	(*)				ILADELCRQPKPSTVQACNRFNCPPAWYPAQ
		l	ł			WQPCSRTCGGGVQKREVLCKQRMADGSFLE
1		i				LPETFCSASKPACQQACKKDDCPSEWLLSDW
		1		}		TECSTSCGEGTQTRSAICRKMLKTGLSTVVNS
	1	l		1		TLCPPLPFSSSIRPCMLATCARPGRPSTKHSPH
1				}		AAARKVYIQTRRQRKLHFVGGGFAYLLPKTA
	1			1		VVLRCPARRVRKPLITWEKDGQHLISSTHVT
1	1				ì	VAPFGYLKIHRLKPSDAGVYTCSAGPAREHF
		1				VIKLIGGNRKLVARPLSPRSEEEVLAGRKGGP
		1		1	1	KEALQTHKHQNGIFSNGSKAEKRGLAANPGS
			)	1		
						RYDDLVSRLLEOGAPCSSSKKKN
220	1500	Δ	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN MKPDNILLDEHGHVHITDFNIAAMLPRETQIT TMAGTKPYMAPEMFSSRKGAGYSFAVDWW
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT  TMAGTKPYMAPEMFSSRKGAGYSFAVDWW SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT  TMAGTKPYMAPEMFSSRKGAGYSFAVDWW  SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET  TVVTYPSAWSOEMVSLLKKLLEPNPDQRFSQ
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT  TMAGTKPYMAPEMFSSRKGAGYSFAVDWW  SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET  TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVONFPYMNDINWDAVFQKRLIPGFIPNK
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT TMAGTKPYMAPEMFSSRKGAGYSFAVDWW SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRI NCDPTFELEEMILESKPLHKKKKRLAKK
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT  TMAGTKPYMAPEMFSSRKGAGYSFAVDWW  SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET  TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVONFPYMNDINWDAVFQKRLIPGFIPNK
239	1589	A	2636	1	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT TMAGTKPYMAPEMFSSRKGAGYSFAVDWW SLGVTAYELLRGRRPYHIRSSTSSKEIVHTIFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVQNFPYMDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIINRE KVNRDCI
						RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT TMAGTKPYMAPEMFSSRKGAGYSFAVDWW SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIIINRE KVNRDCI FILDPTTPMRTKCIELLYAALTSSSTDQPKAD
239	1589	A	2636	389	678	RYDDLVSRLLEQGAPCSSSKKKN  MKPDNILLDEHGHVHITDFNIAAMLPRETQIT TMAGTKPYMAPEMFSSRKGAGYSFAVDWW SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIINRE

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	i	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide			09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	1	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	l	1	914			T-Threonine, V=Valine, W=Tryptophan,
İ	İ		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		]	residue of	sequence	Y=1 yrosine, A=0hkilowii, '-stop codoli,
ļ				peptide	1	/=possible nucleotide deletion, \=possible
	1		1	sequence		nucleotide insertion
	ļ	<b>├</b> ──	<del> </del>	Soquette		EMANKELKQLRASYTESCIQEHYLPQVIDGTL
	İ	l				Y
					<del> </del>	IRLTILRCVFMRLATICVLVFTLGSKITSCDDD
241	1591	A	2640	392	3	IKLIEKCYFWKEATICVETTOVCOPMYKI MIED
		1	1	1		TCDLCGYNQKLYPCWETQVGQEMYKLMIFD
	1	}	}	1	1	FIIILAVTLFVDFPRKLLVTYCSSCKLIQCWGQ
	1			Į.		QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM
		1		1	1	Ϋ́
		<b>↓</b>		105	1	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR
242	1592	A	2642	405	\ 1	MVLMAGAKPGMLLLCFMCCTTLLSMWLSNT
	ì	1	1			MYLMAUARI GIVILLECI MECTILLECI VAGNEN
		1		1	1	STTAMVMPIVEAVLQELVSAEDEQLVAGNSN
	ł		ł			TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK
	l		1	1		SPLMISQACI
	1.500	+	2646	412	2	CLAMIKGIOSSGKIIYFSSLFPYVVLICFLIRAF
243	1593	Α	2046	412	1 ~	LLNGSIDGIRHMFTPKLEIMLEPKVWREAATQ
			}	1		VFFALGLGFGGVIAFSSYNKRDNNCHFDAVL
		1	1			VFFALGEGFGGVIATGSTRIGGERANVINEKCIT
	ļ	1	1		1	
	İ	ĺ		1		QNSETV
244	1594	A	2650	i	1271	MTTTLIGLLKTARLLRLVRVARKLDRYSEYG
244	1394	^	2030	1	1	AAVLMLLMCIFALIAHWLACIWYAIGNVERP
	-	1	ł	Ì	1	VI_TDKIGWI_DSLGOOIGKRYNDSDSSSGPSIK
,	Ì		1			DKYVTALYFTFSSLTSVGFGNVSPNTNSEKIF
	1	1	1	İ		SICVMLIGSLMYASIFGNVSAIIQRLYSGTARY
l		1	1	1	1	HMQMLRVKEFIRFHQIPNPLRQRLEEYFQHA
1	}			l	ì	HMOMEKA VELIKA HÖLLIK EKÖNEDELI ÖLLIK
	l	}	ļ	Į.		WTYTNGIDMNMVTNGTCSSCTSDDGHFILVS
ļ						NHHQGGLIYSWNDAASMQRPFNHIKSSLLGS
	1	-	1	1		TSDSNLNKYSTINKIPQLTLNPSEVKTEKKNSS
1	1	1	1			PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA
	1	1	l l	ļ		DVLPEYKLQAPRINKFTILHYSPFKAVWDWLI
	ì					LLLVIYTAIFTPYSAAFLLNDREEQKRRECGY
			į.			SCSPLNVVDLIVDIMFIIDILINFRTTYVNQNEE
	ĺ					
1	1	-	- }			VVSDPASV
245	1595	A	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFFLDNVIMW
243	1373	1			1	WESLLLLTAYFCYVVFMKFNVQVEKWVKQ
	1	1			Ì	MINRNKVVKVTAPEAQAKPSAARDKDEPTLP
	- {	1	i	<b>!</b>	-	AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD
	1	ļ	Į	· ·	{	PHV
1.				<del></del>	506	VLVLQMNYYQMLIIYYVLFFKVNEFLAFEGPI
246	1596	A	2660	200	506	LLDMRIKHLIKTNQLSQATALAKLCSDHPEIG
			1	1		PEDINKING MESONICKI BEAGAGES
	1			1	1	IKGSFKQTYLVCLCTSSPNGKLIEEVSMFSFIS
		1	1 .	1	}	NYFLS
0.15	1505		2678	3	267	DAWVKNDIIFNQTERKQKISENLKHLASVRV
247	1597	Α	20/8	٦	1 ~~ ′	VQKNLVFVVGLSQRLADPEVSPLVFFVILIFF
				1	}	VSLSYLEIIFDPAQLCDSSEHIIS
1	1	_1_		1	<del></del>	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF
248	1598	A	2687	1	404	DELITE ANIMALITY OF ANIMALS ALD
	1	1			1	GAAIKSVKNPDKKSIENQVLDSLVPLLLYSQD
1		- 1		1	1	ENDAVAEESRQVLTICAQFLKWKLPREVYSK
1	1	1	- 1		1	DPWHIKPTEAGTICRFFEKKCKGKINILEQTL
			1		1	MYSKNPKI
				<del></del>	140	FRRRRRRERDCAAQGARRHCRHLAECKLV
249	1599	Α	2692	1	440	SFPIGIYKVLRNVSGQIHLITLANNELKSLTSK
					1	PLAIN I LA LUIL AND LINE DELICATION A
				ļ	1	FMTTFSQLRELHLEGNFLHRLPSEVSALQHLK
1	1					AIDLSRNQFQDFPEQLTALPALETINLEENEIV
i		1				DVPVEKLAAMPALRSINL
				150	<del>-   -   -   -   -   -   -   -   -   -  </del>	LLPGSLGVPILHSQPWDPSPQCPHRAPSTPRRL
250	1600	Α	2693	459	21	PPLGALSQALTFLSRAAKNHSQDPGKGTKPFP
1		1	1			PELOAL DADDE DADE DA LOS ADOS ADOTTE
	1	1				AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF
į	1			•	1	
			İ			NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG
						ISSCPDLKLTKSSTP
251	1601	A	2694	2	404	NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG ISSCPDLKLTKSSTP FVFDLKLRVPGFAALLIHGASSVPGPETVRLR

EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
uci-	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence	)	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	defice	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience	1	ļ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	ł	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	ļ	<del>  </del>		sequence		OKRKKAPDHSSGRKEELVTTHTVDKLETKK
	1	İ	ļ		ļ	PVGRVLCGLSGELLHSLLLPRRKTEKRALGSH
		1	1		Į.	RKAGFPEHPVAPEPLSNSCQISKEGREQVLSEI
	1	1	1		]	GAGDCI.
				<u> </u>	<del>                                     </del>	POKSHSGAYQCFATRKAQTAQDFAIIALEDG
252	1602	Α	2697	421	1	TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPT
	ļ	1	l	1		VTWALDDEPIVRDGSHRTNQYTMSDGTTISH
	l	1	į			MNVTGPQIRDGGVYRCTARNLVGSAEYQARI
	1	l	1			NVRGPPSIRAMRNIT
	1	1	1			ACCQWRTLIPAKSTTVSCTISTPHHPFRGSYS
253	1603	A	2698	65	401	ACCOWREILIPARSTIVSCIISTIFILITROSTS
233	1003	1		Ì	1	FDDHITDSEALSRSSHVFTSHPRMLKRQPAIEL
	ļ	l l	1	1		PLGGEYSSDVPRPLSTQLSSSLLGYFSTLMTG
	l l		ļ	1	}	AAFTNNIASSTIIL
051	1604	A	2699	438	301	GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ
254	1604	^	20))	130		RVRGPWEAGPGVGY
	1.55-	A	2700	1	842	LONREDSSEGIRKKLVEAEELEEKHREAQVS
255	1605	A	2/00	1 1	1 0.2	A OHI EVHI KOKEOHYEEKIKVLDNQIKKDLA
		1				DEET FINMMORHEEEAHEKGKILSEQKAMIN
					}	AMDSKIRSLEORIVELSEANKLAANSSLFTQR
		1		1		NIMIK A OPEMISELROOKFYLETOAGKLEAQN
	1	ł	i	1		DEL FEOT EKISHODHSDKNRLLELETRLREVS
	}	1	l			LEHEEQKLELKRQLTELQLSLQERESQLTALQ
			1			AARAALESQLRQAKTELEETTAEAEEEIQALT
		1		}	ì	VGLGSNIFRLLKASARMSVELALSILAHP
	1	1				FVGGPGADPPVAVMWDPRAARMDLTAYAE
256	1606	A	2701	2	405	LLKESGNQVLKNGNFSLAIRKYDEAIQILLQL
		1				YQWGVPPRDLAVLLCNKSNAFFSLGKWNEA
		1				FVAAKECLQWDPTYVKGYYRAGYSLLRLHQ
	İ	[	[			FVAARECLQWDF11VRG11RAG13DEIGMIQ
	- 1	1	\		\	PYEAARMFFEGLR
257	1607	A	2702	2	399	FVESASSRPPGCFSGDGRFWLVSEGSRRGWD
231	1.00			1		FNPSFSFLDPRYSVGGDENIGTVTTLANILREF
	}		ł			NPSLKGFSVGTGKETSPNAFLNQAVAGGRAE
	1		ì			DLPVQARRLVDLMKNDTRIHFQEDWKIITLFI
i	ļ		1		Į.	GGNDL
	1600	A	2709	<del>                                      </del>	1097	SVGARQGEARDRIRRFFPKGDLEVLQAQVER
258	1608	l A	2109	1 -		MTRKELLTVYSSEDGSEEFETIVLKALVKACO
		. 1		- }		SSEASAYLDELRLAVAWNRVDIAQSELFRGD
1						OWR SEHT EAST MDALLNDRPEF VKLLISHOLS
l				1		I GHELTPMRLAOLYSAAPSNSLIRNLLDQASH
1		}	1	1	1	SAGTKAPALKGGAAELRPPDVGHVLRMLLG
1				1		KMCAPRYPSGGAWDPHPGQGFGESMYLLSD
	-			1	}	KATSPLSLDAGLGOAPWSDLLLWALLLNRA
i	1	i		[		QMAMYFWEMGSNAVSSALGACLLLRVMAR
ļ	1	1			1	LEPDAEEAARRKDLAFKFEGMGVDLFGECY
		1	'	(	{	SSEVRAARLLLRRCPLWGDATCLQLAMQAD
Į			Į.		1	22EAKWAKTTTWKCLT ACDALCTÓRIAIÓUR
				1	<u> </u>	ARAFFAQDGVQSLPTQKWWGDMARR
259	1609	A	2721	1	403	VYLGAGPGLFFSNEGAKEGEKANIPKLMLPR
239	1009	'`			• [	GGFSQREMVTGERSPSPEEEEEEEEGFGERA
1		1	1	ł		SCRRGLFRVRLTRVGLAAPSKASRGQEGDAA
1						PKSPVREKSPKFRFPRVSLSPKARSGSGDQEE
1		1		[	ŀ	GGLRVRLP
				<del></del>	477	LI GGDLRYHLOONVHFTEGTVKLYICELALA
260	1610	Α	2728	1	7//	I FYLORYHIIHRDIKPDNILLDEHGHVHITDFI
						IATVVKGAERASSMAGTKPYMAPEVFQVYM
						DRGPGYSYPVDWWSLGITAYELLRGWRPYE
						HSVTPIDEILNMFKVERVHYSSTWCKGMVAI
1			1	}		
			1	1		LTITDFILVLYRYYRSPLVQIYEIEQHKIETWR
1			0220	<del>-   1</del>	547	I LITTDFILVLYKYYKSPLVQIYEIEQHAIEI WA
261	1611	l A	2730	3	1 347	EIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIH

	C 10 10	) (-A	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	nod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			214	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	}	}	peptide	Sequence	/=possible nucleotide deletion, \=possible
	1	1	1	1 * *	ļ	nucleotide insertion
			ļ	sequence	ļ	RI PVI DPVSGNVLHILTHKRLLKFLHIFGSLLP
	İ	ĺ	[	1	Į	RPSFLYRTIODLGIGTFRDLAVVLETAPILTAL
			1	1		DIFVDRRVSALAVVNECGTHPQDERLGLGW
	1		1	i		GLGEPGSEERLEPAAITSR
			<u> </u>		431	GPEFPGSAKLVFLDLSYNNLTQLGAGAFRSA
262	1612	Α	2733	3	431	GRLVKLSLANNNLVGVHEDAFETLESLQVLE
	l	ł	Į.	1		LNDNNLRSLSVAALAALPALRSLRLDGNPWL
		1		1		CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM
	ļ	ì	l			ESRRISLRACRRPASRV
	}	1			<del></del>	PARISGVDPPVRKATKGGENCSFEDNKNWQF
263	1613	A	2736	2	343	LWGLNGNFNFFKEPWGGRNNHAKGFRTTW
			ł	į		ARSSSQNNRTFQNNRNFLRLQRDSQKKGQFA
		1	1	ļ	1	RLISPLVNLPQSPGGLEFQYQAT
		ł	1 _	l		RAMLKCLREGOPPPSYNWTRLDGPLPSGVRV
264	1614	A	2738	2	245	DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH
20 .		1	ł	1	}	DGDILGFPPLITERSOIT AND THE SOLESAN
	l		1	1	<u> </u>	DTVDVLDPPEDSGKQVDL AAGDAPLRSLEQANRTRFPFFSDVKGDHRLV
265	1615	A	2752	2	388	LAAVETTVLVLIFAVSLLGNVCALVLVARRR
205	1011		}	1	1	RRGATACLVLNLFCADLLFISAIPLVLAVRWT
		l .				RRGATACLVLNLFCADLLFISAILLVLAVICITI
		Ì			1	EAWLLGPVACHLLFYVMTLSGSVTILTLAAV
	(	1	l	ł		SLER
266	1616	A	2755	192	1	AFREVGGYWGLLCEHLYAIPSKTSEGNWTAK
200	1010			ţ	ļ	LQGYLPLQDAFHIFQDPLTGDLPWPELILGLP
	İ	1	i			V
267 1	1617	A	2760	434	714	ASRLEKQNSTPESDYDNTPNDMEPDGMGYM
207	1017	1.	1 2,00	1	1	HRTSVPGEGLPRARDLAGLGQQKQFTTHTPF
	ł		1	Ì		LYFQTHKGLKDSSIRSEVTCLGISQCWRKGFF
268	1618	A	2762	1	405	IACTFCGQDEWSPERSTRCFRRSRFLAWGER
268	1010	Δ.	2702	-		AVLLLLLLSLALGLVLAALGLFVHHRDSPL
		1	1	1		VQASGGPLACFGLVCLGLVCLSVLLFPGQPSI
			1	1		ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESI
	- 1	Ì	İ	ļ		LPLSWAE
200	1619	A	2772	3	243	TRPAEKIQYLVLFFVMSHPSQAYDKLSLSDHI
269	1019	Ι Δ	2,,2			LIAVLNLLRREVSEHGRHLQQYFNLFVMYAN
	1		]		ł	LSKNLSFSEFCFDVSY
			2789	<del>-   1</del>	486	ELQSQQACTHTKETEQLRSQLQTLKQQHQQA
270	1620	Α	2/09	1 '		VEOLAY AFFTHSSI SOFLOARLOTVIREKEEL
				1		I OI SIERGKVLONKOAEICOLEEKLEIANEDK
ł	- 1	-	<b>\</b>		1	KHALERFEOEAVAVDSNLRVRELQRKVDGIC
}	Į.	1	ı	1	1	KAYDELRLQSEAFKKHSLDLLSKERELNGKL
			1	1		RHI SP
				<del></del>	568	KEKR VT VOLPTESIOKNOEDKLKM VPRKQRI
271	1621	A	2795	1	300	ESCSOR GKI PGSEEKNOGPSMIGRKEERLITE
			-	1		DENENI KNKSAPKVVKOKVIDAHLDSQTQN
1		1				FOOTOIOTAESKAEHKKLPOPYNSLQEEKCL
1					1	VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE
		1				SQRDDGKGALNIVEFLRKREELHQILSTVKQI
	}	1				KCMQGKYAGAMESEPCVCTEADFDCDYGY
272	1622	A	2797	8	523	RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNS
	1	1				GYRKVVSNNCTDGVREQYTAKPQKCPGKAI
	1		ĺ			RGLRIVTADGKLTAEQGHNVTLMVQLEEGD
1	1			1		KULKIV I ADUAL I AEQUIN Y I LIVI Y QLEBOD
				1		VQRTLIQVDFGDGIAVSYVNLSSMEDGIXHV
	1	1	}	1		YQNXGIXRXTVQVDNSLGS
		į		1	1206	HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS
272	1622	<del> </del>	2801	72	395	111 0110111
273	1623	A	2801	72	393	DEEGONOLGIRIHODIPLPPRRRELPALRTING
273	1623	A	2801	72	395	DEEGQNQLGIRIHQDIPLPPRRRELPALRTING KADSLNVSRNSVMQELSELEKQIQVIRQELQ
273	1623	A	2801	72	395	DEEGQNQLGIRIHQDIPLPPRRRELPALRTING KADSLNVSRNSVMQELSELEKQIQVIRQELQ
273	1623	A	2801	72	320	DEEGONOLGIRIHODIPLPPRRRELPALRTING

EO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
	peptide	100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl- otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq- ience	dence	ĺ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ì		peptide	}	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
275	1625	A	2812	208	321	GSLATCQLSEPLLWFILRVLDTSDALKAFHD
			ĺ		<u></u>	MGKIIFQ
276	1626	Α	2813	41	266	AGRSLHGAGDRAWVGISPTDWSPKVVELCK
			1	ļ		KYQQQTVVAIDLAGDETIPGSSLLPGHVQAY
			1			QVGPVRRNGEAGPG VLQERLDNFQRKCIQLASSTEGKVDKLLMRN
277	1627	A	2817	3	410	LFISYLHTPKHKQHEVLQAMGSILGITGEEME
			1			PLFQEEHGTATRWMTGWLEGGSKSVPKTPL
		1	1	1	l	GLNQQPALNGSFSELFVKFLKTESLSSTLPTX
		İ				LPPHNSPGKIK
	1	1	ļ	\		GLSGPSCSCPHSPLPTIISRAQLETALKWRNYE
278	1628	A	2821	238	457	VKLRLLLHLEELQMEHDIRHYDLESVPMTWD
		ł				PVDQNPRLV
					ļ	PLIPANLPAHSNPLQPLPSLPHPFLPATHKFPT
279	1629	Α	2822	342	1	TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS
		Ì		l .		CRLPSRPSVSRELPPQSGPASSVPLAPTPLPDS
				ţ		VPSQRHPTXPPPAS
				207	177	PSMVWSYHWGVKQKRLALCVFSFEEGGRRK
280	1630	Α	2825	307	''	CGQYWPLEKDSRIRFGFLTVTNLTGAVGEPG
						VAFQCDGQRRREPTC
			2007	81	381	KMGTAVWVPKEKEKRDKASOEGGDVLGAR
281 1631	A	2827	81	301	ODCTPSLKSLVATGNLLDLEETAKAPLSTVSA	
	ì	1				NTTNMDEVPRPQALSGSSVVWVSGCVASRS
		ł				VII SLTSG
	1622	A	2830	471	160	KLPXDKYELEPSPLTQYILERKSPHTCWQVFV
282	1632	A	2830	471	100	TSSGKYNELGYPFGYLKASTTLTCVNLFVMP
				1	l l	YNYPVLLPLLDDLFKVHKLKPNLKWRQAFDS
		-				YLKTLPPYYL
283	1633	$+_{A}$	2835	462	148	VSPALSLTPTIFSYSPSPGLSPFTSSSCFSFNPEE
203	1033	1	1 2055			MKHYLHSQACSVFNYHLSPRTFPRYPGLMVP
	1		ì		1	PLQCQMHPEESTQFSIKLQPPPVGRKNRERVE
						SSEESAP
284	1634	A	2836	2	384	KTLPRTLLDILADGTILKVGVGCSEDASKLLQ
201	1					DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL KSLAETVLNFPLDKSLLLRCSNWDAETLTED
		l l				QVIYAARDAQISVALFLHLLGYPFSRNSPGEK
	İ	1				
	İ					KR PIRPYYSYSGLDRDCSWLPLAKAWLPDVMIL
285	1635	A	2843	20	271	VCDRVSEDGINRQQAQEWCIKHGFELVELSP
	}	-		l		EELPEEDGKCLCVRRKYGTYI
		1				TAEDVLTVAYEHGVNLFDTAEVYAAGK
286	1636	Α	2845	197	278	FVAEVRREWAKYMEVHEKASFTNSELHRAM
287	1637	A	2851	2	427	NLHVGNLRLLSGPLDQVRAALPTPALSPKDK
						AVLQNLKRILAKVQEMRDQRVSLEQQLRELI
ļ	İ	ı		1		QKDDITGSLVTTDHSQMKKLFEEQLKKYDQL
						KVYLEQNLAAQDRVLCALT
					1460	FVNLGILTCIECSGIHREMGAHISRIQSLELDK
288	1638	A	2859	2	469	LGTSELLPAKNVGNNSFNDIMEANLPSPSPKP
[	}			1	i	TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA
					+	KLNELLEAIKSRDLLALIQVYAEGVELMEPLL
1	}	Ì				EPGQELAETALHLAVRTADQTSLHLVE
				<del></del>	454	FVASGGPATARMSDSOFFCVAEERSGHCAV
289	1639	_   A	2861	2	454	DGNFLYVWGGYVSIEDNEVYLPNDEIWTYD
	1	}		1		DSGLWRMHLMEGELPASMSGSCGACINGKL
İ					1	YIFGGYDDKGYSNRLYFVNLRTRDETYIWEK
{				1	1	ITDFEGQPPTPRDKLSCWVYKDRLIYFG
					270	FRQGQLYKVFLHGSQGQVYHSQQVGPPGSA
290	1640	A	2868	1	378	SPDLLLDSSGSHLYVLTAHQVDRIPVAACPQI
1	1		İ	1		PDCASCLQAQDPLCGWCVLQGRCTRKGQCC
Í	1					

			1 050	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	İ	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	{	i	1	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		nucleotide insertion
	l	<u> </u>	<u> </u>	sequence		RAGQLNQWLWSYEEDSHCLHIQSLLPGHHPR
		}	ł			OE
		i				FRYMPNNRQQLLRKRHIGNDIVTIVFQEPGAL
291	1641	A	2870	1	385	PFTPKSIRSHFQHVFVIVKVHNPCTENVCYSV
		1	i	]		GVSRSKDVPPFGPPIPKGVTFPKSAVFRDFLL
	1	1	1	ļ		AKVINAENAAHKSEKFRAMATRTRQEYLKD
		ì		ļ		1
	}		<u> </u>		<u> </u>	LA RPTRPPPATTQSPESTMDTSLKKEKSAILDLYI
292	1642	A	2877	3	188	PPPPAVPYSPRYVAVHCHGMLVSCWCHL
	1		ļ	L		REKEEEVEEEDKVVKETEKEAEQEKEEDSL
293	1643	A	2878	1	427	GAGTHPDAAIPSGERTCGSEGSRSVLDLVNYF
	ł	1	l l	1		LSPEKLTAENRYYCESCASLQDAEKVVELSQ
	ì	İ	l.		1	GPCYLILTLLRFSFDLRTMRRRKILDDVSIPLL
	1	1				GPCYLILILLRESPOERTMARKALEDDVSHEE
	1	1	1	1		LRLPLAGGRGQAYDL
294	1644	A	2879	109	245	QLCCFCFRQTTLIVYILSFIGMVIFTFTLDLRYI
254	1.011		ì			IIVFVTGGVLG
295	1645	A	2880	3	320	LASSQHGILNNLSLLFSICKTCIRTMDHHCPRA
293	10.15			ł		NNCVGEQNHRFFCALHCKSKHFCIEFTLNTNF
	1.		ì	ì		FNCFLPGAEKSTIDAPFSLQPFLQDSKYNTALS
	ľ	1	j	Ì	İ	LSESISQ
296	1646	A	2892	209	363	SQYSHSLDYHLLQVTKNPFTLGDSSNPGQTE
290	1040	1 **			ì	RLQEFSQKMDQVRGHWPVST
297	1647	A	2893	8	424	SPXTLXLDTFILLGIQDNILVLILATPPFMAGG
297	1047	1	2073			KLYSTMGRFLRDRKNPACREMAVVLLANLA
	1					QGDSLAARAIAVQKGSIGHLLGFLEDSLAAT
	1	1				QIQQSQASLLHMHNPPFEPTSVDMMRRACRA
i		1	l			LLALAKVDDNHSEF
298	1648	A	2894	310	445	FWIYFPSFFMTGYLPLGFEFAVEITYPESEGTS
298	1040	1 ^	20,	3.0		SGLLNASAQVNL
299	1649	A	2898	1	492	KIKAKNLTNYDLCSIFLGTSTLLVWVGVIRYL
299	1049	1 ^	20,0	] -	l .	GYFQAYNVLILTMQASLPKVLRFCACAGMIY
	ì		1		Ì	LGYTFCGWIVLGPYHDKFENLNTVAECLFSL
)	1	}	}	1	ľ	VNGDDMFATFAQIQQKSILVWLFSRLYLYSFI
			1			SLFIYMILSLFIALITDSYDTIKKFQQNGFPETD
	-	ŀ				LQEF
200	1650	- <del> </del> A	2901	1	445	PVWWNSLNGASEVTFSVHVKDGGSFPKTDST
300	1030	1^	2,01	1		TVTVRFVNKADFPKVRAKEQTFMFPENQPVS
	1		1	1		SLVTTITGSSLRGEPMSYYIASGNLGNITQIDQ
1	1		ì			LTGOVSISQPLDFEKIQKYVVWIEARDGGVPP
	1		i			FSSYEKLDITVLDVNDNAPIF
<u></u>	1.55		2002	162	433	THEICLPLGYCFPLLDKDLQLPSGFNCNFDFLE
301	1651	A	2902	102	133	EPCGWMYDHAKWLRTTWASSSSPNDRTFPG
	İ	1				KPAVSEDMKELRPACSTYFNPRFPYKL
		<del></del>		<del>  2</del>	412	GPOMLCKKIYFIWVTRSQCQFEWLADIMQEV
302	1652	A	2909	4	712	FENDHODLVSVHIYVTOLAEKFDLRTTMLYI
		1				CERHFOKVLNRSLFTGLRSITHFGRPPFEPFFN
	- 1		- {	1		SLQEVHPQVRKIGVFSCGPPGMTKNVEKACQ
				]		LVNRQDRAHFM
İ	ļ			<del></del>	462	KLNRWLCFFYSWSFGILLYEMVTLGAPPYPE
303	1653	Α	2914	291	453	VPPTSILEHLQRRKIMKRPSSCS
						PGVPSQALRKAESLKKCLSVMEAKVKAQTAP
304	1654	A	2926	179	354	NKDVQREIADLGEVGAASLPPSSGPGA
1	}	}			120	GMGYLHAKGILHKDLKSKNVFYDNGKVVIT
305	1655	A	2938	135	438	DFGLFSISGVLQAGRREDKLRIQNGWLCHLA
1		1			l .	DIGETSISOVE AND THE PROPERTY OF THE PROPERTY O
1	]	1			İ	PEIIRQLSPDTEEDKLPFSKHSDVFALGTIWYE
1		1				LHAREWP
306	1656	A	2944	2	329	VRWNSCVNCSCAFGNGASLSTSLGESSGCLW
1 300	1 .350	1 **	1			EIGKWLSCSLLSFPSPLAVLITTFCIVTVLGREA
İ	1		J	)	1	LTKGALWAVFLLAGSALLCAEVTGVIWRQPE

						A Alanine CarCysteine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		ļ		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		nucleotide insertion
	l	L		sequence	ļ	SKTKLSFKVSSSA
	T				ļ <u></u>	NYLCIAKNSAGSAMGKTRLVVQVPPVIENGL
307	1657	A	2950	2	411	PDLSTTEGSHAFLPCKARGSPEPNITWDKDGQ
	1					PVSGAEGKFTIQPSGELLVKNLEGQDAGTYT
			1			CTAENAVGRARRRVHLTILVLPVFTTLPGDRS
			1			LRLGDRLWLR
		<u> </u>		<u> </u>	407	PTRPPRVRFDNEFDAESQRKRTTSVSKMERM
308	1658	Α	2951	1	407	DSSLPEEEEDEDKEAINGSGNAENRERHSESS
ŀ		1				DWMKTVPSYNQTNSSMDFRNYMMRDETLEP
						LPKNWEMAYTDTGMIYFIDHNTKTITWLDP
	}		ŀ	1		RLCKKAKAPEDC
			J		179	QDFLTLTLTEPTGLLYVGAREALFAFSMEALE
309	1659	A	2954	2	179	LOGAVRGGAVGGSRACORARPRGAVLG
		<del>   </del>	10050	<del>                                     </del>	419	ODMMERAIDTEVGHDVVEPGSYVQMFPYPC
310	1660	A	2959	1	417	VTRDDFLFVIEHMMPLCMVISWVYSVAMTIQ
1			1			HIVAEKEHRLKEVMKTMGLNNAVHWVAWFI
		1				TGFVQLSISVTALTAILKYGQVLMHSHVVIIW
		}		1	1	I FI AVYAVATIMFCF
	<u> </u>		2963	3	465	MKPOMPGLGAPNGYGPGRGRAGVPGGPERR
311	1661	A	2963	3	405	PWVPHILPESSPGYLGVMKAQKPGAGEGMK
1			1	ł		POKPGLRGTLKPOKSGHGHENGPWPGPCNA
1		ł		1		RVAPMLLPRLPTPGVPSDKEGGWGLKSQPPS
		-	İ			AVQNGKLPGHQPPNGYGPGAEPGFNGGLEPQ
		}	1			KI
212	1662	A	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM
312	1002	1 ^	2507			HTGGCSPKTKPHIKEECIVPTPCYKPKEKLPV
į.		1		}		EAKLPWFKQAQELEEGAAVSEEPSFIPEAWS
	1	- 1		Į.		ACTVTCGVGTQVRIVRCQVLLSFSQSVADLPI
						DECEGPKPA DECEMPED OF THE PART WIT
313	1663	I A	2969	2	430	VVADNCRQGYLDALRFLERRGLTKEPVLWT
1 3.3	1000					LVSKEPPAPADGNWDAGCDQRRKGGLSLNW
-		1				KVPHVQVKDVPNFEQLSPELEAALKKACTRD PSRWARFWHSGPGQVLTYLLLPCTLPFEYIYF
			İ	Ī	1	PSRWARF WHSGPGQVLI I LLLI CILII IIII
		1	<u> </u>			RSRRLVVWLPDVPADLWWMQ LDXSHNALQRLRPGWLAPLFQLRALHLDHNE
314	1664	A	2971	422	33	LDALGRGVFVNASGLRLLDLSSNTLRALGRH
		ł		1		DLDGLGALEKLLLFNNRLVHLDEHAFHGLRA
		J		,	1	LSHLYLGCNELASFSFDHLHGLSATHLLTLDL
·{		1				SSNRM
L						ITVSTHASGSPFGLEPQSGWLWVRAALDREA
315	1665	A	2973	1	525	OFI YII KVMAVSGSKAELGOOTGTATVRVSI
	ļ					INONEHSPRISEDPTFLAVAENQPPGTSVGRV
	1			1		FATORDSGPNGRLTYSLOOLSEDSKAFRIHPQ
		-	1			TGEVTTLQTLDREQQSSYQLLVQVQDGGSPP
		1	1			RSTTGTVHVAVLDLNDNT
					400	FI VVELVSAGKSGPERNTYEVQVVTGNVPKA
316	1666	A	2978	2	400	GTDANVYLTIYGEEYGDTGERPLKKSDKSNK
1						FEOGOTOTETTYAIDLGALTKIRIRHDNTGNR
1	1					AGWFLDRIDITDMNNEITYYFPCQRWLAVEE
					i	DDGOLSRE
					440	VINCOGRPTRPVRINGDGOEVLYLAESDNVR
317	1667	_ A	2981	3	1 440	L GCPYVL DPDDYGPNGLDIEWMQVNSNPAH
				1	1	HRENVELSYODKRINHGSLPHLQHRVRFAAS
	1					DPSOYDASINLMNLQVSDTATYECRVKKTIM
						ATRKVIVTVOARPAVPMCWTEGQ
			2005	119	414	1 PEKEFPIIRKSSSLKVTKCLFTEOPKPIIILRFA
318	1668	Α	2995	117	""	ENVIDARILRIDIANTLREOVOELFNKTYGKQ
		1	- 1	1		RRTPGEGHVAAVDREVAGFPVPAEGISGETIH
L	1	<del>-   -</del>	2999	2	332	GFFAYTYGRLVVVEDLHSGAQQHWSGHSAEI
319	1669	A	2999		1 2 2 2	

<u> </u>	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
10: of	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	цепсе		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	ļ		714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	{	ĺ	l l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	ļ	ì	peptide		/=possible nucleotide deletion, \=possible
			Ì	sequence		nucleotide insertion
	l			sequence	<del> </del>	STLAI SHSAOVLASASGRSSTTAHCQIRVWD
	1	}	Į	l		VSGGLCQHLIFPHSTTVLALAFSPDDRLLVTL
	Į.	į		ļ		GDHDGRTLALWGTGHL
	}		J			IDESTGLIITVNYLDYETKTSYMMNVSATDQA
320	1670	A	3000	693	322	PPFNQGFCSVYITLLNELDEAVQFSNASYEAA
		1		1	1	ILENLALGTEIVRVQAYSIDNLNQITYRFDAY
		ł	1			TSTQAKALFKIDAITVRGWGQGAPFFPI
	1	1	1	Į.		RIPRGKACXTVLGRSTGELEGFASSRLPPQPC
321	1671	A	3001	6	383	RIPRGKACXI VLGKSI GELEGI ASSIGLI QI O
321	1071	11	1 333.			GWGQSSDLLSRIDLDELMKKDEPPLDFPDTLE
	1	1	1		)	GFEYAFNEKGQLRHIKTGEPFVFNYREHLHR
	i		<b>\</b>		1	WNQKRYEALGEIITKYVYELLEKDCNSKKVS
	J.,	<del> </del>	3007	192	447	ERVRNSLFPGRGDSQCACCPSSPVWVFLETGF
322	1672	Α	3007	192	1 '''	LFPWLFLOVEVIKKAYMQGEVEFEDGENGK
	ł		i	1	1	DCAASPRNVGHNIYILAHOLARH
	\			J	245	KELL EVHLIVNNINFFNTRYAKIHIPIIASVSEH
323	1673	Α	3019	18	243	QPTTWVSFFFDLHILVCTFPAGLWFCIKNIND
	1.					PRICERRGE
		Į			<u> </u>	LCYFSARYHQRKIFGILYIFTLSAINRKEPNLFI
324	1674	A	3020	523	797 .	YLFIFFEMESHSVTHAGVQRHNLNSLQPLPPG
J	1	1	(	1		FKRFSCLCFLSSWNYRGAPPGPANF
	ļ	1	ļ	ł		NDFLPLYFGWVLTKKSSETLRKAGQVFLEEL
325	1675	A	3022	2	156	NDFLPLYFGWVLIKKSSEILKRAGQVI EDED
323	1073	1	, 552			GNHKAFKKELRQCRWQVGAL
167	1076	A	3023	38	172	KMVRGSKKLISFFPGGPYGILAGRDPSKGLAT
326	1676	^	3023	1 30		FCLNKEALKDEFE
	<del></del>	<del></del>	3027	+1	385	LTLEFLLLPAASELAHGKRLACCIVDHKLPEC
327	1677	Α	3027	1 '	505	GEVGLYDKILLFKHDPTSANLLQLYKSSGDIQ
	1	ì	1			FGDI VEVVI SASATFEDFOIRPHALTVHSYRA
	j	- }				PAFCDHCGEMLFGLVRQGLKCDGCGLNYHK
	Ì	1				RC .
	1				660	ITRPTISCQRPGPGLAAGMLPYTVNFKVSART
328	1678	Α	3030	13	569	I TGAI NAHNK AAVDWGWOGLIAYGCHSLV
	l		1			VVIDSITAQTLQVLEKHKADVVKVKWAREN
1	1		i	1		YHHNIGSPYCLRLASADVNGKIIVWDVAAGV
}	1	ì	1	ì		AQCEIQEHAKPIQDVQWLWNQDASRDLLLA
	- 1	İ				HPPNYIVLWNADTGTKLWKKSYADNILSFSF
1	1	i	- 1	1		1 _
ŀ	1		ļ	}		D D CONTROL V COPE A ED
220	1679	A	3038	90	744	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAED
329	1019	1	70,50			GNIEYKKLVNPSQYRFEHLVTQMKWRLQEG
1						RGEAVYQIGVEDNGLLVGLAEEEMRASLKTI
						HRMAEKVGADITVLREREVDYDSDMPRKITI
1	1		)	)		VI VRKVPDNOOFI.DLRVAVLGNVDSGKSTL
Į.			l l			I GVI TOGEI DNGRGRARLNLFRHLHEIQSGR
ł				ļ		TSSISFEILGFNSKGEVHGINGTQWGQTLRMC
ļ	1			1		w
		1				LCSTLLLLTIPSWVLSQITLKESGPTLMKPTET
330	1680	A	3040	3	397	LTLTCTFSGFSLNTSGVGVAWIRQPPGKALE
550	1117					WLALIYWDDDKRYSPSLNDRLTIAKDTSRNO
1			1		1	WLALIY WDDDKRYSPSLNDRLTTARDYGGN VVLTMTNMGPVDTATYYCAQFARGARGSN
ļ	]	i	1	l		
1		1				WFDPWGQ
1	<del>- 1</del>	<del></del>	3043	<del>-   3</del>	1509	AGIRHEAPPTTSNRHRRQIDRGVTHLNISGLK
331	1681	Α	3043	١		MDDGIAIDWVAGNVYWTDSGRDVIEVAQMI
						GENERAL ISOMIDEPHAIVVDPLRGTMYWSL
				1		WGNHPKIFTAAMDGTLRETLVQDNIQWPIC
		ļ		j		I A VOYHNERLY WADAKLSVIGSIRLING I DP
1		1	1	- {		VAADSKRGLSHPFSIDVFEDYIYGVTYINNK
1		į			Į.	FKIHKFGHSPLVNLTGGLSHASDVVLYHQHI
	1			1		QPEVTNPCDRKKCEWLCLLSPSGPVCTCPNC
F						KRLDNGTCVPVPSPTPPPDAPRPGTCNLQCF
1		- 1	ı	1	ł	- KRIDNGILVEVESETEEDAFAFGIGADQUE
	İ	ļ	ļ	1	į.	GGSCFLNARRQPKCRCQPRYTGDKCELDQC

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	1		'	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	į į		!	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		ļ	peptide	Soquemes	/=possible nucleotide deletion, \=possible
	Ì		ļ	,		nucleotide insertion
	_	i	<u> </u>	sequence		WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC
				ļ		TQQVCAGYCANNSTCTVNQGNQPQCRCLPG
	}	1	1		1	FLGDRCQYRQCSGYCENFGTCQMAADGSRQ
	ļ		1		}	FLGDRCQ YRQCSG I CENT OT CQUAR IN CONTROL
	1		1	1		CRCTAYFEGSRCEVNKCSRCLEGACVVNKQS
	İ	1	1	1		GDVTCNCTDGRVAPSCLTCVGHCSNGGSCT
	1	}		1	1	MNSKMMPECQCPPHMTGPRCEEHVFSQQQP
	1	}	ì		1	GHIASILIP
	1	<del> </del>	3045	3	952	TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG
332	1682	A	3043	13	752	AVDEEVGDYFPEFLDMLEESPFLKMTLPWGT
	1	}	1			LSSLRLQCRSQSDDGPIMWVRPGEQMIPTAD
	ļ	1	1			MPKSPFKRRSMNEIKNLQYLPRTSEPREVLF
	Į.	1	}	}	}	EDRTRAHADHVGQGFDWQSTAAVGVLKAV
	{	1	1			QFGEWSDQPRITKDVICFHAEDFTDVVQRLQ
		-				OF THE BUTTON OF THE TOTAL TOT
	<b>\</b>		1		}	LDLHEPPVSQCVQWVDEAKLNQMRREGIRY
	1		1		l	ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW
			İ		İ	HIRLKQYHPVVEATQNTESNSNMDCGLTGKR
	1	1	1	1		ELEVDSQCVRIKTESEEACTEIQLLTTASSSFP
		1				PASE
				497	167	SACSTGPELPGRATRSLTRPANQKGCDGDRL
333	1683	Α	3046	497	107	VVDGCAMIAMNGSVFAQGSQFSLDDVEVLT
	[		1	ì		ATLDLEDVRSYRAEISSRNLAVSAPVDTCVG
	İ	1	1			CSSKTWKVAPFVRAWWRP
	l	1				VITDLEEQLNQLTEDNAELNNQNFYLSKQLD
334 1	1684	A	3053	37	276	EASGANDEIVQLRSEVDHLRREITEREMQLTS
	1		1			EASGANDEIVOLKSEVDHERREITEREMQETS
1		İ	1	1		QKQVRRVNKVVRSLEDF
335	1685	A	3054	2	846	WDAWGDWSDCSRTCGGGASYSLRRCLTGR
333	1005	1 1	1 303 .	1		NCEGQNIRYKTCSNHDCPPDAEDFRAQQCSA
	1		ļ			YNDVQYQGHYYEWLPRYNDPAAPCALKCH
	-	1	]			AOGONLVVELAPKVLDGTRCNTDSLDMCISG
		1	ı	1		ICOAVGCDROLGSNAKEDNCGVCAGDGSTC
	1	1	l			RIVRGOSKSHVSPEKREENVIAVPLGSRSVRI
ŀ		- 1	1	1		TVKGPAHLFIESKTLOGSKGEHSFNSPGVFVV
1		1	1	ì	1	ENITVEFORGSEROTFKIPGPLMADFIFKTRY
		1				TAAKDSVVQFFFYQPISHQWRQTDFFPCTVT
		1		ļ		
1	}	1				CGGG VVGKQEAGAHSDSCCLLHTPPRLTPAHSRKA
336	1686	A	3058	54	347	A ARKAGAMUS AND A THE ALL ALL ALL ALL ALL ALL ALL ALL ALL AL
330	1.000	1		į		LRNSRIVSQKDDVHVCIMCLRAIMNYQVSRG
	-	1				AWDWRLGSPACPHWGLHKLPRLWDPLSLYP
1	1			1		VLCWGT
2==	1.05	<del></del>	3059	12	709	ILTSLVELTRFETLTPRFSATVPPCWVEVQQE
337	1687	Α	3039	[ ~	1	OOORRHPOHLHOOHHGDAAQHTRTWKLQT
	I	1		1		DSNSWDEHVFELVLPKACMVGHVDFKFVLN
ł	1	1	1			SNITNIPOIOVTLLKNKAPGLGKVNGLRLCPF
İ	-	1	[	1		LEDHKEDILCGPVWLASGLDLSGHAGMLTL1
		1				SPKLVKGMAGGKYRSFLIHVKAVNERGTEEI
	1					CNGGMRPVVRLPSLKHQSNKGYSLASLLAK
1	1	-				CNGGMKPY VKLPSLKTQSNKU I SDASELAK
	Į.					VAAGKEKSSNVKNENTSGTRK
220	1200	A	3060	85	384	KAFYNYHVLELLQMLVTGGVSSQLEQHLDK
338	1688	A	3000	1 55	- '	DKVYGVADSCTSLLSGRNRCKLGLLSLHETII
	1					SDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDI
1		1	1	Ì		FFIND
					100	CFLCLSGDFMVMTIFFNVSRRFGYVAFQNYV
339	1689	A	3063	236	362	
1		1		1 .		PSSVTTMLSWV
340	1690	A	3065	3	1249	DLWQFTPLHEAASKNRVEVCSLLLSYGADPT
3-40	1000	1.	1		1	LLNCHNKSAIDLAPTPQLKERLAYEFKGHSLI
			1	1		OAAREADVTRIKKHLSLEMVNFKHPQTHETA
						I HCAAASPYPKRKOICELLLRKGANINEKTK
1	ì	ĺ				FI TPI HVASEKAHNDVVEVVVKHEAKVNAL
	Ţ	- 1				DNLGQTSLHRAAYCGHLQTCRLLLSYGCDPI

				- T	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1		314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l	Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		<del> </del>	<del> </del>	1		IISLQGFTALQMGNENVQQLLQEGISLGNSEA
						DRQLLEAAKAGDVETVKKLCTVQSVNCRDIE
	}	ì				GROSTPLHFAAGYNRVSVVEYLLQHGADVH
						AKDKGGLVPLHNACSYGHYEVAELLVKHGA
	1					VVNVADLWKFTPLHEAAAKGKYEICKLLLQ
			1			HGADPTKKNRDGNTPLDLVKDGDTDIQDLLR
	İ					GDAALLDAAKKGCLARVKKLSSPDNVNCRD
		1				TQGRHSTPLHLAGK
341	1691	A	3070	1	547	GVLIPSFQNQLFADILAGIESVTSEHNYQTLIA
3.11	1071	}				NYNYDRDSEEESVINLLSYNIDGIILSEKYHTI
	1					RTVKFLRSATIPVVELMDVQGERLDMEVGFD
	1				Ì	NRQAAFDMVCTMLEKRVRHKILYLGSKDDT
	j	}	ļ		}	RDEQRYQGYCDAMMLHNLSPLRMNPRAISSI
	ļ	ļ	1			HLRMQLMRDALSANPDLDGVFCTN
342	1692	A	3073	463	3	RINRCRKPSDADILVPGDTISLIGTTSLRIDYNE IDDNRVTAEEVDILLREGEKLAPVMAKTRILR
		1				AYSGVRPLVASDDDPSGRNVSRGIVLLDHAE
		}				RDGLDGFITITGGKLMTYRLMAEWATDAVC
Ì		1	1	}		RKLGNTRPCTTADLALPGSQEPAKVP
· ·					<del></del>	LLIYLAIFAPVAMSALAGVKSVQQVRIRAAQS
343	1693	A	3075	250	1	LGASRAQVLWFVILPGALPEILTGLRIGLGVG
1	ļ					WSTLVAAELIAATRGLGFM
1					120	LYFDAYLQSLQVAAISTFCCLLIGYPLAWAV
344	1694	A	3076	2	138	AHSKPSTRNILLLL
			2070	460	3	LKIRGQRIELGEIDRVMQALPDVEQAVTHAC
345	1695	Α	3078	469	) 3	VINQAAATGGDARQLVGYLVSQSGLPLDTSA
1		l			1	LQAQLRETLPPHMVPVVLLQLPQLPLIANGKL
			Į.		1	DRKALPLPELKAQAPGRAPKAGSETIIAAAFS
		1				SLLGCDVODADADFFALGGHSLLAMKLAT
246	1696	+ <u>-</u> -	3082	404	2	ONITSKOLDVRLDPQTVPIELEQLVLSFNHMI
346	1090	A	3002	707	) -	ERIEDVFTRQSNFSADIAHEIRTPITNLITQTEI
	1			1		ALSQSRSQKELEDVLYSNLEELTRMAKMVSD
		1	1	i	1	MLFLAQADNNQLIPEKKMLNLAHEVGKVFD
					_	QFEALPE
347	1697	A	3084	3	340	NELTFKEAEISKLYTKVHPAYRTLLEKRQALE
34,	107.	1		1	1	DEKAKLNGRVTAMPKTQQEIVRLTRDVESGQ
		İ			1	QVYMQLLNKEQELKITEASTVGDVRIVDPAIT
	-			1		QPGVLKPKKGLIILGAI
348	1698	A	3086	723	10	TQAMVWQQKACAEDDPQLSGRHWLHAATL
	1	1		1	1	YNIAAYPHLKGDDLAEQAQALSNRAYEEAA QRLPGTMRQMEFTVPGGAPITGFLHMPKGDG
			1	1	1	QRLPGTMRQMEFTVPGGAFTTGFLHMFRGDG PFPTVLMCGGLDAMQTDYYSLYERYFAPRGI
1		1				AMLTIDMPSVGFSSKWKLTQDSSLLHQHVLK
		1		1		ALPNVPWVDHTRVAAFGFRFGANVAVRLAY
		}			1	LESPRLKAVACLGPVVHTLLSGLKCQQQVPE
1				1		MYLDVLASRLGMHDASTKSSTRENH
					240	RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV
349	1699	Α	3087	2	249	GFGVAMSQALGPFSLRAGVASSTLGIAQVCG
		1	1		{	SSLWIWLAAVVGIGAWNM
					424	EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR
350	1700	A	3099	3	424	ANTPDSDITEKTEDSSVPETPDNERKASISYFK
		1				NORGIQYIDLSSDSEDVVSPNCSNTVQEKTFN
		1				KDTVIIVSEPSEDEESQGLPTMARRNDDISELE
						DLSGMEDLK
				<del></del>	404	IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG
351	1701	Α	3108	2	404	MFGIVVMVIETELSWGAYYKAPLYSLALKCL
		1				ISLFTIILLGLTIVYHAREIQLFMANYGADDWR
						SALTYEPIFLILLEALRGVIHATPCRVSLSLWD
		J			1	GLDLP

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
			i	amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	}	1	residue of	Seducine	/=possible nucleotide deletion, \=possible
	Ì	\	1	peptide		nucleotide insertion
	1 _	L	1	sequence	<del> </del>	AQLAEVCPPQTLLTTNTSSISITAIAAEIKNPER
352	1702	A	3110	341	2	VAGLHFFNPAPVMKLVEVVSGLATAAEVVE
	1	1	ì			QLCELTLSWGKQPVRCHSTPGFIVNRVARPY
		ļ	1		}	YSEAWRALEEQVAAPEVI
	1		<u> </u>			HFSLFRIAFAVFLTYMTVGLPLPVIPLFVHHEL
353	1703	A	3111	3	188	GYGNTMVGIAVGIQFLATVLTRGYAGRLA
	Ì			1		WQLFHLNGTFLNIGETDTESCVNGWVYDRSS
354	1704	A	3116	367	225	FPFSNMTEVRGLVFLS
	1	Ì	i			VINLVYLISSPRPELKPVDKESEVVMKFPDGF
355	1705	A	3117	101	53	EKFSPPILQLDEVDFYYDPKHVIFSRLSVSADL
			1			ESTICVVGENGAGKSTMLKLLLGDL\APVRGI
	1		1	}		ESRICY VGENGAGAS I MILALLEGIDE VA VICT
	1	1	Į.			RHAHRNLKIGYFSQHHVGAAGT*TFSACGNL
						LGTQVFLGRPEEEY\RHQLGFGMGISGELGHA
			· ·	j		SSLPACLGGQKEAEVAFCSDGLLPCPNFL\IL\
	1	(				DEPTNHLGHGRAIEALGPCLQTISGVGVILVS
	1		Į.			HE*SALSRLVCREYLWVC*GRSTSPF
356	1706	A	3121	137	466	RGGRDWGEHNQRLEEHQARAWQGAMDAG
330	1700	1			-	AASREHARWQGTGLAPGTRVAVAPTCVQGL
	1	}	1		1	PQERSVCRPFFSSRWREGPVWALGAGAHGKP
	1	-			į	RWSGGVRCVVRGGRWFTPAPH
357	1707	A	3124	1249	229	MLEAPGPSDGCELSNPSASRVSCAGQMLEVQ
337	1707	1	312.	12.0	j	PGLYFGGAAAVAEPDHLREAGITAVLTVDSE
	1	1	[		1	EPSFKAGPGVEDLWRLFVPALDKPETDLLSH
	1					LDRCVAFIGQARAEGRAVLVHCHAGVSRSV
	1	1	ł			AIITAFLMKTDQLPFEKAYEKLQILKPEAKMN
	- {	1	į.			EGFEWQLKLYQAMGYEVDTSSAIYKQYRLQ
]	- 1	ļ	ļ			KVTEKYPELQNLPQELFAVDPTTVSQGLKDE
			1			VLYKCRKCRRSLFRSSSILDHREGSGPIAFAH
	Ì	ł	1			KRMTPSSMLTTGRQAQCTSYFIEPVQWMESA
ŀ					j	LLGVMDGOLLCPKCSAKLGSFNWYGEQCSC
1	· ·		{			GRWITPAFOIHKNRVDEMKILPVLGSQTGKI
	1700	<del>-                                     </del>	3127	816	139	EVETLGPRTPGP/EAQSPTPGSCPGWQEPSPGP
358	1708	, A	3127	010		TPPP*I SGPGPOGAPVLGKLLPDPEETPAGKTP
	- {	:		1		LGKHFWWGL\PVTSANFSPGAAA*FGGALSPP
1		ļ	1			GGDL/GHMLLOGPPSPFRLQQQ*QTPPGSHSP
	1	-	1	ļ		PTANREINPGPAAAADTRSCWGHKRSWRGW
ļ	Į.		ł		1	RGLAPWRLGFGSPGIP*PAPAGIP/GRPTWEGG
			1			KGAGGKPSETLTRSPPVWRGKRGSANGFLSW
			<b>\</b>	1		VOILO
				1-	191	HEHLLLLLCVFLVKSQGVNDNEEGFFSARG
359	1709	Α	3132	3	191	HRPLDKKREDAPNLRPALADVITVCDYRAQIA
}				1		*AASTPKRAASIAHNAVSCR*AQIA
L					1206	PEDPRPALLEF*DRVSLCCPGWNAVVQSQLT
360	1710	Α	3134	1	286	AAPTSQVQ/SDSPTFPSSWDYRHVPEYPANFL
1	1	1		}	1	*RQGFPMLPRLVSNSWAQTVHPPRPPKVLDL
	'	1				· · ·
1	i	Į				QA PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA
361	1711	A	3135	56	1449	AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR
		1		1		VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N
			İ	1		GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA
1		ì				CONTROL A VIEW DITTO CHEET AND CHEET A PARTICULAR A VIEW CHICAL A VIEW C
	{	1				GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD
		ı	1	Ì		PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ
		1			j	APGLPHRTSIRPGWRRLTEPEAWARRHRRPW
	1	İ		1	1	GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT
		1		- 1		PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ
	[	1		1		SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA
į					1	GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT
1	1	1	1	I .	ı	
			1	1		F/LIPSPT*MSPALVIQPPVPPTQMGLRISGLPR QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP
						GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT

		77-	I CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid E=Glutamic Acid,
10: of	NO: of	noa	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	Ì	1	ng to first	acid residue	O-Glutamine R=Arginine, S=Serine,
ience	}		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	l	ł		sequence	/=possible nucleotide deletion, \=possible
	1	l		peptide		nucleotide insertion
	1	<u> </u>	<u> </u>	sequence	ļ	RNQSPLGNDTLSSGLPMGPRRQVWPLARVG
						GHSSPREPQVLKKPLWGQTDIAGVGSASLYP
	}					
	)	}			L	DNL RVGMVLGTREVGDSTPPPSPPLYPFTGNEFVQ
362	1712	A	3136	1270	274	HNTWQLSRVYPSDLRTDSSNYNPQELWNAG
302	1,,,,		1	}		HNT WQLSKV IPSDLKIDSSIVINI QLEWING
	1	1	ł		\	CQM/V*GGSRDWEEGVEEQQVGNKFSSDGR
	1		1	1		VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS
	ļ		1	1		LKEGLEGLHGESCSSFLLGPSVAMNMQTAGL
	[	1		1		EMDICDGHFRQNGGCGYVLKPDFLRDIQSSF
	1		ļ	1		HPEKPISPFKAQTLLNQVISVQQLPKVDKTKE
	ļ		ļ			GSTUDPLVKVOIFGVRLDTARQETNYVENNG
	1		ļ	1		FNPYWGOTLCFRVLGPDFPMLRFGKMDYDW
		Ì			ľ	KSRNDLLGKTPCPGTCMQQGYRHIHLLSKDG
		1	1		1	ISTRPASIFVYICIOEGLEGDES
		1		<del></del>		MFAGSYGKSMFSFSKKVLNCLPKWRYHFVIA
363	1713	C	3139	60	248	PAMNESPLAPHLHQHLVFSVFQVLTILIGV**
	1	-				SAFKTLQLPAFSLYFDLGSLKLLILRIHTSIVK
364	1714	A	3140	57	418	NHKVESPRTMSPG*DPQSFLQIPQPRPPQLRV
	1					GLTSGLIQHFHSPSSCQFPLLRGPPFPRQPPLGI
	1	1	1			SGASLCPVLSPPR*PLQPSSL
		1	Į			LLPYPSLFVFLRQCHFVT/RLECNGVVSAHCN
365	1715	A	3145	122	413	LLPYPSLFVFLRQCHFV FIXLECTOV CULTUL IE/VF
303	1713	1		}		LHLPGSSDSPASAS*VAGTTGVCHHTRLIF\VF
	i	1	1			LV*TGFHYVAQAGLELLTA*S\PPQLPKVVGL
	1		}			QA
	1.716	A	3150	247	2	VGEKLHDIRFGNDFDMTPKAQATKEKIDKLN
366	1716	A	3130	1 2 17		FIKIKKLCIEGYY/NREPQNGRKIFANYVS\DK
		- }		}		GIMATIYEELLKLSNKLIQ
		_		3	2367	OKIKONOPKRAHVEDGGSRSKQGNEQSKKT
367	1717	A	3152	3	2507	PIEKSDEAAATHPRAFYLSKPDETPNAWMSD
	l	-		ļ		SGTGLTYWKLEEKDMHHSLPETLEKTFISLSS
l	- 1	\	j			TDVSPNOVLTLDPTLHMKPKQQISGIQPHGLP
	1	- 1	1			NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN
	- 1	- 1				VISOI PGEPKYPSHTKASPVDSWKNQIFQNE
	1	}	1	Ì		SPITSSTEPSVYTITSNDISVNTVDEENTVMVAX
			Į			ASVSQSQLPGTANSVPECISLTSLEDPVILSKIF
			1			QNLKEKHARHIADLRAYYESEINSLKQKLEA
	]	ļ	1			KEISGVEDWKITNQILVDRCGQLDSALHEATS
1		}	İ	ł	1	RVRTLENKNNLLEIEVNDLRERFSAASSASKI
	Į	1			į	LQERIEEMRTSSKEKDNTIIRLKSRLQDLEEAF
1	ļ	-	i	]		LOEKIEEMK 155KEKDATIKLKSTOOGDESSE 2
	Į.	Į	i i	1		ENAYKLSDDKEAQLKQENKMFQDLLGEYES
		1	j			LGKEHRRVKDALNTTENKLLDAYTQISDLKR
	1	i	i			MISKLEAQVKQVEHENMLSLRHNSRIHVRPS
	1	1		Ì		RANTLATSDVSRRKWLIPGAEYSIFTGQPLDT
		1	]	}		QDSNVDNQLEETCSLGHRSPLEKDSSP/GSSS
1		ĺ	ì			SILIKKORETSDTPIMRALKELDEGKIFKNWC
		j		1		TOTEKEDTSNSLL*/INPROTETSVNASRSPEK
	}	}	1			CAOOROKRINSASORSSSLPPSNRKSSTPTKR
		-			1	FIMI TPVTVAYSPKRSPKENLSPGFSHLLSKN
1	1			1		ESSPIREKTYSEKATDNHVNHSSCPEPVPNGV
	i			1		KKVSVRTAWEKNKSVSYEQCKPVSVTPQGN
				1		DFEYTAKIRTLAETERFFDELTKEKDQIEAAL
i		1		- (		OF THE TAKE TEACHER TO THE MOUNT OF MILE
				1	1	SRMPSPGGRITLQTRLNQVKCLSLNLL
260	1710	A	3163	2	2350	EFKSGGCGAGLVAAGAVLVLYPASRAGERT
368	1718	A.	3103	-	· ·	RVPGSPAPSSLPLHSPGACGTEVDMDPQRSPI
						1 EVK GNIELKRPLIKAPSOLPLSGSRLKRRPD
1			İ			MEDGI EPEKKRTRGLGATTKITTSHPRVPSL
1		- 1			}	TVPOTOGOTTAOKVSKKTGPRCSTALATGLK
	1					1117171717171
			{			NOKPVPAVPVOKSGTSGVPPMAGGKKPSKR
						NOKPVPAVPVQKSGTSGVPPMAGGKKPSKR AWDLKGQLCDLNAELKRCRERTQTLDQENC

SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
eotide seq- uence	seq- uence		09/496	correspondi ng to first amino acid residue of peptide sequence	to last amino acid residue of peptide sequence	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						OLODQLRDAQQQVKALGTERTTLEGHLAKV QAQAEQGQQELKNLRACVLELEERLSTQEGL VQELQKKQVELQEERRGLMSQLEEKERRLQT SEAALSSSQAEVASLRQETVAQAALLTEREER LHGLEMERRRLHNQLQELKGNIRVFCRVRPV LPGEPTPPPGLLLFPSGPGGPSDPPTRLSLSRSD ERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDE VFEEIAMLVQSALDGYPVCIFAYGQTGSGKTF TMEGGPGGDPQLEGLIPRALRHLFSVAQELSG QGWTYSFVASYVEIYNETVRDLLATGTRKGQ GGECEIRRAGPGSEELTVTNARYVPVSCEKEV DALLHLARQNRAVARTAQNERSSRSHSVFQL QISGEHSSRGLQCGAPLSLVDLAGSERLDPGL ALGPGERERLRETQAINSSLSTLGLVIMALSN KESHVPYRNSKLTYLLQNSLGGSAKMLMFV NISPLEENVSESLNSLRFASKVEPSVLFGTAQS NRKWKTDPDLCVCVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGGFIGWRAPCPRAIK
369	1719	A	3165	365	12	GYTSQGRWIDIERGPLTANTESLHENNFNALP GYIRKIE*I*IYKKN*INFGGVGLLNIVKISILS/K IYRFDAIPVKILTRFFINLDKLILKFVLKTKIAK NRIKTFYIMRRKKLGDSS
370	1720	Α.	3170	393	42	GASISPSAVIDGVEGLKPMQEQEAQEAGPCLD *HMAPEQWVAPR\RLLFRLIFSVLHALIIAAAA QSSAEEDEDPRN*GQSSEDQAPNQNGLIVIVH RVHVPLGAAATVPVHRSHFPR
371	1721	A	3173	770	510	GNGGCGLSQIPPSHLGAFSRGSLLSRG\DPRGP PPHPVIFFVFVVE\QGFTVLARMVSIS*PCDPP ALASQSAGITGVSHLARPQNLYF
372	1722	A	3180	381	76	RVLHHDNVPAHSSPQKREISQEFQLEIRHLP*S PDLAPSGCFLFLNLKNIFK\GTHFSLVDNVKK TVSTWLH/SQNAQFYKDRLNGWYHCLQKCL QHY*AYVEK
373	1723	A	3181	410	14101	RREVAGPEGKGLLLASAHTMLTPPLLLLLPLL SALVAAAIDAPKTCSPKQFACRDQITCISKGW RCDGERDCPDGSDEAPEICPQSKAQRCQPNE HNCLGTELCVPMSRLCNGVQDCMDGSDEGP HCRELQGNCSRLGCQHHCVPTLDGPTCYCNS SFQLQADGKTCKDFDECSVYGTCSQLCTNTD GSFICGCVEGYLLQPDNRSCKAKNEPVDRPP VLLIANSQNILATYLSGAQVSTITPTSTRQTTA MDFSYANETVCWVHVGDSAAQTQLKCARM PGLKGFVDEHTINISLSLHHVEQMAIDWLTGN FYFVDDIDDRIFVCNRNGDTCVTLLDLELYNP KGIALDPAMGKVFFTDYGQIPKVERCDMDG QNRTKLVDSKIVFPHGITLDLVSRLVYWADA YLDYIEVVDYEGKGRQTIIQGILIEHLYGLTVF ENYLYATNSDNANAQQKTSVIRVNRFNSTEY QVVTRVDKGGALHIYHQRQPRVRSHACEN DQYGKPGGCSDICLLANSHKARTCRCRSGFS LGSDGKSCKKPEHELFLVYGKGRPGIIRGMD MGAKVPDEHMIPIENLMNPRALDFHAETGFI YFADTTSYLIGRQKIDGTERETILKDGIHNVE GVAVDWMGDNLYWTDDGPKKTISVARLEK AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW TDWEEDPKDSRRGRLERAWMDGSHRDIFVT SKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI LLNGTDRKIVYEGPELNHAFGLCHHGNYLFW TEYRSGSVYRLERGVGGAPPTVTLLRSERPPI

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
			Ì	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	1		1	residue of	sequence	/=possible nucleotide deletion, \=possible
1	1	1		peptide	İ	nucleotide insertion
				sequence		FEIR/MYDAQHQQVGSNKCRVNNAGCSSLCL
						ATPGSRQCACAEDQVLDADGVTCLANPSYVP
		1				PPQCQPGEFACANSRCIQERWKCDGDNDCLD
			1			NSDEAPALCHQHTCPSDRFKCENNRCIPNRW
						LCDGDNDCGNSEDESNATCSARTCPPNQFSC
ļ	-	1		Ì		ASGRCIPISWTCDLDDDCGDRSDESASCAYPT
			1			CFPLTQFTCNNGRCININWRCDNDNDCGDNS
		-			j	DEAGCSHSCSSTQFKCNSGRCIPEHWTCDGD
		-	-	1	1	NDCGDYSDETHANCTNQATRPPGGCHTDEF
						QCRLDGLCIPLRWRCDGDTDCMDSSDEKSCE
						GVTHVCDPSVKFGCKDSARCISKAWVCDGD
	{		Ì	1		NDCEDNSDEENCESLACRPPSHPCANNTSVC
1	1	-	1	1		LPPDKLCDGNDDCGDGSDEGELCDQCSLNN
			}		1	GGCSHNCSVAPGEGIVCSCPLGMELGPDNHT
				1	1	COLOSYCAKHLKCSOKCDQNKFSVKCSCYEG
		Į		ł	1	WVI_EPDGESCRSLDPFKPFIIFSNRHEIRRIDLH
	j	-		1		KGDYSVLVPGLRNTIALDFHLSQSALYWIDV
	1	1				VEDKIYRGKLLDNGALTSFEVVIQYGLATPEG
	Ì					LAVDWIAGNIYWVESNLDQIEVAKLDGTLRT
	1		1	1		TILLAGDIEHPRAIALDPROGILFWTDWDASLP
			Ì			RIEAASMSGAGRRTVHRETGSGGWPNGLTV
		i i	İ			DYLEKRILWIDARSDAIYSARYDGSGHMEVL
			ľ	1		RGHEFLSHPFAVTLYGGEVYWTDWRTNTLA
1	\		ļ			KANKWTGHNVTVVQRTNTQPFDLQVYHPSR
						QPMAPNPCEANGGQGPCSHLCLINYNRTVSC
	Ì		1		1	ACPHLMKLHKDNTTCYEFKKFLLYARQMEIR
	1					GVDLDAPYYNYIISFTVPDIDNVTVLDYDARE QRVYWSDVRTQAIKRAFINGTGVETVVSADL
	}	j			1	PNAHGLAVDWVSRNLFWTSYDTNKKQINVA
						RLDGSFKNAVVQGLEQPHGLVVHPLRGKLY
	1					WTDGDNISMANMDGSNRTLLFSGQKGPVGL
					1	AIDFPESKLYWISSGNHTINRCNLDGSGLEVID
	Ì	Ì			İ	AMRSQLGKATALAIMGDKLWWADQVSEKM
		-				GTCSKADGSGSVVLRNSTTLVMHMKVYDESI
		1	Į.	1	*	QLDHKGTNPCSVNNGDCSQLCLPTSETTRSC
		İ	1	İ		MCTAGYSLRSGOOACEGVGSFLLYSVHEGIR
	İ	-				GIPLDPNDKSDALVPVSGTSLAVGIDFHAEND
	1	1	1	1	1	TIVWVDMGLSTISRAKRDQTWREDVVTNGIG
· ·		Ì	Ì			RVEGIAVDWIAGNTYWTDQGFDVIEVARLNG
						SFRYVVISOGLDKPRAITVHPEKGYLFWTEW
						GOYPRIERSRLDGTERVVLVNVSISWPNGISV
		-				DYODGKLYWCDARTDKIERIDLETGENREVV
		-		1		LSSNNMDMFSVSVFEDFIYWSDRTHANGSIK
		1				RGSKDNATDSVPLRTGIGVQLKDIKVFNRDR
		ļ				QKGTNVCAVANGGCQQLCLYRGRGQRACA
			j			CAHGMLAEDGASCREYAGYLLYSERTILKSI
						HLSDERNLNAPVQPFEDPEHMKNVIALAFDY
						RAGTSPGTPNRIFFSDIHFGNIQQINDDGSRRIT
1		- }				IVENVGSVEGLAYHRGWDTLYWTSYTTSTIT
İ						RHTVDQTRPGAFERETVITMSGDDHPRAFVL
1	1					DECONLMENTINWNEQHPSIMRAALSGANVL
			1			TLIEKDIRTPNGLAIDHRAEKLYFSDATLDKIE
						RCEYDGSHRYVILKSEPVHPFGLAVYGEHIF
		-				WTDWVRRAVQRANKHVGSNMKLLRVDIPQ
	- 1	1		1	1	QPMGILAVANDTNSCELSPCRINNGGCQDLCL
1					1	LTHQGHVNCSCRGGRILQDDLTCRAVNSSCR
		- 1		1		AQDEFECANGECINFSLTCDGVPHCKDKSDE
		- 1		(		KPSYCNSRRCKKTFRQCSNGRCVSNMLWCN GADDCGDGSDEIPCNKTACGVGEFRCRDGTC
1			ļ	İ		GADDCGDGSDEIPCNKTACGVGEFRCEDGTC IGNSSRCNQFVDCEDASDEMNCSATDCSSYF
						IGNOSKUNGF VDCEDASDEMINGSATDOSSTT
L						

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
l				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	,	/=possible nucleotide deletion, \=possible
	[	1		sequence		nucleotide insertion RLGVKGVLFQPCERTSLCYAPSWVCDGAND
<del></del>		+	<u> </u>			CGDYSDERDCPGVKRPRCPLNYFACPSGRCIP
	1					MSWTCDKEDDCEHGEDETHCNKFCSEAQFE
	1					CONHRCISKOWLCDGSDDCGDGSDEAAHCE
		ì	ĺ			GKTCGPSSESCPGTHVCVPERWLCDGDKDCA
						DGADESIAAGCLYNSTCDDREFMCQNRQCIP
						KHEVCDHDRDCADGSDESPECEYPICGPSEF
	İ					RCANGRCLSSRQWECDGENDCHDQSDEAPK
		i				NPHCTSPEHKCNASSQFLCSSGRCVAEALLCN NPHCTSPEHKCNASSQFLCSSGRCVAEALLCN
	}	1				GQDDCGDSSDERGCHINECLSRKLSGCSQDC EDLKIGFKCRCRPGFRLKDDGRTCADVDECS
1				1		TTFPCSQRCINTHGSYKCLCVEGYAPRGGDP
						HSCKAVTDEEPFLIFANRYYLRKLNLDGSNY
			1			TILKOGLNNAVALDFDYREOMIYWIDVIIQ
	1	1				GSMIRRMHLNGSNVQVLHRTGLSNPDGLAV
						DWVGGNLYWCDKGRDTIEVSKLNGAYKIVL
	}	-				VSSGLREPRALVVDVQNGYLYWTDWGDHSL IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTE
						RIYWADAREDYIEFASLDGSNRHVVLSQDIPH
			Ì			IFALTLFEDYVYWTDWETKSINRAHKTTGTN
	}	ì				KTLLISTLHRPMDLHVFHALRQPDVPNHPCK
		\ \				VNNGGCSNLCLLSPGGGHKCACPTNFYLGSD
						GRTCVSNCTASQFVCKNDKCIPFWWKCDTE
						DDCGDHSDEPPDCPEFKCRPGQFQCSTGICTN PAFICDGDNDCQDNSDEANCDIHVCLPSQFK
						CTNTNRCIPGIFRCNGQDNCGDGEDERDCPE
	İ		Ì			VTCAPNQFQCSITKRCIPRVWVCDRDNDCVD
	-	1				GSDEPANCTOMTCGVDEFRCKDSGRCIPARW
		ì				KCDGEDDCGDGSDEPKEECDERTCEPYQFRC
		1				KNNRCVPGRWQCDYDNDCGDNSDEESCTPR
		i		1		PCSESEFSCANGRCIAGRWKCDGDHDCADGS PCSESEFSCANGRCIAGRWKCDGDHDCADGS
						DEKDCTPRCDMDQFQCKSGHCIPLRWRCDA DADCMDGSDEEACGTGVRTCPLDEFQCNNT
			-			LCKPLAWKCDGEDDCGDNSDENPEECARFV
	}		j			CPPNRPFRCKNDRVCLWIGRQCDGTDNCGD
	}	ļ	j			GTDEEDCEPPTAHTTHCKDKKEFLCKNQKCL
-		Ì				ccci pCNMFDDCGDGSDEEDCSIDPKLISCAI
	Ì	İ				NASICGDEARCVRTEKAAYCACRSGFHTVPG
						QPGCQDINECLRFGTCSQLCNNTKGGHLCSC ARNFMKTHNTCKAEGSEYQVLYIADDNEIRS
		i				LFPGHPHSAYEQAFQGDESVRIDAMDVHVKA
						GRVYWTNWHTGTISYRSLPPAAPPTTSNKHR
	1			1	[	POIDEGVI'HI NISGLKMPRGIAIDWVAGNVY
		1				WTDSGRDVIEVAOMKGENRKTLISGMIDEPH
					1	A INJUDDI ROTMYWSDWGNHPKIETAAMDGI
						LRETLYQDNIQWPTGLAVDYHNERLYWADA
		-				KLSVIGSIRLNGTDPIVAADSKRGLSHPFSIDV FEDYIYGVTYINNRVFKIHKFGHSPLVNLTGG
1						LSHASDVVLYHQHKQPEVTNPCDRKKCEWL
j		1				CLISPSGPVCTCPNGKRLDNGTCVPVPSP1PP
		1				PDAPRECTOLOCENGGSCFLNARRQPKCRC
			1	1		OPPVTGDKCELDOCWEHCRNGGTCAASPSG
	1	1				MPTCP CPTGFTGPKCTOOVCAGYCANNSTCI
		- 1				VNOGNOPOCRCLPGFLGDRCOYRQCSGYCE
				1		NEGTCOMAADGSROCRCTAYFEGSRCEVNK
						CSRCLEGACVVNKQSGDVTCNCTDGRVAPS CLTCVGHCSNGGSCTMNSKMMPECQCPPHM
		j				TGPRCEEHVFSQQQPGHIASILIPLLLLLLVL
i						VAGVVEWYKRRVOGAKGFQHQRMTNGAM
					ļ	NVEIGNPTYKMYEGGEPDDVGGLLDADFAL
						1 - 1 - 1 - 1

			1.000	Deadisted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	1 -	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	]	_	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ì	09/496	ng to first	acid residue	O=Giutamine, R=Arginine, S=Serine,
uenœ	Ì	i	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	!		1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	residue of	Sequence	/=possible nucleotide deletion, \=possible
	}	}		peptide	Ì	nucleotide insertion
				sequence		DPDKPTNFTNPVYATLYMGGHGSRHSLASTD
				1		EKRELLGRGPEDEIGDPLA
				<u> </u>	<u> </u>	CLELASAGKIPEESKALSLLAPAPTMTSLMPG
374	1724	Α	3187	191	1815	AGLLPIPTPNPLTTLGVSLSSLGAIPAAALDPNI
		1				AGLLPIPTPNPLTTLUVSLSSLUAITAAALDITA
		ì	1	1		ATLGEIPOPPLMGNVDPSKIDEIRRTVYVGNL
		1	]		ļ	NSQTTTADQLLEFFKQVGEVKFVRMAGDET
	1				1	QPTRFAFVEFADQNSVPRALAFNGVMFGDRP
	\		1		1	LKINHSNNAIVKPPEMTPQAAAKELEEVMKR
		i		1	<u> </u>	VREAQSFISAAIEPGWLHSTSLCNDFLGCF*RR
		1		1	1	RMYRE*APCTICGTFHLCLIINWDL*LF*AYTA
	1					K*FFPPRVWKEQ*KKRR\RSRSHTRSKSRSSSK
	ļ	1	1		ľ	SHSRRKRSQSKHRSRSHNRSRSRQKDRRRSK
	1	İ	1	1		SPHKKRSKSRERRKSRSRSHSRDKRKDTREKI
	İ	1	1			KEKERVKEKDREKEREREKEREKERGKN
		Į.	1			KDRDKEREKDREKDKEKDREREREKEHEKD
	1	1				RDKEKEKEQDKEKEREKDRSKEIDEKRKKDK
	1	}	}			KSRTPPRSYNASRRSRSSSRERRRRRSRSSSRS
	[	Į.	ì			PRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
	1	ĺ	1	i		HISERRERERSTSMRKSSNDRDGKEKLEKNST
·	i	1	ì	į		S
275	1725	A	3192	415	101	AHSSHQTRAILQEFQWDIIRHPPL\SPNLALSG
375	1723	^	31,72	} ~~~	, , , ,	F\FPNLKKSLRGTHFSSVKK\TTLTWLNSQDP
	[					WF/FFYP*SPDLQIPSSFRNGLNDWYHHSQKC
		1	1	}		PDLDGAYVKK
<u> </u>	170		3199	931	418	GV*WCDLGSPOPPPPGFKQFCLGRSSSWDYR
376	1726	Α	3199	731		HVPPHPANFVFLLETGFLHAGQAGL\GDPPAS
			i			ASQSAGITGVSHTWPKNHLIFYACLVIRSKRI
l						ĸ
L	<del></del>	+	3201	274	1285	KTGYTSRGSPLSPOSSIDSELSTSELEDDSISM
377	1727	Α	3201	2/4	1203	GYKLQDLTDVQIMARLQEESLRQDYASTSAS
			j	İ	1	VSRHSSSVSLSSGKKGTCSDQEYDQYSLEDEE
ļ				ļ		EFDHLPPPQPRLPRCSPFQRGIPHSQTFSSIREC
1	1		j	}		RRSPSSOYFPSNNYOOOOYYSPQAQTPDQQP
		1				NRTNGDK/PPKKYA*PSPDAKYNCH**QH\SSP
				1		VTVRNSQSFDSSLHGAGNGISRIQSCIPSPGQL
				ļ		OHRVHSVGHFPVSIROPLKATAYVSPTVQGSS
1	}	1	- 1			NMPLSNGLQLYSNTGIPTPNKAAASGIMGRS
	1		ļ			ALPRPSLAINGSNLPRSKIAQPVRSFLQPPKPL
		1				SSLSTLRDGNWRDGCY
1		<u> </u>			1.500	VPGVTESRPSVLRGDHLFALLSSETHQEDPIT
378	1728	A	3202	112	1789	YKGFVHKVELDRVKLSFSMSLLSRFVGWG*
1		1		1		PFKVNFY/TFNRQPLRV\QHRALELTGRWLLW
						PEKANEA/LEUKAKATERI OKATERI
1		ı				PMLFP\VAPRDVPLLPSDVKLKLYDRSLESNP
	Į	ł	l			EQLQAMRHIVTGTTRPAPYIIFGPPGTGKTVT
]	1		}	1		LVEAIKQVVKHLPKAHILACAPSNSGADLLC
		1		1		QRLRVHLPSSIYRLLAPSRDIRMVPEDIKPCCN
				1		WDAKKGEYVFPAKKKLQEYRVLITTLITAGR
1						LVSAQFPIDHFTHIFIDEAGHCMEPESLVAIAG
	Ì					LMEVKETGDPGGQLVLAGDPRQLGPVLRSPL
				1		TOKHGLGYSLLERLLTYNSLYKKGPDGYDPQ
1		1				FITKLLRNYRSHPTILDIPNQLYYEGELQACA
}	}		ļ			DVVDRERFCRWAG\LPRQGFPIIFHGVMGKD
		ĺ	İ	1	1	EREGNSPSFFNPEEAATVTSYLKLLLAPSSKK
		1	ļ			GKARLSPRSVGVISPYRKQVEKIRYCITKLDR
		1				FLRGLDDIKDLKVTCCSTVTPCLPCAPTCPLP
1		j	Į	1		ETSSSFHSSPRPRPTPAALNRARALPEPLTPGD
1	1			1		SNLRVWDGIRKPACLTNTSCHS
1			1	1	1	United to Donate the State of t
				120	120	PKAAPSVXI WEPPEL*GSFKPTKGHTXCVXIK
379	1729	A	3206	432	130	PKAAPSVXLWFPPFL*GSFKPTKGHTXCVXIK *LSTREAXDSXPGRQIAXXRQGGKVETTTAL

PCT/US01/03800

					Dunglinend d	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	Į	ì	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		1	}	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknowii, -Siop codoii,
	1		1	peptide		/=possible nucleotide deletion, \=possible
	ł		1	sequence		nucleotide insertion
<b> </b>	<del> </del>	+	-	<del> </del>		XKQSNNKGTRASSYXEPDAXEQWKFPHKKL
Í		1		1		QLPGXTHE
200	1730	A	3207	187	507	GGTGHPHPARPPLSGVGGCQCSHSKPWTAGS
380	1/30	^	3207	107		PEQRDHPAPHKQIEAGQGLPGPQAWGG*KGP
	Į.	1		}	1	AXLLPGPGGGPGPVASLEARAQASSGVTPNG
{	ſ	1	1	ļ		GGRTYPYPTFSSGE
		<del> </del>	2005	<del>                                     </del>	840	GTRPGHLPAPSDGFCV/HL*SIPSWGSF*GESL/
381	1731	A	3225	1	040	FMOLITSLGLOEFDIARNVLELIYAQTLVWIGI
Ì		1	1	1	ļ	FFCPLLPFIQMIMLFIMFYSKNISLMMNFQPPS
ļ		1	1			KAWRASQMMTFFIFLLFFPSFTGVLCTLAITI
	Į.	ļ	1	1		WRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRP
1			}	1		GYLWVVWIYRNLIGSVHFFFILTLIVLIITYLY
	1	1				WQITEGRKIMIRLLHEQIINEGKDKMFLIEKLI
	}				ļ.	KLQDMEKKANPSSLVLERREVEQQGFLHLGE
	ì		1	ł		KLQDMERKANPSSEVERKEVEQQ01 BXB0B
			1	]		HDGSLDLRSRRSVQEGNPRA
382	1732	A	3238	256	38	LLMIKVSSTCFSCHLHHHHHHHHHHHHQGHNS
302	1.52	1	1			LFFSLKSSSNSSTLPVYLSYNIILVFSKCLVFDF
}	1	1	1	İ		LFSNACL
383	1733	A	3241	1542	343	KGAPSFVRLYQYPNFAGPHAALANKSFFKAD
303	1/33	1 "	32	1		KVTMLWNKKATAVLVIASTDVDKTGASYYG
1	1	1	1			EQTLHYIATNGESAVVQLPKNGPIYDVVWNS
i	ł	ł	ł			SSTEFCAVYGFMPAKATIFNLKCDPVFDFGTG
1			1			PRNAAYYSPHGHILVLAGFGNLILQI*AD/IMK
1	İ		}			VWNVKNYKLISKPVASDSTYFAWCPDGEHIL
1	1	İ				TATCAPRLRVNNGYKIWHYTGSILHKYDVPS
	1		ł			NAFL WOVSWOPFLDGIFPAKTITYQAVPSEVP
	1		ł			NEEPKVATAYRPPALRNKPITNSKLHEEEPPQ
1	i		ì			NMKPOSGNDKPLSKTALKNQRKHEAKKAAK
	1	-				QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP
<u> </u> '	ļ	1	1	ľ	Ì	EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK
	i	1				NQLEKIQKETALLQELEDLELGI
1	i				(70	IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP
384	1734	Α	3242	3	678	RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP
		- 1				LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS
1	1		į	i	j	ASLVRATVRAVSKRKLQPTRAALTLTPSAVN
ļ				]		KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL
1				1		EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL
1		1		ļ		GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES
		1		1	-	
						FNI VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL
385	1735	A	3243	3190	664	VAMGIPKAQHPPPPQLLFLILLDGCFWIQQLFL
300					1	KEEEILPEPGSETPTVASEALAELLHGALLRR
	1	1		1		GPEMGYLPGPPLGPEGGEEETTTTIITTTVTT
1	ļ			}		TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL
	1	1		1		GLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELL
						VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT
			}			NRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFP
						PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG
1						FETLICLNGTRPSWNGETPSCMASCGGTIHNA
1				į .		TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL
1		1		}		HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS
						DMDDVPERGLISDAQSLYVELLSETPANPLLL
		1	ļ			SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG
	Ì	}	1			THE PROPERTY OF THE PROPERTY O
						ALATESCLPGYALEPPGPPNALECVDFTEPHW
						ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NITTEPACKAMCGGELSEPAGVVLSPDWPQS
						NDTEPACKAMCGGELSEPAGVVLSPDWPQS
						NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGODCVWGVHVQEEKRILLQVEILNVREG
						NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEILNVREG DMI TLFDGDGPSARVLAOLRGPQPRRRLLSS
						NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEILNVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLOFOAPPGPPNPGLGQGFVLHFKEVPR
			-			NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEILNVREG DMI TLFDGDGPSARVLAOLRGPQPRRRLLSS

		_				(A Alasina Carataina
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	{		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	}	peptide	]	/=possible nucleotide deletion, \=possible
	1	ļ	ļ	sequence		nucleotide insertion
<del></del>	-		+	37.7	<del> </del>	MTCADPGEIANGHRTASDAGFPVGSHVQYRC
			1		<b>\</b>	LPGYSLEGAAMLTCYSRDTGTPKWSDRVPKC
			Ì			ALKYEPCLNPGVPENGYQTLYKHHYQAGESL
	İ	1	1			RFFCYEGFELIGEVTITCVPGHPSQWTSQPPLC
	(					KVTQTTDPSRQLEGGNLALAILLPLGLVIVLG
	i		1			SGVYIYYTKLQGKSLFGFSGSHSYSPITVESDF
		1			ŀ	SNPLYEAGDTREYEVSI
		<u> </u>	ļ		2004	GTSTVTMATKKHFSIILNLLGMLLKKDNQDT
386	1736	A	3250	5725	3984	RKLLMTWALEVAVVMKKSETYAPLFCLPSF
		1				HKFCKGLLADTLVEDVNICLQACSSLHALSSS
1	1		ł			HKTCKGLLADILVEDVNICLQACSSLIALSSS
			1			LPDDLLQRCVDVCRVQLVHRGTCIRQAFGKL
	1	İ	ł			LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP
		ì				SNTFHPQDFSD/VISFILYGNSHRTGKDNWLE
		1	İ			RLFYSCORLDKRDQSTIPRNLLKTDAVLWQW
l		1	1	1	1	AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIR
			1	1		SLAGHTLNPDQDVSQWTTADNDEGHGNNQL
					İ	RLVLLLQYLENLEKLMYNAYEGCANALTSPP
	]	1	1		}	KVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLA
		1	1			GQPAVTVRHGFDLLTEMKTTSLSQGNELEVSI
	ł	1			ļ	MMVVEALCELHCPEAIQGIAVWSSSIVGKHL
1	1	}	l l		1	LWINSVAQQAEGRFEKASVEYQEHLCAMTG
		ļ	1			VDCCISSFDKSVLTLASAGCKSASLKHCLNGE
						SRKSVLSKPTDSSPEVINYLGNKACECYISTA
	1		ļ		1	DWAAVQEWQNAIHDLKKSTSSTSLNLKADF
1	1		İ			NYIKSLSSFESGKFVECTEQLELLPGENINLLA
	1				1	GGSKEKIDMKKLLRNM
205	1737	<del>                                     </del>	3255	380	76	MDIFLYNCKYQVQTEI*NSIQHIMA\SKKLSRF
387	1/3/	A	3233	360	1 70	LKYVHNL*AENYKTLMK*INEDLNKQRDVPY
		1				S*TARLNKMSIPTKTIFRFKAIYIKIPATYFIET
1		1	i	1		NMQ
	<del></del>	┵	2260	685	428	POWLGLQVYALPPANFVFFVEMRSTILAQTG
388	1738	A	3260	685	420	FELLDSSDLPASASKSAGITCMSHHARTLSLK
		1	j	1		*WPFCLSATQEKFC*PASEGVAW
L		┧	<del> </del> _	<del> </del>	1222	LDGYHTPIYMLNRIIRLPAAL*IISDQTGHALTI
389	1739	A	3269	1	332	LTRLETQMINADYQNKLTLDYLLTTDREVYE
		İ	1	1		PFNLTNYCLHIHNQRLGAYDLG*V*Q/KLAHV
i		1	1	ĺ	•	PHOLINICEDE VICES
		į.				PVQV*HGFDPEAMFR
390	1740	A	3270	2	372	GRCHDQNKGKS\DGPDAQAEACGGESTYQEL
1				1		LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH
					1	SPRGVKKVHKFVNKGEKGIMVLAGDTLGIGV
	1	{				YCLLPCMC*DRKLTYAHIPSTTDLGAGAGY
391	1741	A	3273	1	187	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ
	1	-		1	1	HVETFFQ\EELTRSQEGMKLGENFLMFAMPP
		1		1	{	DDSKESKGK*FFQEMLDIMKAISDMMGKCTY
		ļ		1		PVLKEDAPRQHVETFFQVGINQKSRGHEVRR
						KFPDVCHAPR
202	1742	A	3281	901	521	FFFGDGVSPCRQAGV*WHDLDSLQNLPPGFK
392	1/42	A	3201	"	1 22.	RESYLSLPSSW\DYRHVLPRQANFCIF/M*RRG
	1		}	1		FTMLARMVSIS*PRDLPALASQSAGITGVSHH
		1		1	1	APPOMDFTFALLCFALKGCLPRQKEGGTLNLI
i	1.5.5	<del>   </del>	1000	705	3	RNRSVVPEFVLLGLSAGPQTQTLLFVLFVVIC
393	1743	A	3283	385	٦	LLTVMGNLLLLVVINADSCLHTPMYFFLGQL
		}		1		SFLDLCHSSVTAPKLLENLLSEKKTISVEGCM
						5 LULUNDO Y LATALLENLLOERA LIO YEUCIVI
	Ì			1		A*VFFVFATGGTESSLLAVMAYDRYVAIRTR
1				1		G
394	1744	A	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYLHLGKC
1	1			1		LDNCPEGLEANNHTMECVSIVHCEVSEWNP
1	1					WSPCTKKGKTCGFKRGTETRVREUQHPSAKG
		1	j	1	1	NLCPPTNETRKCTVQRKKCQKGERGKKGRE
1	1	- 1	<b>I</b>	ŀ		NLCFF INETRICT VOICECCROENCIA

250 15	DEC ID	1401	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-			USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ļ	Į.	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ĺ	ļ	1	peptide	Sequence	/=possible nucleotide deletion, \=possible
	1	{		sequence		nucleotide insertion
		<u> </u>	<b>↓</b>	sequence		RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN
	Į.		]			KQQQ
			-	<del> </del>	340	RVLYVPSMGFCILVAHGWQKISTKSVFKKLS
395	1745	A	3286	1	340	WICLSMVILTHSLKTFHRNWDWESEYILFMS
	İ	1				ALKVNKNNAKLWNNVGHALENEKNFERAL
					1	KYFLQATHVQPDDIGAHMNVGR
	l			ļ. <u>.</u>	170	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL
396	1746	A	3293	1	172	IAFMKQRRMGLNDFIQKIANNSYACKQ
	1				101	AEPACGASSCTPPSLRSSSSQSVGPLRPGRPL
397	1747	Α	3295	12	401	WSEACAFL*AAAPQGPASPCCGLPSGFPRVW
	1	1	ļ	ļ	1	AQCCPPGGALRFPEGLGSVLSPRRCPQVSRGS
	1	1	1		1	GLSAVPQEVPSGFLGPGLRACPQEAPSRFLRA
		}		1		1
	1	į		J		GLT KQRRWQNIQRKGPKRYIVIAGNSQSHQPMIFS
398	1748	A	3300	1912	2768	MLRKLPKVTCRDVLPEIRAICIEEIGCWMQSY
	[			}		STSFLTDSYLKYIGWTLHDKHREVRVKCVKA
		1				LKGLYGNRDLTARLELFTGRFKDWMVSMIV
						DREYSVAVEAVRLLILILKNMEGVLMDVDCE
	1	1	ł			SVYPIV*ASN*GLASAVGEFLYWKLFYPECEI
		1	}			SVYPIV*ASN*GLASA VGETLI WALI I I BEEVESK SI
		i	1			RTMGGREQRQSPGAQRTFFQLLLSFFVESKSI
	1	ì	1	ł		SVTQAGVQWQFSAHRDLCLPGSSNSHVSASR
	-	1	1	1		VAGIAGAHRHTWLIYVFFSWRQGFAVLAGL
		1	1		<u> </u>	VSNS TO THE PROPERTY OF THE PR
399	1749	A	3301	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSE
	1	]		1		SPPPITDSWAPFISLTHHVLSQSQSPLSSNCWI
	İ	1	1			CLSTHTQ*FTALPADLLTWTQSNVSLHISYLA
	Ì	-	1			PFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
	1		ľ			GRAVALLHLIASGLTSIQTNTASSKPPIWGYL
	1		}			STQTSFISPPPLCLSRTYPNPAHATMVGQVPQ
	İ	1	1			SLCGLIFTL/RTPCRPSILHPNYKIISTSAWQKV
		1		l		LCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAAN
	1	-	]	]		SALYVSSLKGPPGKNVTIPSPVTGT*QPPHRG
	1		l l			N/RLTVDKDNFFLSPKPNSLHQLPSQ\TPYQAL
						TGAALAGSYPIWENENTLSWLPTFTYNFCLS
			Ì	i		PSLFFLCDTN*YLCLPANWSGTCTLVFQAPTI
	ļ			Į		NILPPNQTILISVEASISSSPIRNKWALHLITLLT
		1		1		GLGITAALGTGIAGITTSITSYQTLFTTLSNTV
	-	ŀ	l l			DMHTSITSLQRQLDFLVGVILQNWRVLDLLT
			1			TEKGGTCIYLQEECCFCVNESGIVHIAVRRLH
	1		1			DRAAEL*HQVADSWWQGSSLLRWIPWVAPF
	1	-	i		1	LGPLIFLFLLLMIGPCIFNLVSRFISQRLNCFIQ
		1	1	Ì		ASMQKHIDNIFHLCHV*YQSLRGNHSEAPEPI
						P
400	1750	A	3303	2	453	THWRHSSGVPGSTTARRRRELEIATSDNQE
400	1/30	1 ^	1 3303	! -	1	YYNRLCQEVTNRERNDQKMLADLDDLNRTI
	- [	1			1	VVI FERI IFI I ROKDAL WOKSDALEFQQKLS
		1	1		1	AFERWLGDTEANHCLDCKREFSWMVRRHH
				1		RICGRIFCYYCCNNYVLSKHGGKKERCC
46:		<del></del>	3304	1	626	MAPOHSSLDDKVPOOASTVCFEFQDILQHSQ
401	1751	Α	3304	1 1	020	CTEHKDSLWGPGARSQPFGAHNTRLSPDSCP
	1			l		FKIVI RALKDSRAGMPEODKDPGVQENPDD
		)	}	1		ORRVPOGTGDAPSAFRPLWDNGGLSPFVSRF
[				Ţ		GPLERDLHAQRSEVTYNQRSQSSWMSSFPKI
						NAFVSPYSSMGQAQP/GLPKTNPIGESCCWEG
				1		LSLSTQILG*QKPSKYIPSLCKR
		<u> </u>			150	MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA
402	1752	A	3305	1678	172	PVGFCLLVLRLFLGIHVFLVSCALPDSVLRRF
402		1	ı	- 1	1	LAQLCTTATEFORTAL FARCUET DRAFTER
402	ļ	1		į.	1	AND THACAVI OF MADOEDS OF ROHSVRVI ISI
402						VVRTMCAVLGLVARQEDSGLRDHSVRVLIST HVTPFDHNIVNLLTTCSTVSESEAESATGRFP

PCT/US01/03800

EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
ucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
æq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ieuce			717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
i	l			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
\	. !			peptide	004	/=possible nucleotide deletion, \=possible
	i		1	sequence	ł	nucleotide insertion
				sequence	ļ	GAOLKAPLSPLAFRMEDTEALPLTPILYPTCQ
			ļ	ĺ		FEEE/IFI NIFLLAFSSPGSOPLLNSPPSFVCWSR
			1			GFMEMNGRGELVESLKRFCASTRLPPTPLLLF
Ì						PEEEATNGREGLLRFSSWPFSIQDVVQPLTLQ
	ļ		1	Ï		VQRTLVSVTVSDASWVSELL\WSLFVPFTVY
	ļ	ł	1	Ì	1	QVRWLRPVHRQLGEANEEFALRVQQ\LVAKE
	,			İ	1	LG\QTGTRLTPA\DKAEHMKRQRHPR\LRPQS
	1		1			AQSSFPPSPWVLSS/SDVQTGQTLGFREFKESF
	İ	1	ĺ	ſ		CPHVAIGVFIPERPWPKTGCCKTLTIHLILL*G
	ļ	1	l			CPHVAIGVFIPERPWPATOCCATETHIELES O
	1	1	1	ļ	1	GPVSFSCPE\DIHPRGT*VPTQQASGLPSFPSYG
	Į.	1				PARGGVL*HPSAQQPLTFA\KSS\WARAGRAL
	ì		1	(	}	QERKQ\ALYEYARRFTERRAPGGLD
702	1753	A	3307	44	447	DPSPSLLAVALGLRAGERTRSGPGSSSPSGGIS
403	1/33	^	3307	1		GGASAGLASSPECACGRSHFTCAVSALGECT
		l		1	1	CIPAOWOCDGDNDCGDHSDEDGCILPTCSPL
	1	1	Ì			DFHCDNGKCIRRSWVCDSDNDCEDDSDEQD
	i	1	1	ļ.		CPPRECEED
		<u> </u>		409	1	PRHGWGRRVLGRDRPRLOKVKKSVKAIYIPG
404	1754	A	3311	409	1	ODHVONEFIYARVLDKFGSNFLSRDNADLGT
	1	1	1			AFVKESTI TK*LSALLKNLLOGLSRNVIF1LDS
	ı	1	İ	}		LLKGDLKGVKGDLKKPFDKAWKDYETKFAK
		1	)		ļ	IEKEKREREWR
	1	l		<del> </del>	450	AAVPVENPWDDPRVRPRVRIFTWEDCIAGQA
405	1755	Α	3322	12	458	KVLCNDSYGVTIDWSPKGAFIRLTSQSVGNG
	1	1	1		İ	HPASKENDQMVDTIKNTTKVPIIWTYGDMVE
			1	i	ļ	PRPOMIRPAVGAKHKELWKILMALKKIKVWE
	1	1	1		l	GKYTKPSQYNPNYMLELAHNDSVW
	1					LSMLSTISTEHRLSVLWPIWYCCHCPTHLSAV
406	1756	A	3324	1	426	MCVLLWALSLLQSILEWMFCSFLFSDVDSDN
	1	}		)		WCQILDFLTAVWLIFLILVLCGFTLVLLVRIIC
	-	-	l l	!		GSQKMPLTRLYVTILLTGLVFLFCSLPLSIQ*F
						GSQKMPLIKLTVITELTGLVTET-CBELDBIQ
	}	1	1	1		LLYWIEKDLDDL
407	1757	1 <sub>A</sub>	3328	213	1841	SGDLSPAELMMLTIGDVIKQLIEAHEQGKDID
407	1,3,	1.				LNKVKTKTAAKYGLSAQPRLVDIIAAVPPQY
		-		ļ	ì	RKVLMPKLKAKPIRTASGIAVVAVMCKPHRC
	- 1	l	ł		!	PHISFTGNICVYCPGGPDSDFEYSTQSYTGYEP
	1	Ì	Ì		ì	TSMRAIRARYDPFLQTRHRIEQLKQLGHSVD
1	1		ł	l .		KVEFIVMGGTFMALPEEYRDYFIRNLHDALS
	ļ		1			GHTSNNIYEAVKYSERSLTKCIGITIETRPDYC
		- 1	l	ì		MKRHISDMLTYGCTRLEIGVQSVYEDVARD
		1	Ì	1		TNIDGHTVKAVCESFHLAKDSGFKVVAHMMP
					1	DIPNYGLERDIEOFTEFFENPAFRPDGLKLYP
				1		TI VIRGTGLYELWKSGRYKSYSPSDLVELVA
1		-	1	1		RIT AT VPPWTRVYRVORDIPMPLVSSGVEHG
}						MI REI AT ARMKDI.GIOCRDVRTREVGIQEIH
1		1		1	1	HIVERPYOVELVERDYVANGGWETFLSYEDP
	1	-	1		1	DODILIGLERIKCSEETFRFELGGGVSIVREL
	<b>3</b>	1	1	1		HVYGSVVPVSSRDPTKFQHQGFGMLLMEEA
	İ			1	1	TA 102 A AL ADDICOL LIG GLIGOL CHINDS
						EDIADERUCSGKIAVISGVGTRNYYRKIGYKL
						ERIAREEHGSGKIAVISGVGTRNYYRKIGYRL
						OGPYMVKMLK
408	1758	A	3335	3	467	QGPYMVKMLK ATA SPRAA GIRHELTSTMAAGKNKRLTKGGK
408	1758	A	3335	3	467	QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG
408	1758	A	3335	3	467	QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFFFSLADLOND/TDGYLLRVI*VAFTT
408	1758	A	3335	3	467	QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESLADLQND\TDGYLLRVI*VAFTT FRINOI/REVFNKLIPDSIGKDIEKACQSIYPLH
408	1758	A	3335	3	467	QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESLADLQND\TDGYLLRVI*VAFTT ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPLH DDFARKVKMLKKPKFELRKLMELHGEGSS
						QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESLADLQND\TDGYLLRVI*VAFTT ERTNQI/REVF\NKLIPDSIGKDIEKACQSIYPLH DDFARKVKMLKKPKFELRKLMELHGEGSS PRWR\SARDEILLSFPONYYIQWL\NGSLIHGL
408	1758	A	3335	3	1252	QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESLADLQND\TDGYLLRVI*VAFTT ERTNQI/REVF\NKLIPDSIGKDIEKACQSIYPLH DDFARKVKMLKKPKFELRKLMELHGEGSS PRWRNSARDEILLSFPQNYYIQWLNGSLIHGL WNI ASI.FSNLCLFVLMPFAFFFLESEGFAGLK
						QGPYMVKMLK  AIASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESLADLQND\TDGYLLRVI*VAFTT ERTNQI/REVF\NKLIPDSIGKDIEKACQSIYPLH DDFARKVKMLKKPKFELRKLMELHGEGSS PRWR\SARDEILLSFPONYYIQWL\NGSLIHGL

PCT/US01/03800

NO: of NO: of hod ID NO: beginning nucleotide D=As	o acid sequence (A=Alanine C=Cysteine,
NO: of NO: of hod ID NO: beginning nucleotide	spartic Acid, E=Glutamic Acid,
	enylalanine, G=Glycine, H=Histidine,
nucl-   peptide   III	leucine, K=Lysine, L=Leucine,
ectide (Sch.	lethionine, N=Asparagine, P=Proline,
sea-   ucnce   05/450   conceptual	lutamine, R=Arginine, S=Serine,
uence 914 ng to first acid residue	reonine, V=Valine, W=Tryptophan,
	yrosine, X=Unknown, *=Stop codon,
residue of sequence Y=T	ssible nucleotide deletion, \=possible
peptide /=pos	ssible nucleonide deletion, —possible
sequence nucle	eotide insertion
LLL	CTPVGL\SRMFTVMGQLLVKPTILEDLDE
QIYI	ITLEEEALQRPTKWAVFIRW/KYNIMELE
QEL	ENVKTLKTKLERRKKASAWERNLVYPA
	VLLLIETSISVLLVACNILCLLVDETAMPK
GTR	GPGIGNASLSTFGFVGAALEIILIFYLMVS
SVV	GFYSLRFFGNFTPKKDDTTMTKIIGNCVS
	SSALPVMSRTLGITRFDLLGDFGRFNWL
CNF	VIVI SYNLLFAIVTTLCLVRKFTSAVREE
LFK	ALGLHKLHLPNTSRDSETAKPSVNGHQK
1422 GSI	RFSLASPLDPEVGPYCDTPTMRTLFNLL
410 1760 A 3337 127	ALACSPVHTTLSKSDAKKAASKTLLEKSQ
WL/	KPVQDRGLVVTDLKAESVVLEHRSYCSA
TSD VAT	RDRHFAGDVLGYVTPWNSHGYDVTKVFG
KAI	TQISPVWLQLKRRGREMFEVTGLHDVDQ
SKI SKI	MRAVRKHAKGL\P*CLGSCLRTGLTMISG/
	DSEDEIEELSKTVVQVAKNQHFDGFVVE
	NQLLSQKRVGLIHMLTHLAEALHQARLL
	VIPPAITPGTDQLGMFTHKEFEQLAPVLD
ALL	VIPPATIPUTOCONIA DI CUVIR A CVOV
GFS	SLMTYDYSTAHQPGPNAPLSWVRACVQV
LDF	PKSKWRSKILLGLNFYGMDYATSKDAREP
VV	GARYIQTLKDHRPRMYWDSQVSEHFFEY
	SRSGRHVVFYPTLKSLQVRLELARELGVG
VSI	WELGQGLDYFYDLL*VGIAASAVDVFFSK
PW	SE
411 1761 A 3342 74 2701 VA	TRKLAKGFTQFAKMTEGTKKTSKKFKFFK
411 1701 A 3572 FK(	GFGSFSNLPRSFTLRRSSASISRQSHLEPDTF
[ ] EA	TQDDMVTVPKSPPAYARSSDMYSHMGTM
PRI	PSIKKAQNSQAARQAQEAGPKPNLVPGGV
	PRI EAAKEVMVKATGPLEDTPAMEPNPS
	FVDPIRKPEVPTGDVEEERPPRDVHSERAA
GFI   GFI	PEAGSDYVKFSKEKYILDSSPEKLHKELEE
	CLSSTDLRSHAWYHGRIPREVSETLVQRN
	FLIRDSLTSLGDYVLTCRWRNQALHFKIN
)	VVK AGESYTHIOYLFEQESFDHVPALVKY
	GSRKAVSEOSGAIIYCPVNRTFPLRYLEAS
YG Y	LGOGSSKPASPVSPSGPKGSHMKKKSVIM
	CLTADK VTRSDGCPTSTSLPRPRDSIRSCA (
191	MDQIPDLHSPMSPISESPSSPAYSTVTRVHA
LOSI	AAPSATALPASPVARRSSEPQLCPGSAPKT
Ar.	ESDKGPHTSPSHTLGKASPSPSLSSYSDPDS
I I I I I I I I I I I I I I I I I I I	YCQLQPPVRGSREWAATETSSQQARSYGE
OH DY	KELSENGAPEGDWGKTFTVPIVEVTSSFNP
	FOSLLIPRONRPLEVGLLRKVKELLAEVDA
	LARHVTKVDCLVARILGVTKEMQTLMGV
	LAKH VIK VUCL VARILO VIKLING I DING V
i i i i la	CONTRACTOR DESCRIPTION OF THE PROPERTY OF THE
RT	GMELLTLPHG\RKLRLDLLERFHTMSIML
RT RW	DII GCTGSAEERAALLHKTIQLAAELRGT
RT RW AV	DILGCTGSAEERAALLHKTIQLAAELRGT SNIMESEAAVMGALDMAOISRLEQTWVTLR
RT RW AV MC	DILGCTGSAEERAALLHKTIQLAAELRGT SNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAII YEKKLKPFLKSLNEGKEGPPLSN
RT RW AV MC QR	DILGCTGSAEERAALLHKTIQLAAELRGT SNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITI.LECDSAPPEGPEPWGSTEHGV
RT RW AV MC QR TT	DILGCTGSAEERAALLHKTIQLAAELRGT SNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG
RT RW AV MC QR TT EV	DILGCTGSAEERAALLHKTIQLAAELRGT SNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA
RT RW AV MC QR TT EV FQ	DILGCTGSAEERAALLHKTIQLAAELRGT SNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA YFKFDKVLTALSHKLEPAVRSSEL
RT RW AV MC QR TT EV FQ	DILGCTGSAEERAALLHKTIQLAAELRGT GNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA YEKFDKVLTALSHKLEPAVRSSEL
RT RW AV MC QR TT EV FQ RR RT RW RT RW RT RW MC QR TT RW RT RW RT RW RT RW RT RW RT RW RT RW RW RT RW RW RW RW RT RW	DILGCTGSAEERAALLHKTIQLAAELRGT GNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA YEKFDKVLTALSHKLEPAVRSSEL RAAECRTKPLPMAVSIRGNADSIVACLVLM VIJKKRIJVACAAVFYGFAVHMKIYPETYI
RT RW AV MC QR TT EV FQ RR IDJ	DILGCTGSAEERAALLHKTIQLAAELRGT GNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSQA YEKFDKVLTALSHKLEPAVRSSEL RAAECRTKPLPMAVSIRGNADSIVACLVLM YLIKKRLVACAAVFYGFAVHMKIYPETYI ITI HI LPDRDNDKSLRQFRYTFQACL*ELL
412 1762 A 3347 1 898 IDI	DILGCTGSAEERAALLHKTIQLAAELRGT GNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA YEKFDKVLTALSHKLEPAVRSSEL RAAECRTKPLPMAVSIRGNADSIVACLVLM YLIKKRLVACAAVFYGFAVHMKIYPETYI ITLHLLPDRDNDKSLRQFRYTFQACL*ELL
412 1762 A 3347 1 898 IDI	DILGCTGSAEERAALLHKTIQLAAELRGT GNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA YEKFDKVLTALSHKLEPAVRSSEL RAAECRTKPLPMAVSIRGNADSIVACLVLM YLIKKRLVACAAVFYGFAVHMKIYPETYI ITLHLLPDRDNDKSLRQFRYTFQACL*ELL
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412 1762 A 3347 1 898 IDI KR WI AF	DILGCTGSAEERAALLHKTIQLAAELRGT GNMFSFAAVMGALDMAQISRLEQTWVTLR HTEGAILYEKKLKPFLKSLNEGKEGPPLSN FPHVLPLITLLECDSAPPEGPEPWGSTEHGV VLAHLEAARTVAHHGGLYHTNAEVKLQG ARPELLEVFSTEFQMRLLWGSQGASSSQA YEKFDKVLTALSHKLEPAVRSSEL RAAECRTKPLPMAVSIRGNADSIVACLVLM YLIKKRLVACAAVFYGFAVHMKIYPETYI ITLHLLPDRDNDKSLRQFRYTFQACL*ELL

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	nucleotide	location	F=Pnenylalanine, G=Olychie, n=riscidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence	1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	<b>\</b>	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	Y=1 yrosine, A-Olikhowii, -Stop codon,
	1			peptide	1	/=possible nucleotide deletion, \=possible
	l .			sequence	1	nucleotide insertion
	<del> </del>	<del>↓</del>	<del> </del>	Boque	<del> </del>	VMPLVRMPWKRAVVLLMLWFIGQAMWLAP
	1	i	1	1		AYVLEFQGKNTFLFIWLAGLFFLLINCSILIQII
	1	1	1	ł		SHYKEEPLTERIKYD
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413	1763	A	3361	3	474	PIPVRWNSLEGRLLRGYEQHANDGKDYISRN
413	1	1	1			*DLRSWTAADMAAQITKRKWEAEEFAEQIKA
	1	l				YLEGTCVER/LRTHLENGKETLQLTEQSSQPTI
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414	1764	A	3363	1488	453	HQILELKKKILKTYNPDYDEDLVQEASSEDVL
714	1.704	1 11		1		GVHMVDKDTERDIEMKRQLRRLRELHLYST
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	1	1		1		PEILSETLPGSVKKRVCFPSEDHLEEFIAEHLP
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415	1765	A	3369	431	315	IPWSWVGRLSVRKMSILF*LTYNYNAILNKTP
413	1703	1 1	3307	'''		PSFSPSL
	<del></del> -	<del></del>	2272	42	651	RQEKMGLGEIGASGVLRSMLKERKKQNMKG
416	1766	A	3373	42	1 031	NGNVTLTPLLPAVQCGCHLQPAGRSPLPSSHS
1	1		l l		Ì	APGLCSPLHPLQPQQEASTCPSGTLQGREKAA
	}	1		ł		PGQGRPLCSLWAGGAGA\PGERGAEGRGPSD
1	1	1	ļ		1	PGOGRPLCSLWAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
[	[					QAPDPKSGPWLFPPGLGAPAEVRLHNVPHNL
}	ì	Ì	1			RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG
į.			ļ			PKPQCSLPSQVPGDTH
			2202	12	2061	EAQDPRACGPDAGGRFAARDAPGNSLRPPPS
417	1767	A.	3382	2	2001	SPP/GWPGQLRLLPRVPGSELRCGKPERGRLP
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1	1					WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP
1	l	1				KNAGRCGGA\RGPRLSLGPPPGPPPAPALPAR
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1	ļ			1		TRGSRRGPGSRPARAAAAPRAGDHGRRPVRV
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			1	}		R\GPGWDCALLPSPGPRSPRAVGCAEPEIWDP
	ļ	1	- 1		Į.	SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY
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Ĭ	1	1	1	1		PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC
	- [	1	1			SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD
	1					2WDHANKIKOPOVEI 2NKCL2ULTO/ODOC2D
1	1		1			HSSCEGHPDLHAGREMPAAPGLSELERVRFT
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						GTGTEP*TPTTSIPFFPQPSGVYPSRATLLPMPS
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1		- 1		1		Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA
		-				KGIGQLSEIPLLNVETAFWSMWVTYFRK
1	_ <del></del>		2200	204	2121	EEEEEEDEDDDDNNEEEEFECYPPGMKVQV
11.	1 1740	A	3398	304	2121	RYGRGKNQKMYEASIKDSDVEGGEVLYLVH
418	1768				I	VIORORIAGIZITI PURPUTANDO LEGODI PIETI
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418	1700	}				YCGWNVRYDEWIKADKIVRPADKNVPKIKH
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418	1700					RKKIKNKLDKEKDKDEKYSPKNCKPPALGPN PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI EITSILNGLOASESSAEDSEQEDERGAQDMDN
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NO: of nucl-peptide eotide sequence  NO: of nucl-peptide eotide sequence  NO: of nucl-peptide eotide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  NO: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location corresponding to last amino acid residue of peptide sequence  No: of nucl-otide location nucleotide do nucleotide insertion nucleotide sequence  No: of nucleotide location nucleotide nucleotide nucleotide nucleo	lycine, H=Histidine, c, L=Leucine, paragine, P=Proline, nine, S=Serine, e, W=Tryptophan, own, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
NO: of nucleotide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  No: of peptide seq	lycine, H=Histidine, c, L=Leucine, paragine, P=Proline, nine, S=Serine, e, W=Tryptophan, own, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
eotide sequence  USSN location corresponding to last amino acid residue of peptide sequence  USSN location corresponding to last amino acid residue of peptide sequence  USSN location corresponding to last amino acid residue of peptide sequence  W=Methionine, N=Aspiration of peptide sequence  W=Tyrosine, X=Unkno /=possible nucleotide dinsertion  NKVHADLVISKPVSI  YEEDEVTKKRKDVF RYCNTEECLKTGSPO SSNSSSDEDEETKA  SLRTTGFYSGFSEVA	c, L=Leucine, paragine, P=Proline, paragine, S=Serine, e, W=Tryptophan, pwn, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
seq- uence  09/496  914  09/496  109/496  914  09/496  109/496  914  109/496  109/49	paragine, P=Proline, nine, S=Serine, e, W=Tryptophan, nwn, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
uence  914  ng to first amino acid residue of peptide residue of peptide sequence  914  ng to first amino acid residue of peptide sequence  914  ng to first acid residue of peptide sequence  914  ng to first acid residue of peptide sequence  915  N=Tyrosine, R=Argir  7=Threonine, V=Valin  Y=Tyrosine, X=Unkno  /=possible nucleotide de nucleotide insertion  NKVHADLVISKPVSI  YEEDEVTKKRDVK  RYCNTEECLKTGSPO  SSNSSSDEDEETKA  SLRTTGFYSGFSEVA	nine, S=Serine, e, W=Tryptophan, own, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
amino acid residue of peptide sequence sequence of peptide sequence sequence of sequence sequence sequence of peptide sequence sequence of	e, W=Tryptophan, own, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
residue of peptide sequence Y=Tyrosine, X=Unkno /=possible nucleotide d nucleotide insertion  NKVHADLVISKPVSI YEEDEVTKKRKDVK RYCNTEECLKTGSPO SSNSSSDEDEEETKA SLRTTGFYSGFSEVA	wn, *=Stop codon, eletion, \=possible  KSPERLRKDIEVLSEDTD
peptide /=possible nucleotide d nucleotide insertion NKVHADLVISKPVSI YEEDEVTKKRKDVI RYCNTEECLKTGSPC SSNSSSDEDEETKA SLRTTGFYSGFSEVA	eletion, \=possible KSPERLRKDIEVLSEDTD
sequence nucleotide insertion  NKVHADLVISKPVSI YEEDEVTKKRKDVI RYCNTEECLKTGSPO SSNSSSDEDEETKA SLRTTGFYSGFSEVA	KSPERLRKDIEVLSEDTD
NKVHADLVISKPVSI YEEDEVTKKRKDVK RYCNTEECLKTGSPO SSNSSSDEDEETKA SLRTTGFYSGFSEVA	KSPERLRKDIEVLSEDTD
YEEDEVTKKRKDVI RYCNTEECLKTGSPO SSNSSSDEDEETKA SLRTTGFYSGFSEVA	
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SLRTTGFYSGFSEVA	KMTPTKKYNGLEEKRK
	AEKRIKLLNNSDERLQNS
RAKDRKDVWSSIQO	GOWPKKTLKELFSDSDTE
A A A SPPHPAPEEGV	AEESLOTVAEEESCSPSV
	IEEKTVEVNDRKAEFPSS
GSNFSA*IPLPYLHL	NRLHQSL*QKGSRQQSS
VTVSEPLAPNOEEV	RSIKSETDSTIEVDSVAGE
LODLOSERE*LASRI	F*COCELKQ**SARTRTS*
KSLYRSEKSERCSG	RRKFIKKAEKKP*SNSGK
QQKEGK	
419 1769 A 3399 206 463 QRECLSIHIGQAGIQ	IGDACWELYCLEHGIQP
NGVVLDTQQDQLE	NAKMEHTNASFDTFFCE
TRAGKHVPRALFVI	OLEPTVIDGIR
420 1770 A 3408 1010 685 RRLSFFF*IWSSVLV	TQARVQWRDLGSPQPLP
PGFKRFSCLSLPSSV	VDYRHPSPRPVNF/HVFLV
VMGFHHVGQAGLE	ELLTSGDLPALASQSARIT
GVNHCAQPRGHFH	T CDWGCDWBWEOVGAS
421 1771 A 3409 355 1326 ADSNLIESCWQELG	LGPWGGDWRVEQVGAS
	FTAVSLLSLFLSAFWLGL
LYLVSPLENEPKEM	ILTLSEYHERVRSQGQQL VSTVRAANSERVAKLVF
QQLQAELDKLHKE	ALSSVGASIDLQKTSHDY
QRLNEDFYRRPD 17	FWNYARPPTVILEPHVFP
ADKNIA IT WINTO	VVIQLPGRVQLSDITLQHP
DROVEUTGGANSAF	RDFAVFFLLSFFTHQGLQ
VVDETEVSI GKETE	DVEKSEIQTFHLQNDPPA
A EDK VKIOII SNWG	HPRFTCLYRVRAHGVRT
SEGAEGSAQGPH	
421 FEDA OPSIGAL VVF	KRP*ATTGSDPGPKRGMN
42Z 177Z A STIZ YLVSCSMRSPESGK	GEPGTARDYTPMGRPPP
PVPSVSPGPLPGSLA	<b>ALAPHSPEPHPWEQQPPRG</b>
QARSPPGGWLGSA'	T/RVRRPHNHP/RGH/HSP
VDTAGAPASPGPD	VCE
DAORAIYSSVGPAV	/SLRQRQQDGAVKESGR/
RGGVRSFSRAAAA	MAPIKVGDAIPAVEVFEG
EPGNKVNLAELFK(	GKKGVLFGVPGAFTPGCS
KTHLPGFVEQAEAI	LKAKGVQVVACLSVNDA
FVTGEWGRAHKAI	EGKVRLLADPTGAFGKET
DLLLDDSLVSIFGN	RRLKRFSMVVQDGIVKA
LNVEPDGTGLTCSL	LAYNIISUL
424 1774 A 3421 4 7688 RQVTRVGTRVLGS	TTAAVFLSVEDDNDNAPQ
FSEKRYVVOVRED	VTPGAPVLRVTASDRDKG
SNAVVHYSIMSGN	ARGQFYLDAQTGALDVV
SPLDYETTKEYTLR	VRAQDGGRPPLSNVSGL
VTVQVLDINDNAP	IFVSTPFQATVLESVPLGY
LVLHVQAIDADAG	DNARLEYRLAGVGHDFP AELDREEVDFYSFGVEAR
FINNOIGWISVAA	SVTALDVNDNNPTFTQPE
DHGIPALIASASV	SVIALDVNDNNFIFIQIE
YTVRLNEDAAVGI	SQSGGGLVSLALPLDYKLE
QIISGNIRNRISIIS	RQDTAQIVVNVTDANTH
RQYVLAVIASDGI	NEDRPAGTTVVLISATDE
RPVFQSSHYIVNV	DSIPQFRIDADTGAVTTQA
DIGENARIITEME	ITARDNGIPQKSDTTYLEI
ELDYEDQYSYILA	RDSYQGSVYEDVPPFTSV
LVNDVNDNAPQFL	RVFYTFQGGDDGDGDFI
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LGRFELFNNYVTNISSSFFGGAIGRVPAHDP DISDSLTYSFERGNELS.VLIANFGLEKLSR ALDNNRPLEAMMSVLVSDOVHSVTAQCALRY TIIIDEMLTHSITLRLEDMSPETLSPLLGLFIQ AVAATLATPDHVVVFNVQRDTDAYGGHIN VSLSVQQPPGGGPFIPSPLQERLYINRS LLTAISAQRVLPPDDNICLREPCENYMRCVSV LRPDSASPILASSVLFPRIPVGGURCRCPPGF TGDYCTTEVDLCYSRPGGHRGCRSRGGYT CLCRDYTGEHEVSASSGRETGVVCNGTGT CLCRDYTGEHEVSASSGRETGVVCNGTGT CVILLVGGFKCDCPSGFERPYCQVTTRSPP AHSFITTRGLRQRFHFTLALSFATKERGGLI YNGRFNEKHDFVALEVIGROVQLTFSAGEST TIVSPFVGGVSDGQWHTVQLXYYXFGEST TTVSPFVGGVSDGQWHTVQLXYYXGGEST TTVSPFVGGVSDGQWHTVQLXYYXGGEST TTVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGVSDGQWHTVQLXYYXGGEST TVSPFVGGGSGGCQGXASSLDGTGGTLAGG VLGNYSGCAAQGTGGGSKKSLDLTOPLLAGG VLGNYSGCAAQGTGGGSKKSLDLTOPLLAGG VLGNYSGCAAQGTGGGSKKSLDLTOPLLAGG VLGNYSGCAAQGTGGGSKKSLDLTOPLLAGG VLGNYSGCAAGGTGGGKGCAQGAMAPQHF LGSSLVAWHGLSLPISQFWYLSLMFRTRQAD GVLLQAITTGGSTTLLAGGGFWMLSVEGTGL QASSLRLFGRANDGDWHHAQLALGGGP GHALLSFDYGGQGAAGGLAGGPMCMLSESTTQAD GVLLQAITTGGRAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			ì				QIVEGNIPEVFQLDIFSGELTALVDLDYEDRPE
DISSELTYSERGNELS.VLINASTGELKJ.SR ALDNRPLEARMSVLYSDOVHSVTAQCALRY TIITDEML.THSTIT.RLEDMSPERFLSPLLGFIQ AVAATLATEPDHVVENVPKQUDTDAPGHLIN VSLSVQPPCPGGGPFLPSEDLQERLYLNS LLTALSQRVLYPEDDMICLAFENYMCVSV LRPDSSAPFLASSSVLFRPIHPVGLRCRCPPGF TGDYCETEVDLCYSRPCOPHGRESSEGOTT CLCRDYTGEHEVSARSGRCTPGVCKNGGT CVILLVGGFKCDCPSGPFEKPYCQVTTRSPF AHSFITTRGLRGKFHFTLALSTATERERGLLL YNGRPEKHDFVALEVIQEQVQLTPSAGEST TTVSPFVPGGVSDQWHTVQLKYYNKPLLG QTGLPQGPSEQKVAVVTVDGCDTGVALREGS VLGNYSCAAQGTOGSKSKLDLTOPLLLGG VPDLPESFPVRMCPVGCMRNLQVDSRHDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAFSCECFLGFGGKSCAQEMANQHF LGSSLVAWHGLSLPISQPWYLMFTRQAD GVLLQATRGRSTITLQLREGHVMLSVETGL QASSRLFEFGRANDGDWHHAQLALGAIGGP GHALSFDYQQQRAEGNLGPRHOLLISNITV GGPQPAGGVARGFRGCLQGVAVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCTANSY CSNDWDSYSCSCOPGYV3DNCTNVCDLNPC EHQSVCTRKPSAPHGYTCSCPPNYLGPYCET RIDQCPRGWWGHPTOGPCNOWSKGFDPDC NKTSGECHCKENHYRPGSPTCLLCDCYPTG SLSRVCDPEDQCPCKPGVIGRQCDRCDNPF AEVYTNGCENNTDSCPRAEGAIWWPRTFRG LPAAARCPKGSFGTAVHCDEHRGWLJPNLF NCTSITTSELKGFGRAVHCDEHRGWLJPNLF NCTSITTSELKGFGRAVHCDEHRGWLJPNLF NCTSITTSELKGFGRAVHCDEHRGWLJPNLF NCTSITTSELKGFGRAVHCDEHRGWLJPNLF NCTSITTSELKGFGRAVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPNLF NCTSITTSELKGFARVHCDEHRGWLJPRAYAS ALAQNMHTITJSFTTITTNIVSVVRLDKGN FAGAKLPRVEALRGGPPDLETTVLIPSSVPR ETTPVVVRAGGFGAQFGEALGRRENGRIPELSQ GEAVASVITRTLAGLIPHNYDPOKRARGE EFERTRPLCYFWHISILVSGTGGWSARGC EVYRNESHVSQCCHHMTSVIJVUNGDYRLDKGN PAGAKLPRVEALRGGPPDLETTVLIPSSVPR ETTPVVRAGGFGAQFGEAQPPELATRALTLASTPLTLL RILBSRQGGRAFKFCLAGRRENGENSPR ETTPVVRAGGFGAQFGEAQPPELATRALTLASTPLTLL RILBSRQGGGRAFKGCAGFFKG PVSGGPFGAQFFECALHDRSVTRUMDVSRE MGELPLKTLTYVALAGTLAALLLTFFFLILL RILBSRQGGGRAFKFCLGGFKKG PVSGLOPSFAVLLLLSATVLLALLSVNDTLL LAVELPFGGFGRAVLLLASTVLLALLSVNDTLL LAVELPFGGFGRAVLLLASTVLLALLSVNDTLL LAVELPFGGFGROPPOCONSTRATICL READANPGGOFFKKG PVSGLOPSFAVLLLLSATVLLALLSVNDTLL LAVELPFGGFGRAVLLLASTVLLALLSVNDTLL LAVELPFGGFFKGFKG PVSGLOPSFAVLLLLSATVLLALLSVNSDT	1	1	1	i		Ì	YVLVIQATSAPLVSRATVHVRLLDRNDNPPV
DISSELTYSERGNELSLVLLMASTGELKLSR ALDNINPLEARMSVLYSDOVHSVTAQCALRY TIITDEMLITISTILRLEDMSPERFLSPLLGEFIQ AVAATLATEPDHVVETNYGQMTDAPGGHLIN VSLSVQOPPGGGOPPFLPSEDLQEELYLNS LLTAISAGRVLPPDDIVICLERCPSTMGCVSV LRDSSAPFLASSSVLFPBIPVGGLRCCPPGF TGDYCFIEVDLCYSRPCOPHGRSBEGGYT CLCRDAYTGEHEVSARSGRCTPGVCKNGGT CVNLLVGGFKCDCPSGDFEKPYCQVTRSGF TGYCFIEVDLCYSRPCOPHGRSBEGGYT CLCRDAYTGEHEVSARSGRCTPGVCKNGGT CVNLLVGGFKCDCPSGDFEKPYCQVTRSGP AHSFITTRGLRGKFHFTLALSTATERERGLLL YNGFPEKHIDFVALEVQEDVQLTFSAGEST TTVSPFVPGGVSDGQWHTVQLXYYNKPLLG QTGLPQGPSEGKVAVVTVDCDGTGVALRFGS VLGNYSCAAQGTGGSKSKSDLDTOPLLLGG VPDLPSSFPVRRGPVGCMRNLQVDSSRTIDM ADPIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAFSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLFISQPWYLDSKFLDMANSVEGTGL QASSRLFEFGRANDGDWHHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL GASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGL QASSRLFEFGRANDGDWHAUSVEGTGGLANSY CSNDWSYSCEOPGYYGDNCTNVCDLNGC REGGRANGGRANDGTANSY CSNDWSYSCEOPGYYGDNCTNVCDLNGC ANGERGRANGGRANDGTANSY CSNDWSYSCEOPGYYGDTCNDYFCTG RIDQCPGWGGCAGPGGCAGDFEGAGGRANDGTANSY CSNDWSYSCEOPGYYGDTCNDYFOTG ANTONICATION ALTANATHTAGYTGGGTAWLCORTEGASY PASACHAUSVEGGGAAGAGGAGGAAGAGGGGGAAGAGGAGGAAGAGGAGG		1		ì			LGNFEILFNNYVTNRSSSFPGGAIGRVPAHDP
ALDNINPLEAMSVLVSDOVHSVTAQCALRY TITIDEMLTHSITLRLEDMSPERLSFLLGLFIQ AVAATLATPEDHVVVFNVQRDTDAYGGHIN VSLSVQQPPGGGPFIPSEDLQEELYLNIS LLTAISAQRVLPPEDNICLREPCENYMRCVSV LRFDSSAFFLASSSVLFPEIPWGGLRCCCPGGF TGDYCETEVDLCYSRPCGPHGRCRSREGGYT CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT CVNLLVGGFKCDYSGDFEKPYCQVTTRSFP AHSTITRGLRQRFHFTLALSTATEREDGLLL YNGRFMEKLIDEVALEVUGEVQULTESAGEST TTVSPFVPGGVSDQWHTVQLKYYNFYLLG QTGLPGGPSEGKVAVVTVDCDTGVALRFGS VLGNYSCAA\QGTQGGSKKSLDLTOPLLLG VPDLPSSFPVMRQFVGCMRNLQVDSRTHMD ADFLANNGTVGGCSKKSLDLTOPLLLG WYDDLFSSFPVMRQFVGCMRNLQVDSRTHMGTC VNQWDAYSCSCPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLQATTRGRSTTILQLREGRSTTLLQLREGRYSTTLAGGT VNQWDAYSCSCPLGFGGKSCAQEMANPQHF GGGPAGGVAGGNAGGNLQPRLHGLH.SNITTV GGTGPAGGVAGGNAGGNLGPRLHGLH.SNITTV GGTGPAGGVAGGNAGGNCGCQCRVSDSTPEGVN SLDPSHGESINVQGGCLFPPCDSNFC7ANSY CSNDWSYSCSCDPGYYGDNCTNVCDLNFC EHGSVCTRKPSAPHGYTCSCPPNYLGFYCET RIDQPCRGGWWGHPTCGFCNDVSKGFDPDC NKTSGECHCKENHYXPPGSFTCLLCDCYPTG SLSRVCDPEDGGCCKFGGCDRCDNFF AEYTTNGCEVNYDSCPRALEAGIWWPRTRFG LPAAAPCKGSGTAVRLDGHRGWLPPTGF LPAAAPCKGSGGTAVRLDGHRGWLPPTGF AEYTTNGCEVNYDSCPRALEAGIWWPRTRFG LPAAAPCKGSGTAVRLDGHRGWLPPTGF AEYTTNGCEVNYDSCPRALEAGIWWPRTRFG LPAAAPCKGSGTAVRLDGHRGWLPPTGF LANGCHGRAGGAGALAGARGGAGAAAA ALQNMRHTJNSFTTIVINIVISVVRLDKGN FAGAKLPRVEALRGGPPDLETTVLLPSSVR ETTPVVRRAGGGGAGATCHAUTYSEAVR GGEAVASVIJVRTLAGLLPHNYDPDKRSLRVFR FETPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR GGEAVASVIJVRTLAGLLPHNYDPDKRSLRVFR RIPTTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLLFSVRR ETTPVVRRAGGFGAQFECHTIVLTSVRALLALLTFFFLLL LRLERSNGHGIRRSLLTAGTLAGGREKG PVSRSSVSVDDEELLFRALDKFVTVQFR RLITTERTRALLTAGTTSWALLSVRF RLITTERTRALLTAGTTSWALLSVRF RLITTSFTRALLLALLSVRSDTLL HLTEERTRAPCVTYOPMRSLAAALLLTFFFLLL LRLERSNGHGFFRKG PVSGLOPSFRALLLSANTYLLALLSVRSDTLL HLTEERTRAPCVTYOPMRSTYMLDWGVPAFTG LAVCLOPSFGALLLSANTYLLALLSVRSDTLL FFLALARPSCOPPGLGCFGFKKG PVSGLOPSFAALLLSANTYLLALLSVRSDTLL FFLALARPSCOPPGLGCFGFGKKG PVSGLO	Ì	1	Ì	l			DISDSLTYSFERGNELSLVLLNASTGELKLSR
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AVAATLATPDHUVVFNVQRDTDAFGHILN VSLSVGOPPGGGPFILSEDLQRLYLNRS LLTAISAQRVLPFDDNICLREPCENYRCVSV LRFDSSAPILASSNI.FRIPPVGGLRCRCPPGF TGDVCFTEVDLCYSRPCOPHGRCRSREGGYT CLCRDGYTGEHCEVSARSCCTPGVCKNGGT CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP AHSFITTRGLRQRHFITLALSFATKERGLLL YNGRFINEKHDFVALEVIGEQVQLTFSAGEST TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG QTGLPQCPSGCKVAVVTVDGCDTGVALRIGS VLGNYSCAAQGTGGGSKKSLDLTGPLLLGG VPDLPSSFPVRMQFVFGGNSLQVDSRHDM ADFIANNGTVFGCFAKKNVCDSKTCHNGGTC VNQWDAFSCEPULGFGGSKCAQEMANPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLQATTRGRSTHTQLAGFHVMLSVSCTGL QASSLRLEFGRANDGDWHHAQLALGAIGGF GHAILSFDYGQQRAEGONLGPHAGHLSNITV GGPGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESRNVEGGCSLFDFCDSNPCFANSY CSNDWDSVSCSCDFQYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNTLGFYCET RIDQPCPRGWWGHTCGCPNCDVSKGFPDDC NKTSGECHCKENNYRPPGSPTCLLCCYPTG SLSRVCTPEDGQCCKEPGUGRQCDRCDNFF AEVTTNGCEVNYDSCPRAEAGIWWRTRFG LPAAAPCFRGSGTAVRHCDEHRGWLFPNLF NCTSITFSELKGFAERLQRNESGLDCDNPF AEVTTNGCEVNYDSCPRAEAGIWWRTRFG LPAAAPCFRGSGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRQQL ALLIRNATQHTAGYFGSDVKAVAQLATRLL AHESTQRGGGLSATQDVHFTENLLRVGSALL DTANKRHWELQCTEGGTAWLDHYFELSAYA ALQNMRHTYLSPFTIVTPNIVISVVLDKGN FAGAKLPRYSALRGQPPDLETTVILPESVFR ETPPVVRPAGFGGGALGRURGNSRRVLDSKRSRVK RPIINTPVVSSVSHDDEELLPRALDKFVTVQFR LLETERTKPICVYFNHSILVSGTGGWSARGC EVVFNESHVSCOCNINNFSAVLMDVSRRE NGELPLKTLTYVALGVTLALLLITFFLTLL RILRSNOHGRRNITAALGLJFFHLTLLS RLATRSDGGGRSTALCHTHURSPAGP VAFAVSMSVFLYLLAARASCAAQRGFEKKG PVSCLQFSFAVLLLLSXTMLALLLSVNSSTLL HTYLFACTNCIQGFFILSTVVLSKGVRKAQFEKKG PVSCLQFSTAVLLLLSXTMLALLLSVNSSTLL HTYLFACTNCIQGFFILSTVVLSKGVRKALK LACSRKPSPDALTTKSLTTSSYNCPSFYALD LACSRKPSPDALTTKSLTTSSYNCPSFYALD LACSRKPSPDALTTKSLTTSSYNCPSFYALD EFSALNFROGOPPOLGGTGRGCRLCCHGRKDQF			1	1			TUTDEMI THSTTLRLEDMSPERFLSPLLGLFIO
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LLTAISAGRVLPFDDNICLREPCENYRKCVSV LRFDSSAPIFASSSVLFPHPVGGLRCRCPPGF TGDVCFTEVDLCVSRPCGPHGRCSSEGGYT CLCRDGYTGEHCEVSASGGCTPGVCKNGGT CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP AHSFITFRGLRQRFHFTLALSFATKERBGLLL YNGRFNEKHPVALEVIGEQVQLTFSAGEST TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG GTGLPQGPSGCKVAVVTVDGCDTGVALRFGS VLGNYSCAAQGTOGGSKKSLDLTGPLLLGG VPDLPESFPVRMRQFVGGCMRNLQVDSRHDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAFSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLPISGPWYLSLMFTRQAD GVLLQATTRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHAQLALGIGGP GHAILSFDYGQQRAEGNLGPRLHGLHSNITV GGPGPAGGVARGFRGCLGGVRVSDTPEGVN SLDPSHGESINVEGGCSLPPCDSNFCPANSY CSNDWDSVSCSCDFGYGGCDKPCNSFCPANSY CSNDWDSVSCSCDFGYGGDCDKOFKPANSY CSNDWDSVSCSCDFGYGGDCDKOFKPANSY CSNDWDSVSCSCDFGYGGCDKCDNFF ABCVTTNGCGCSLPPCDSNFCPANSY CSNDWDSVSCSCDFGYGGCDRCDNFF ALSTVTNGGCEVNYDSCFRAGTWPRETRFG LPAAAPCFKGSFGTAVRHCDEHRGVLPPNL NCTSHTSELKGFAERLQRNESGIDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL DTANKRHWELIQQTEGGTAWLQHYEAYAS ALAQMMRHTYLSFTIVTFNIVSVXLDKGN FAGAKLPRYALRGGCPPDLETTVLIPESVR ETPPVVRPAGFGGAQEPELARRQRRIPELSQ GEAVASVIRTALAGLLBYTVDFFK RPINTTPVSISVHDDEHLLRAGAGLAG FETPPVVRPAGFGGAQEPELARRQRRIPELSQ GEAVASVIRTALAGLLBYTVDFKR RPINTTPVSISVHDDEHLLRAGTGRAARG EVYFRNESHYSCQCNIMTSFAVLMDVSRE NGEILPLKTLTYVALGVTLAALLITFFLTLL RILRSKOHGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHEILYCTSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALGLAHLY RALTSVRDVGRRNLTAALGLAQLVFLLGINQA VAFAVSMSVFLYLLAARSCAALQRGGFEKG PVSGLQPSFAVLLLLSATWLALLLSVNSDTLL FRYLLFACTNCGGFFILEGGRACCFGGGFRCAGFGAGFGFALCFT,GRFKDQQ		ł	1	1			WANTE ATTENDED CORPORATION OF THE STATE OF T
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AHSFITRGERQRFHFILALSTATKERDGILL YNGRPEKHIDFVALEVIQEVOU.TPSAGEST TIVSPFVPGQVSDGQWHTVQLKYYNKPLLG QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS VLGNYSCAA\QGTQGSKKSLDLTGPLLLGG VPDLPESFPVBMRQFVGCMRNLQVDSRHIDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAPSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLS.INGPW1SLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEFGRANDGDWHHAQLALQAIGGP GHAILSPDYQQQRAEONLGPRLHGLHLSNITV GGGPGPAGGVARGFRGCLQQVRVSDTPEGVN SLDPSHGESINVEQGSLPPDCCDSNFCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCSCPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNFF AEVITNGCEVNYDSCPRALEAGIWWFRTRG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTORGGLSATQDVHFTENLLRVGSALL DTANKRHWELQQTEGGTAWLQHYEAYAS ALAQNMRHTYLSFTIVTENLISVVRLDKGN FAGAKLPRYBALRGCPPDLETTVLLPSSVPR ETPPVVRPAGPGGAGPEELARRQRHPELSQ GEAVASVITYRTLAGLLPHNYDPDKRSLRVPK RPINTTVVSISVHDDEELLFRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNIHMTSFAVLMDVSRE NGEILPLKTLTYVALGVTLAALLLTFFLTLL RILRSNQHGIRRNLTAALGLAQLVFLLGNQA DLFFACTVIALLHFFLYLCTFSWALLEALHLY RALTEVRDVNTGBWRFYYMLGWGVPAFITG LAVGLDFEG GYDFOFCH.STYDTLIWSFAGP VAFA VSMSVFLYLLAARASCAAQROGFEKKG PVSGLQPSFAVLLLSATWLALLSVNSDTLL FHYLFATCNCIQCPFIFLSYVVLSKEVRALK LACSRKPSPDPAJLTLSTLYSYVCLSKEVRALK LACSRKPSPDPAJLTLSTLYSYVCLSKEVRALK LACSRKPSPDPAJLTIKSTLTSSYNCPSFYADG RLYQPYGDSAGSLHSTSRSCKSCPSYTYFLLR				1		1	CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT
AHSFITRGERQRFHFILALSTATKERDGILL YNGRPEKHIDFVALEVIQEVOU.TPSAGEST TIVSPFVPGQVSDGQWHTVQLKYYNKPLLG QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS VLGNYSCAA\QGTQGSKKSLDLTGPLLLGG VPDLPESFPVBMRQFVGCMRNLQVDSRHIDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAPSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLS.INGPW1SLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEFGRANDGDWHHAQLALQAIGGP GHAILSPDYQQQRAEONLGPRLHGLHLSNITV GGGPGPAGGVARGFRGCLQQVRVSDTPEGVN SLDPSHGESINVEQGSLPPDCCDSNFCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCSCPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNFF AEVITNGCEVNYDSCPRALEAGIWWFRTRG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTORGGLSATQDVHFTENLLRVGSALL DTANKRHWELQQTEGGTAWLQHYEAYAS ALAQNMRHTYLSFTIVTENLISVVRLDKGN FAGAKLPRYBALRGCPPDLETTVLLPSSVPR ETPPVVRPAGPGGAGPEELARRQRHPELSQ GEAVASVITYRTLAGLLPHNYDPDKRSLRVPK RPINTTVVSISVHDDEELLFRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNIHMTSFAVLMDVSRE NGEILPLKTLTYVALGVTLAALLLTFFLTLL RILRSNQHGIRRNLTAALGLAQLVFLLGNQA DLFFACTVIALLHFFLYLCTFSWALLEALHLY RALTEVRDVNTGBWRFYYMLGWGVPAFITG LAVGLDFEG GYDFOFCH.STYDTLIWSFAGP VAFA VSMSVFLYLLAARASCAAQROGFEKKG PVSGLQPSFAVLLLSATWLALLSVNSDTLL FHYLFATCNCIQCPFIFLSYVVLSKEVRALK LACSRKPSPDPAJLTLSTLYSYVCLSKEVRALK LACSRKPSPDPAJLTLSTLYSYVCLSKEVRALK LACSRKPSPDPAJLTIKSTLTSSYNCPSFYADG RLYQPYGDSAGSLHSTSRSCKSCPSYTYFLLR	1					1	CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP
TYNGRFNEKHDFVALEVUGEVQVQLTFSAGEST TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS VLGNYSCAA\QTQGGSKSLDLTGPLLLGG YPDLPSSFPVRMRQFVGCMRNLQVDSRHIDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAFSCEPLGFGKSCAQBWANPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEFGRANDGDWHHAQLALGAIGGP GHAILSFDYGQQRAEGNLQPRLHGLHLSNITV GGFQFAGGVARGFRGCLQGVRVSDTFEGVN SLDPSHGESINVEGGCSLPPDCDSNFCPANSY CSNDWDSYSCSCDFGYQDDCTNVCDLNFC EHQSVCTRLFSAPHGYTCECPPNYLGPYCET RIDQPCPRGWWGHFTCGFCNCDVSKGFDPDC NKTSGECHCKENHYRPFGSFTCLLCCYPTG SLSRVCDFEDGQCFCKPGVIGRQCDRCDNFF AEVTTNGCEVNYDSCPALEAGIWWFRTRFG LPAAAPCFKGSFGTAVRHCDEHRGWLPPNLF NCTSITTSELKGFAERLQRNSSCGDLSGRSQQL ALLLRNATQHTAGFSDVKVAYQLATRLL AHESTORGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLLQHVEAYAS ALAQNMRHTYLSFFTIVTPNIVISVVRLDKGN FAGAKLPRYEALRGCQPPDLETTVLLPESVFR ETFPVVRAGFGGAQFPELLARRQRRHFELSQ GEAVASVITYRTLAGLLPHNYDPDKRSLRVPK RPINTPVVSISVHDDEELLFRALDKPVTVQFR LLETERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHMTSFAVLMDVSRE NGELLJKLTLTVAGUTLAALLLTFFLTLL RILRSNQHGRRNLTAALGLQLVFLLGINQA DLPFACTVIALLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRFYYMLGWGVPAFITG LAVGLDPEGYGNPDFCWLSTDTLLWSFAGP VAFAVSNSVFLYLLARRASCAAQRGGFEKKG PVSGLOPSFAVLLLLSATWLLALLSVNSDTLL FHALLATCNCQOFFIFLSYVVLSKEVRKALK LACSRKPSPDFAVLLLLSATWLLALLSVNSDTLL FHYLLFATCNCQOFFIFLSYVVLSKEVRKALK LACSRKPSPDFAVLLLLSATWLLALLSVNSDTLL FFFALLNFGOOFPGLGGFFKNCGTERFKDQG RLYQPYGDSAGSLHSTSRSCKSOPSYFFLLR FFSALNFGOOFPGFGLGGFFKNCTGLGRFKDQG RLYQPYGDSAGSLHSTSRSCKSOPSYFFLLR	ŀ		1				AHSFITFRGLRQRFHFTLALSFATKERDGLLL
TITVSPFVGGVSDGQWHTVQLKYYNKPLLG QTGLPQGPSEQEVAVTVDGCDTGVALRFGS VLGNYSCAA\QGTQGGSKKSLDLTGPLLLGG VPDLPESFPVKMRQFVGCMRNLQVDSRHIDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAPSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLTGPWYLSLWFRTRQAD GVLLQATTRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHHAQLALGAIGGP GHAILSPDYGQQRAEONLGPRLHGLHLSNITV GGGPQPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPPPCSDNFCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCEPPNYLGPYCET RIDQPCRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSPTCLLCDCYPTG SLSRVCDPEDQCPCKPGVIGRQCDRCDNFF AEVTTNGCEVNYDSCPRALEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITTSELKGFAERLQRNESGLDSGRSQQL ALLRNATQHTAGYFGSDVXVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYEAYAS ALAQNMRHTYLSPFTIVTINVISVVRLDKGN FAGAKLPYPSLR GEOPPDLETTVLIPSVFR ETPPVVRPAGPGEAQEPEELARRQRRHPELSQ GEAVASVIYRTLAGLLPHNYDPDKRSLRVPK RPINTFVVSISVHDGELLPRALDKRVTVQFR LLETERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHMTSFAVLMDVSREE NGELLPLKTLTYVALGVTLAALLLTFFFLTL RILSRSNQHGIRRNLTAALGLQLVFLLGINQA DLFFACTVIALLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRFYYMLGWGYPAFITG LANGLDPEGYGNPDFCWLSTDTLIWSFAGP VAFAVSMSVFLYLLAARASCAAQRQGFEKKG PVSGLOPSFAVLLLLSATWLTLALLSVNSDTLL FHYLFATCNCIQGFFETSYVVLSKEVRYK ALCSRKPSSDPALITKSTLSSYNCPSPYADG RLYQPYGDSAGSLHSTSRSCKSQPSYTFLLR					1		YNGRFNEKHDFVALEVIQEQVQLTFSAGEST
QTGLPQGPSEQKVAVVTYDGCDTGVALRFGS VLGNYSCAAQGTGGGSKKSLDLTGPLLLGG VPDLPESFPVRMRQFVGCMRNLQVDSHIDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAFSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQAITRGRSTITI,QLREGHWILSVEGTGL QASSLRLEPGRANDGDWHAQLALGAIGGP GHALLSFDYGQQRAEGNLGPRLHGLHLSNITV GGPGPAGGVAGRAFGRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPPCDSNPCPANSY CSNDWDSVSCSCDPGYVGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCGCPCNTLVCDLNPC EHQSVCTRKPSAPHGYTCGCPCNTVCGLNPC EHQSVCTRKPSAPHGYTCGCPCNCDVSKGFDPDC NKTSGECHCKENHYRPGSPTGLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNFF AEVTTNGGEVNYDSCPRAEAGIWWFRIFRG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL ALLENATQHTAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLUGHYEAYAL ALQNMRHTYLSPFTIVTPNIVISVVRLDKGN FAGAKLPRYEALRGEQPDLETTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRRHFELSQ GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK RPINTPVVSIVAPDEELLFRALDKPVTVOFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHHMTSFAVLMDVSRRE NGEGLPLKTLTYVALGVTLAALLLTFFFLTLL RILRSNQHGIRRNLTAALLLLAUNGVRAC DLPFACTVIALL LHYLTCTSWALLEALHLY RALTEVRD VNTGPMRFYYMLGWGVPAFTG LAVGLDPEGYGRPDFCUSIYDTLIWSFAGP VAFAVSMSVFLYLAARASCAAQRQGFEKKG PVSGLQPSFA VLLLLSATWLLALLSVNSDTILL FHYLFACTNCIQGPFFILSYVVLSKPVRKALK LACSRKPSPDPALITKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTSSGKSQPSYIFFLLR FFSALNFGOGGPFLGSTGFGRSGKSQPSYIFFLLR	Į	}	-	}			TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
VLGNYSCAAQGTQGGSKXSLDLTGLLLGG VPDLPSFPVRMRQFVGGMRNLQVDSRHDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VPQWDAFSCECPLGFGGKSCAQEMAPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQAITRGRSTITLQLREGHYMLSVEGTGL QASSLRLEPGRANDGDWHAQLALGAIGGP GHALLSFDYGQRAEGNLGPRLHGLHLSNITV GGPGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPPPCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSPTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHOEHRGWLPPNLF NCTSTITSELKGFAERLQRNESGLDSGRSQQL ALLRNATQHTAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYEAYAS ALAQNMRHTYLSFTIVTIPNIVSVYLDKGN FAGAKLPRYEALRGCPPDLETTVULPESVFR ETPPVVRPAGPGEAQEPELARRQRRHPELSQ GEAVASVITYRTLAGLLPHNYDPDKRSLRVPK RPINTPVVSISVHDDEELLFRALDKPVTVQFR LLETERSTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCCHHMTSFAVLMDVSRE NGELPLKTLTYVALGVTLAALLLTFFFLTLL RILRSNQHGRRNLTAALGLAQLVFLLGINQA DLPFACTVAILLTHYLTCTSWALLEAHLLY RALTEVRDVNTGPMRPYYMLGWGVPAFITG LAVGLDPEGYGNPDFCKUSTDTLLWSFAGP VAFAVSMSVFLYLAARASCAAQRQGFEKKG PVSGLOPSFAVLLLLSATWLLAALLSVNSDTLL FHYLFATCNCLQFFILSYVVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTTSRSGKSQPSYIFFLLR FFSALNFGOGGPFILSSYVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTTSRSGKSQPSYIFFLLR	1		1	i	1		OTGL POGPSEOK VAVVTVDGCDTGVALRFGS
VPDLPESPVRMGFVGGMRNLQVDSRHDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC VNQWDAFSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQATTRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHHAQLALGAIGGP GHALLSPDYGQQRAEGNLGPRLHGLHLSNITV GGPGPAGGVAGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCPANSY CNDWDSYSCSCDPGYVGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENYPSPGPTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF AEVTTINGGEVNYDSCPRALEAGIWWPTRTFG JPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYSAYAS ALAQNMRHTYLSFTTIVTPNVISVVRLDKGN FAGAKLPRYEALRGQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPELARRQRHPELSQ GEAVSVIYRTLAGLLPHNYPDKRSLRVFK RPINTPVVSISVHDDEELLPRALDKPVTVQFR LLETERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSQCNHMTSFAVLMDVSRRE NGEILPLKTLTYVALGVTLAALLLTFFTLTL RILRSNQHGRRNLTAALGLAQLVFLLGINQA DLPFACTVIALLLHELYLCTFSWALLEALHLY RALTEVRDNTGPMRFYYMLGWGYPAFITG LAVGLDPEGYGNPDFCWLSTYDTLIWSFAGP VAFAVSMSVFLYILAARASCAAQRQGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTILL FHYLFATCNCIGPFTLSYVVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTSRSGKSQPSYIFFLLR FSSALNFGOGGPFTLSSYVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTSRSGKSQPSYIFFLLR			1		Į		VI GNYSCAA\OGTOGGSKKSLDLTGPLLLGG
ADFIANNOTVPGCPAKKNVCDSKTCHNGGTC VNQWDAPSCEQLGFGGKSCAGEMANPQHE LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHHAQLALGAIGGP GHAILSFDYGQQRAEGNLGPRLHGLHLSNITV GGIPGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEGGCSLPDPCDSNPCPANSY CSNDWDSYSCSCDPGYGDNCTNVCDLMPC EHQSVCTRKPAPHGYTCCPPNVLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENIYTRPGSPTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNFF AEVTTINGCEVNYDSCPRAEAGIWWPRTRFG LPAAAPCPKGSFGTAVHLOEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTOGFGISATQDVHIFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYEAYAS ALAQNNRHTYLSPFTIVTPNIVISVVRLDKGN FAGAKLPRVARLAGLUPHDTPLTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRRHFELSQ GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK RPIINTPVVSISVHDDEELLPRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHMTSAVLMDVSRRE NGEILPLKTLTYVALGVTLAALLLTFFFLTLL RILRSNOHGIRRNLTAALGLAQLVFLLGINQA DLPFACTVIALLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRFYYMLGWGVPAFITG LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP VAFAVSMSVPLYLLAARSCAAQRQGFEKKG PVSGLOPSFAVLLLLSATWLLALLSVNSDTLL FHYLFATCNCIGOPFFLSYVLISKEVKKALK LACSRKPSPDALTTKSILTSSYNCPSPYADG RLYQPYYGDSAGSLHSTSSGKSOPSIPFLUR FESALNFGOOPPGLGGPGRLCTLGRFKLDQ		· ·		1	-		VPDI PESEPVRMROFVGCMRNLOVDSRHIDM
VNQWDAFSCEPLGFGKSCAQEMANPQHF  LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD  GVLLQATTRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHHAQLALGAIGGP GHAILSPDYGQRAEGNLGPRLHGLHLSNITY GGIFGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPVCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDDPD NKTSGECHCKENHYRPPGSPTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF AEVTTNGCEVNYDSCPRAEAGIWWPRTREG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITTSELKGFAERLQRNESGLDSGRSQQL ALLLRNATOHTAGYFGSDVVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYEAVAS ALAQNNRHTYLSPFTIVTPNIVISVYRLDKGN FAGAKLPRYEALRGEQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPELARRQRRHPELSQ GEAVASVIIVRTLAGLLEHNYDPDKRSLRVPK RPIINTPVVSISVHDDEELLPRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVYFRNESHVSCQCNHMTSFAVLMDVSRRE NGELPLKTLTYVALGVTLAALLLITFFF.TLL RILRSNQHGIRRNLTAALGLAQLVFLIGINQA DLPFACTVIALLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRFYYMLGWGVFAFITG LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP VAFAVSMSVPLYILAARASCAAQRGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL FHYLFATCROGPFFLSYVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYYGDSAGSLHSTSRSGKSQPSYIFFLLR FESALNGGOGPFGLGGIPGRLCTLGRFKDQQ	1		1				ADEIANNGTVPGCPAKKNVCDSKTCHNGGTC
LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEGRANDGDWHHAQLALGAIGGP GHAILSFDYGQQRAEGNLGPRLHGLHLSNITV GGIPGAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSPTCLLCDCYPTG SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF AEVTTNGCEVNYDSCPRAEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITTSELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL DIANKRHWELIQQTEGGTAWLLQHYEAYAS ALAQNMRHTYLSPFTIVITPNIVISVVRLDKGN FAGAKLPRYBALRGQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRRHFELSQ GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK RPIINTTPVSISVHIDDELLPRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHMTSFAVLMDVSRRE NGEILPLKTLTYVAIGVTLAALLLTFFFLTL RILBSNQHGRRNLTAALGLAQLVFLLGINQA DLPFACTVIAILLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRPYYMLGWGVPAFITG LAYGLDPEGYGNPDFCWLSTYDTLIWSFAGP VAFAVSMSVFLYILAARASCAAQRQGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL FHYLFATCNCLQGFFIFLSYVVLSKEVKRALK LACSRKPSPDPALTTKSTLTSSGKSQPSYPFLIR EFSALNPGGOGPPGLGGIPGRLCTLGRFKDQQ	1			1	1		ADMINIST VI GET REGER SCA DEMANPOHE
GVLLQAITRGRSTITLQLREGHVMLSVEGTGL QASSLRLEPGRANDGDWHHAQLALGAIGGP GHAILSFDYGQRAEGNLGPRLHGLHLSNITV GGPGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESNVEQGCSLDPDCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNDVSKGFDPDC NKTSGECHCKENHYRPPGSPTCLLCDCYPTG SLSRVCDPEDGQCCKPGVIGRQCDRCDNFF AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTORGFGLSATQDVHFTENLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYEAYAS ALAQNMRHTYLSFFTIVTFNIVISVVRLDKGN FAGAKLPRYEAL REGQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRRIPELSQ GEAVASVIJYRTLAGLLPHNYDPDKRSLRVPK RPIINTPVVSISVHIDDEELLFRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHMTSFAVLMDVSRRE NGEILPLKTLTYVALGVTLAALLLTFFLTLL RILRSNQHGRRNLTAALGLAQLVFLLGINQA DLPFACTVIALLLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRFYYMLGWGVPAFTIG LAVGLDPEGYGNPDFCWLSTYDTLIWSFAGP VAFAVSMSVFLYILAARASCAAQRQGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL HTYLFATATCUQGFFITSYVVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTRSGKSQPSYJFFLLR FESALNPGGOGPPGLGGIFGRVLCTLGRFKDQQ		1					VNOWDATSCECTED FOR SCAQLINATION OF THE CAR
QASSLRLEFGRANDGDWHHAQLALGAIGGF GHAILSFDYGQRAEGNLGPRLHGLHLSNITY GGIPGPAGGVARGFRGCLGGVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPGSPTCLLCCYPTG SLSRVCDPEDGQCCKPGVIGRQCDRCDNFF AEVITNGCEVNYDSCPRAEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITISELKGFAERLQRNESGLDSGRSQQL ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL DITANKRHVELIQQTEGGTAWLLQHYEAYAS ALAQNMRHTYLSFTIVTPNIVISVVRLDKGN FAGAKLPRYEALRGEQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRHPELSQ GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK RPINTPVVSISVHDDEELLPRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSCQCNHMTSFAVLMDVSRRE NGELPLKTLTYVALGVTLAALLLTFFFLTL RILRSNQHGRRNLTAALGLAQLVFLLGINQA DLPFACTVIAILLHFLYCTFSWALLEALHLY RALTEVRDVNTGPMRFYYMLGWGVPAFITG LAYGLDPEGYGRPDFCWLSTYDTLIWSFAGP VAFAVSMSVFLYILAARASCAAQRGGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL FHYLFATCNCIQGFFIFLSYVVLSKEVKKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG RLYQPYGDSAGSLHSTRSRGKSQPSYPFFLLR FESALNPGGOGPPGLGGIPGRVLCFLGRFKDQQ		İ		i	1	1	LGSSLVAWHGLSLPISQPWILSLWIFKIRQAD
GHAILSFDYGQQRAEGNLGPRLHGLHLSNITY GGTGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET RIDPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPGSPTCLLCDCYPTG SLSRVCDPEDGQCPCKRGVIGRQCDRCDNPF APYTTINGCEVNYDSCPRAEAGIWWPRTRFG LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITTSELKGFAERLQRNESGLDSGRSQQL ALLRNATQHTAGYFGSDVKVAYQLATRLL AHESTGFGLSATQDVHFTENLLRVGSALL DTANKRHWELIQQTEGGTAWLLQHYEAYAS ALAQNMRHTYLSPTTVTPNIVSVYLDKGN FAGKKLPRYEALRGCQPPDLETTVILPESVFR ETPPVVRPAGPGEAQEPEELARRQRRHPELSQ GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK RPIINTPVVSISVHDDEELLPRALDKPVTVQFR LLETEERTKPICVFWNHSILVSGTGGWSARGC EVVFRNESHVSQCNHMTSFAVLMDVSRRE NGELPLKTLTYVALGVTLAALLLTFFFLTLL RILRSNQHGIRRNLTAALGLAQLVFLLGINQA DLPFACTVIALLHFLYLCTFSWALLEALHLY RALTEVRDVNTGPMRPYYMLGWGVPAFITG LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP VAFAVSMSVFLYILAARASCAAQRQGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL FFFYLFATCNCIQGPFFILSYVVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSSYADG RLYQPYGDSAGSLHSTSRSGKSQPSYIPFLLR		i	1	1	1		GVLLQATTRGRSTITLQLREGHVMLSVEGTGL
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NO: of NO: of nucleotide eotide sequence uence	mino acid sequence (A=Alanine C=Cysteine,  =Aspartic Acid, E=Glutamic Acid,  =Phenylalanine, G=Glycine, H=Histidine,  =Isoleucine, K=Lysine, L=Leucine,  4=Methionine, N=Asparagine, P=Proline,  =Glutamine, R=Arginine, S=Serine,
NO: of nucleotide eotide sequence uence NO: of nucleotide location corresponding uence uence NO: of nucleotide location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location corresponding to last amino acid location location corresponding to last amino acid location location corresponding to last amino acid location loc	=Phenylalanine, G=Glycine, H=Histidine, =Isoleucine, K=Lysine, L=Leucine, 1=Methionine, N=Asparagine, P=Proline,
nucl- eotide seq- uence uence uence   in nucleotide   location   F=  USSN   location   corresponding   I=  correspondi   to last amino   M  ng to first   acid residue   Q  amino acid   of peptide   T=	=Isoleucine, K=Lysine, L=Leucine, 1=Methionine, N=Asparagine, P=Proline,
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residue of sequence Y	'=Tyrosine, X=Unknown, *=Stop codon,
residue ex   sequen	=possible nucleotide deletion, \=possible
, pop	possible insertion
sequence ni	EEEEEEEAAFPGEQGWDSLLGPGAERLPLHS
E	PKDGGPGPGKAPWPGDFGTTAKESSGNGAP
	PKDGGPGPGKAPWPGDFGTTAKESSOTGTA
	ERLRENGDALSREGSLGPLPGSSAQPHKGIL
	KKKCLPTISEKSSLLRLPLEQCTGSSRGSSASE
	GSRGGPPSRPPPRQSLQEQLNGVMPIAMSIKA
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	KAGPHCSRLALTG\SHDFAINFDPENPECEGK
	RGDFHLPRLPADTLHTGAQTPLPRAQLPVPST
	HPRPVFI\EISGVIASYRRCLPQIQLYGPTNVAP
	IINRVAEPAQREQSTGQATKYSVLLVLTDGV
	VSDMAETRTAIVRASRLPMSIIIVGVGNADES
	DMR1_LDGDDGPLRCPRGVPAARDIVQFVPFR
	DEK DVSPPGPFRLKDSSASHPPKSDLKLPPFD
	VI I RTREPSWPP*SPTSPSDDPASPTLPLTPNHI
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	GPA VAFEPI HRPKKELSATKKURVNHULTIU
	FNIVAOSVRNSPEFOKLLGIAMELFLLCSDDA
	ESDVRMVADECLNKVIKALMDSNLPRLQLEL
	VERKINGAPRSLRAALWRFAELAHLVRPQK
	CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP
	KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI
	RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG
	KKIAAGSAVSICQISKKIQIFISWEDITOOOV
	LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV
	KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL
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	ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG
	TOASSPISDSSQTTTEGPDSAVTPSDSSEIVLD
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	A STANKE OF OTOODODEDERY TON DUEYORY
	CTDNOVI GLOIGOPODEDEEATGILPDEASEA
	GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALOOAHLLKNMSHCRQPSDSSVDKF
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	GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGQSTDDDS API VHCVRLLSASFLLTGGKNVLVPDRDVRV
	GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF VI RDEATEPGDOENKPCRIKGDIGQSTDDDS

000 ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uence	delite		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
dence				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
Ì		1		residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
		<u> </u>		sequence		TTEYPEEOYVSDILNYIDHGDPQVRGATAILC
						GTLICSILSRSRFHVGDWMGTIRTLTGNTFSL
•		}	ļ	1	†	ADCIPILIRKTLKDESSVTCKLACTAVRNCVM
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			1			PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK
		- 1			1	SQCWTRSDSALLEGAELVNRIPAEDMNAFM
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of,	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=GlyCille, H=Hasionic,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	,	7.7	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Í		i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1		Sequence	/=possible nucleotide deletion, \=possible
	1			peptide		nucleotide insertion
		1		sequence	<u> </u>	ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
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						LELYSRWILPSSSARRTPAILISEVVRSLLVVS
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431	1781	A	3474	1	441	FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ

NO: of peptide sequence  No: of peptide sequence  No: of peptide sequen						D. dieted and	Amino acid sequence (A=Alanine C=Cysteine,
No. 1  No. 1  Pepide contect of the content of the	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A spartic Acid. F=Glutamic Acid.
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1782   A   3478   416   23   OURRITIPNETTYYSS: IIEIAWI**KNMQID OWFREESPEIDLCKS*YS-ISDREAKAKIWKE CSENRWCYKNWMLHVOKKRI*VOTLHIPS OKL NSKWYKDINVECKTIKLLIQUE/PGOLGY SRAINSGSR     433   1783   A   3504   1876   552   SLGAPGESTILIVRTSKILIVGLIGULLVWILL ORSELIA JOHITISSK PALLAAPTAVCSCSRCS APERCY APPAARTGI PTPAPASSPAPAASPA PAPAPAARTGI PTPAPASSPAPAASPA PAPAPAARTGI PTPAPASSPAPAASPA PAPAPAARTGI PTPAPASSPAPAASPA PAPAPAASPAPASPAPASPAPA		1	ł	1	1 ' '		nucleotide insertion
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WHINLGSLQPLSLEDRLSPGVLGCSALCRSGV RTKFGNMVTSRERGTTRIPKEG  MSLVRAALEALDELDLFGVKGGPQSVIHVLA DEVQHCQSILNSLLPRASTSKEVDASALSVVS FPAFAVEDSQLVELTKQEITIKLQGRYGGCRF LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLKGKNOVPLLPELYSVPPDRVDEEYVOPPT VDRVPMGKLPHMWGQSLYILGSLMAEGFLA PGEIDPLNRFSTVPKPDVVQVYPSLPHGCS SKSPSHQCTIISRITTRKITAPVSILAETEEIKTIL KDKGIYVETIAEVYPIRVQPARILSHTYSSLEIF LPPLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTTETTPQFTDQQQFYLALDNKMIVE MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVYTGKL SEFLITSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMDDYDSTSHARCGDEVARYL DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQYPSVRVEHILPRDQ SGEVDFKALVLQLKETSSLQGADLYMLYT MKGPDWITELTWERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATFGLI MNLSPSAMKNLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSCSFPSA DYQQSSKDRGQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAILVLTMLADIENISIGS INAVEKIVHLANDLFLQEQKTLGADDTMLAKL PASGICTILLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ CPPLTWELIEVKAREVLQDSLDGRYSTPSSCI	1	1	1	1	1		SACTECUTIVIANDI I VEEDESHSVTOAGWVO
RTKFGNMVTSRERGTTRLPKEG  ### MSLVRAALEALDELDLFGVKGGPQSVIHVLA DEVQHCQSILNSLPRASTSKEVDASLLSVVS FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLIKGKNGVPLLPELYSYPDRVDEEYQNPHI VDRVPMGKLPHMWGQSLYILGSLMAEGFLA PGEIDPLNRRSTYPKPDVVVQVYPSLPHGCS SKSPSHQCTISISITTRKTIAPVSILAETEIKTIL KDKGIYVETIAEVYPIRVOPARILSHYSSLEIF LPPLNSVSGCNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFOFDQQQFYLALDNKMIVE MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLTTSCCTHLSFMDPGFEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSHPPQENQVPSVRVEHLPRDQ SGEVDFKALVQLKETSSLQEQADILYMLYT MKGPDWNTELYNERSATVRELITELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATEGL MMLSPSAMKNLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPETYRALLVELTHLADIENHSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTILYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CPPLTWELIEVKAREVLODSLDGRYSTPSSCI		1	1				SAGIIGVKHHAKEL I PEQESHSVI QAGUUQ
435 1785 A 3529 1 3161 MSLVRAALEALDELDLFGVKGGPQSVHVLA DEVQHCQSILNSLLPRASTSKEVDASLLSVVS FPAFAVEDSQLVELTKQEIITKLQGRYGCCFF LRDGYXTPKEDPNRLYYÆNPAELKLFENIEC EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLIKGKNGVPLLPELYSVPPDR VDEEYQNPHT VDRVPMGKLPHMWGQSLYLLGSLMAEGFLA PGEIDFLNRFSTVFKPDVVQVYPSLPHGCS SKSPSHQTIISIRTTRKITAPVSILAETEEIKTLI KDKGIYVETLAEVYPIRQPARILSHYSSLEIF LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFTPQFIDQQGFYLALDNKMIVE MLRTDLSYLCSRWRMTGGPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARGGEVARYL DHILAHTAPKLAPTSQKGGLDRRQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHFRQENQVPSVRVEHILPRDQ SGEVDFKALVLQLKETSSLQEQADILYMLYT MKGPDWNTELYNERSATVRELLTELYGKVG EIRHWGLRYJSGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEMVYLAMYMRTQPGLFAE MFFLRIGLIQVMATELAHSLRCSAEEATEGL MNLSPSAMKNLLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFSAYDQQSSKDSRQGQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLL VEALIVLTIMLADIENISIGS ILAYELVHANDLFLQEQKTLGADDTMLAKL PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ							WHINLGSLQPLSLEDRLSPGVLGCSALCASGV
DEVQHCQSILNSLIPRASTSKEVDASLLSVVS FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF LRDGYXTPKEDPNRLYYENPAELKLFENIEC EWPLFWTYFILDGVPSGNAEQVQEYKEALEA VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHI VDRVPMGKHPIMWGQSLYLLGSLMAEGFLA PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTLL KDKGIYVETTAEVYPIRVQPARILSHIYSSLEIF LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFTPGPIDQQFYLALDNKMIVE MLRTDLSYLCSRWRMTGGPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLITISCCTHLSFMDPGFEGKLYSEDYDDN YDYLESGNWMNDYDDTSHARCGDEVARYL DHLLAHTAPHPKLAPTSQKGGLDRPQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQYPSVRVEHLPRDQ SGEVDFKALVLQLKETSSLQEQADILYMLYT MKGPDWNTELYNERSATVRELTTELYGKVG EIRHWGLIRYISGILRKVVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIIQVMATELAHSLRCSAEEATEGL MNLSPSAMKNLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFPSAYDQSSKLOSRQGQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAILVLTMLADIENHSIGS ILAVEKIVHLANDLFILGEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  **CPPLTWELLEVKKAEVLODSLDGRYSTPSSCI							RTKFGINMVTSRERGTTRLPREG
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FPAFAVEDSQLVELTKQEIITKLQGRYGCRE LRDGYKTPKEDPNRLYYÆNPAELKLFENIEC EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLIKGKNGVPLLPELYSVPPDR VDEEYQNPHT VDRVPMGKLPHMWGQSLYILGSLMAEGFLA PGEIDPLNRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKITAPVSILAETEIKTIL KDKGIYVETLAEVYPIRVQPARILSHIYSSLEIF LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFPQFIDQQFYLALDNKMIVE MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ SGEVDFKALVLQLKETSSLQEQADILYMLYT MKGPDWTELYNERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATEGL MNLSPSAMKNLLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW QRRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAILVLTMLADIENISGS ILAYEKIVHANDLFI-QEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ CPPLTWELLEYKKAEVLODSLDGRYSTPSSCI	433	1/63	^	3323	1 -		DEVQHCQSILNSLLPRASTSKEVDASLLSVVS
LRDGYKTPKEDPNRLYYÆNPÄELKLFENIEC EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHT VDRVPMGKLPHMWGQSLYILGSLMAEGFLA PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTLI KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTTPOFIDQQQFYLALDNKMIVE MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHILLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ SGEVDFKALVLQLKETSSLQEQADILYMLYT MKGPDWNTELYNERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATBGL MNLSPSAMKNLLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSGGSFFSA YDQQSSKDSRQGQW QRRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGELKFSVHVESVL NRVPQPEYRGLLVEAILVLTMLADIENISIGS IHAYEKIVHANDLFI-QEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ CPPLTWELLEYKKAEVLODSLDGRYSTPSSCI	ļ	1					FPAFAVEDSOLVELTKOEIITKLQGRYGCCRF
EWPLFWTYFILDGVFSGNAEQVQEYKEALEA VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHT VDRVPMGKLPHMWGQSLYILGSLMAEGFLA PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTIL KDKGGYVETLAEVYPIRVQPARILSHHYSSLEIF LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFTOPIDQQGYTLALDNKMIVE MLTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ SGEVDFKALVLQLKETSSLQEQADILYMLYT MKSPDDWNTELYNERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPPEREKTISAPLPYEALTQLIDEA SEGDMSISILTQEIMYVLAMYMRTQPGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATEGL MNLSPSAMKNLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFPSAYDQQSSKDSRQGW QRRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTFGEIKFSVHVESVL NRVPQPEYRQLLVEALIVLTIMLADIENISIGS IIAVEKIVHANDLFLQEQKTLGADDTMLAKL PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CPPILTWELLEVKKAEVLODSLDGRYSTPSSCI	į.	Į.	1	1			LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC
VLIKGKNGVPLLPELYSVPPDR VDEEYQNPHI VDRVPMGKLPHMWGQSLYILGSLMAEGFLA PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKJTAPVSILAETEEKTIL KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF LPFINSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFTQFIDQQGFYLALDNKMIVE MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYTGGARVQTGKL SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ SGFVDFKALVLQLKETSSLQEQADILYMLYT MKSPDWNTELYNERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIQVMATELAHSLRCSAEEATEGL MNLSPSAMKNLHHILSGKEFGVERSVRPTD SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPCTSMTPSSGSFPSAYDQGSKDSRQGQW QRRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTFGEIKFSVHYESVL NRVPQPEYRQLLVEAILVLTMLADIENTSIGS IIAVEKIVHANDLFLQEQKTLGADDTMLAKL PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ		1	İ	}	ì		EWPLEWTYFILDGVFSGNAEQVQEYKEALEA
VDRVPMGKLPHMWGQSLYILGSLMAEGIFLA PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTLI KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF LPPLNSVSGCNNRMKLSGRPYRHMGVLGTSK LYDIRKTIFTFTPQFIDQQQFYLALDNKMIVE MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE DGTSLNSSILAALRKMQDGYFGGARVQTGKL SEFLITSCCTHLSFMDPGFEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL DHLAHTAPHPKLAPTSQKGGLDRFQAAVQT TCDLMSLVTKAKELHVQNVHMYLPTKLFQA SRPSFNLLDSPHPRQENQVPSVRVEHLPRDQ SGEVDFKALVLQLKETSSLQEQADILYMLYT MKGPDWNTELYNERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA SEGDMSISILTQEMVYLAMYMRTQPGLFAE MFRLRIGLIIQVMATELAHSLRCSAEEATEGL MINLSPSAMKNLLHHILSGKEFGVERSVRPID SNVSPAISHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFPSAYDQQSSKDSRQQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAILVLTMLADIENHSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  OPPLYWELLEVKKAEVLODSLDGRYSTPSSCI	1	1	1		}		VI INGKNOVPLL PEL YSVPPDR VDEEYONPHT
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SNVSPAISIHEIGAVGATKTERTGIMQLKSEIK QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAILVLTMLADIENHSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI	1		1				MOU SPSAMKNI I HHII SGKEFGVERSVRPTD
QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW QRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAIL\VLTMLADIE\HSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI					1		CHIVED A ICIUEICA VICA TY TED TOMOTI K SEIK
QRRRRLDGALNRVPVGFYQKVWKVLQKCH GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAIL\VLTMLADIE\HSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKT PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI				-			SINASTAISHIEIGUAAGATKI EKI GHIAGEGAGA
GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL NRVPQPEYRQLLVEAIL\VLTMLADIE\HSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKT PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI	}				1		OSPO12W152202L2W1DOMONAGOGA
NRVPQPEYRQLLVEAIL\VLTMLADIE\HSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI					1		QRRRRLDGALNKVPVGFYQKVWKVLQKCH
NRVPQPEYRQLLVEAIL\VLTMLADIE\HSIGS IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI						İ	GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL
IIAVEKIVHIANDLFLQEQKTLGADDTMLAKI PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI	1				1	1	NRVPOPEYROLLVEAIL\VLTMLADIENHSIGS
PASGICTLLYDSAPSGRFGTMTYLSKAAATY VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI							IIAVEKIVHIANDLFLOEOKTLGADDTMLAKD
VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI							PASGICTLLYDSAPSGRFGTMTYLSKAAATY
CP*LTWELLEVKKAEVLODSLDGRYSTPSSCI	1						VOEFI PHSICAMO
436 1786 A 3546 73 SOUTH THE REPUBLIE VALU			:				OPEL TWELLEVILL A EVI ODSI DGRYSTPSSCI
EQPDSCRPTGRSFTALEERAVIPSEDVOLIDI	436	1786	Α	3546	73	393	CONDECED A CONTROL OF THE CONTROL OF
<u> </u>			1	1		1	EOLDSCVL LOVSL LVEEFVILLE SED AGEIDIA

	GEO TO	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=A enartic A cid F=Glutamic Acid,
10: of	NO: of	поа	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	ļ ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence			ng to first	acid residue	O=Glutamine R=Arginine, S=Serine,
ence	1		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	ſ	residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	1		1		Sequence	/=possible nucleotide deletion, \=possible
		ļ	1	peptide	-	nucleotide insertion
	1	1	1	sequence	<b></b>	KGKGKTIRGI*TFKGRKGGTYQREHDANPLA
	1		T	}		PXSARSCWMRKG
	1		_			AVRAEPGLEELSSGLRAHSPSATTVCEPEAQG
137	1787	A	3554	5157	2939	SASGCRYAAHPHWGLGGAAAAGGSWEPQPP
731	1,0,		1	,	1	SASGERIAAHPHWOLGGAAAAGOOWER QA
		1	Ì	]	1	RPVCEPAGRGKPHPPAAPRSPLLPGSRRRPHA
		1	ĺ		}	AQPGARARTSPPPASARNMAARPAATLAWSL
					1	LLLSSALLREGCRARFVAERDSEDDGEEPVVF
	Į.					PESPLQSPTVLVAVLARNAAHTLPHFLGCLER
	ł		j		,	LDYPKSRMAIWAATDHNVDNTTEIFREWLK
	1	(			1	NVQRLYHYVEWRPMDEPESYPDEIGPKHWP
	1	1	Ì	1		TODE A LIVINIKI ROAALRTAREKWSDYILFIDY
				1		DNEI TNPOTI NILLIAENKTIVAPMLESKULYS
					1	NEWCGITPKGFYKRTPDY\VQIREWKKIGCFP
	1	1	1		1	TO MAKE THE TOTAL REASON TO THE TOTAL REPORT OF THE TOTAL REPORT O
	ł	1	1			TEDDITYEAESSROAGIOMYLCNREHYGYLPH
	1	1	1		1	I LEPHOTI OFDIENLIHVOIEAMIDKEPMEPSQ
	1	ŀ	į	1	l .	YVSVVPKYPDKMGFDEIFMINLKRRKGQGGI
	1		1	1		RWLRTLYEQEIEVKIVEAVDGKALNTSQLKA
		1	- !			LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV
	1		Í	{		WKEVIDRELEKTLVIEDDVRFEHQFKKKLMK
			1			LMDNIDQAQLDWELIYIGRKRMQVKEPEKA
	1	1	ı	Ì		LMDNIDQAQLDWELI HUKKKIQ VKEI EIGAOKI V
	{	1	i			VPNVANLVEADYSYWTLGYVISLEGAQKLV
	1	ł		İ	Î	GANPFGKMLPVDEFLPVMYNKHPVAEYKEY
	l l	1	1	1		YESROLKAFSAEPLLIYPTHYTGQPGYLSDTE
	1		l			TSTIWDNETVATDWDRTHAWKSRKQSRIYSN
		- 1	ł			AKNTEALPPPTSLDTVPSRDEL
	1.500	<del></del>	3563	130	527	IFFNSSSLFCRVFCLFLRWSFTLVAQARVQ*C
438	1788	A	3303	130	)	NI SSI OPI PPGFK*FSCLSPPKS*DYKKPPPKP
	ł		{	1		I NET VE**POGETVI GOAGLELLI/S/GDPPISA
	}	1				SQSAGITGVSHRAWPVHAISTHISLVKTRPSL
	ŀ	İ	i			TT C
	1	_			1024	LI OPAMRKSPGLSDCLWAWILLLSTLTGRSY
439	1789	Α	3565	446	1834	GQPSLQDELKDNTTVFTRILDRLLDGYDNRL
1.22		1	1	1		RPGLGERVTEVKTDIFVTSFGPVSDHDMEYT
		ì	ļ	1		DVFFRQSWKDERLKFKGPMTVLRLNNLMAS
	ł	- 1	ł			KIWTPDTFFHNGKKSVAHNMTMPNKLLRITE
i		\ \	- 1			KIWIPDIFFHNUKAS VAINVIINI INDIA
	1	i	l l		1	DGTLLYTMRLTVR\AECPMAFGRDFPM\D\AI
Į.	1	- 1			1	ACPLKFGSYAYTRAEVVYEWTREPARSVVV
	ł			Į.		AEDGSRLNQYDLLGQTVDSGIVQSSTGEYV
	1	İ	1	ļ	1	MTTHFHLKRKIGYFVIQTYLPCIMTVILSQVS
		1			1	WI NDESUPARTVEGVTTVLTMTTLSISARNS
	1			}		PKVAVATAMDWFIAVCYAFVFSALIEFAIVI
		[			1	VETKRGYAWDGKSVVPEKPKKVKDPLIKKN
1		1		1		NTVAPTATSYTPNLARGDPGLATIAKSATIE
1	}	}		}		KEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLI
	}				ļ	ECIENI VVWATYLNREPOLKAPTPHQ
1						STSSCFPAAAAAIMREIVHLQAGQCGNQIGA
440	1790	A	3568	1	350	FWEVISDEHGIDPTGTYHGDSDLQLERINVY
	1 - 1 - 1			- 1		NEATGEAPVPSPTALRGPRGPCLG*RPPVPAG
1		İ			ŀ	NEATUEAR VENETAL ROLL CONTROLL OF THE STATE
1		1		1		GKYVPRAVLVDMEPGTMDSV
141	1791	A	3569	2	1751	FVAVAGAVSGEPLVHWCTQQLRKTFGLDVS
441	1/91	14	7505	-	į	EEIIQYVLSIESAEEIREYVTDLLQGNEGKKG
						FIEEL ITK WOKNDOELISDPLOOCFKKDELL
					1	OVECTHI KRGRKKGRNROEVPAFILEDI IA
		{	1			VKTPEDI AKAOENSNSVKKKTKFVNLYIKE
1						ODDI AVI I PGRHPCDCLGOKHKLINNCLICO
1	1			ļ	!	PTVCEOEGSGPCLFCGTLVCTHEEQDILRGD
	1	- 1	ì	1		NKSQKLLKKLMSGVENSGKVDISTKDLLPH
		1				
	ļ			1		QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQ\

EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
IO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
ucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	i	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ence	donce	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
CHCC	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	ĺ		peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
	<del> </del>		<del> </del>			DDESDYFASDSNQWLSKLERETLQKREEELR
	1					ELRHASRLSKKVTIDFAGRKILEEENSLAEYH
		Ì	Į			SRLDETIQAIANGTLNQPLTKLDRSSEEPLGVL
		1				VNPNMYQSPPQWVDHTGAASQKKAFRSSGF
	1		1		ì	GLEFNSFQHQLRIQDQEFQEGFDGGWCLSVH
	ŀ				}	OPWASLLVRGIKRVEGRSWYTPHRGRLWIAA
	ļ		ļ			TAKKPSPOEVSELOATYRLLRGKDVEFPNDY
			l .	1	1	PSGCLLGCVDLIDCLSOKOFKEQFPDISQESDS
	1		1		1	PFVFICKNPQEMVVKFPIKGNPKIWKLDSKIH
	1	1	1			QGAKKGLMKQNKAV
		l		ļ	1	MPRSHTGERLCEGKEGSQCAENFSPNLSVTK
442	1792	A	3576	1	2019	KTAGVKPYECTICGKAFMRLSSLTRHMRSHT
•			1			AIRAI\EKPYKCKEC\GRAFSLSQILSK\HERSH
		1		1		TGEKPYKCKQCGKTFIYHQPFQRHERTHIGEK
				<b>\</b>		PYECKQCGKALSCSSSLRVHERIHTGEKPYEC
						PYECKOCKARCCCCBRUTERITIOEM TEC
	1			1		KQCGKAFSCSSSIRVHERTHTGEKPYACK\EC GKAFIS\TTSVLTHMITHNGDRPYKCKECGKA
	1	1	l			GKAFIS/ITSVLIHMITHNUDRITREKECKA
			1			FIFPSFLRVHERIHTGEKPYKCKQCGKAFRWS
		1	ļ	į		TSIQIHERIHTGEKPYKCKECGKSFSARPAFRV
		1		1	*	HVRVHTGEKPYKCKECGKAFSRISYFRIHERT
	1		ł	1		HTGEKPYECKKCGKTFNYPLDLKIHKRNHTG
	ļ	1		Į		EKPYECKECAKTFISLENFRRHMITHTGDGPY
	- [	İ	ŀ			KCRDCGKVFIFPSALRTHERTHTGEKPYECKC
	İ	١.	ļ	}		CGKAFSCSSYIRIHKRTHTGEK\PYECKECGK
		ĺ	- 1			AFIYPTSFQGHMRMHTGEKPYKCKECGKAFS
			<b>\</b>	İ	·	LHSSFR\RHTRIHNYEKPLEC*Q\CGKAFSVST
	. i		1	ļ	<b> </b>	LKKPMRNAQSDRKLY/KCEK*EKVFNSNRCF
			1			OSCENSH*REKSCOCK*YRKRDTR*FMYSQV
						PHNHVSVSNGPYR/CGSPIRLYNT*NISINKNL
	ł	!				VAVVTP*CSTLFKCLWCWCKRAALSVV*/IV
			1		Í	DSGRGRWLTPVIPALWEAKAGGSRGQEIKTII
	Ì	1	ł	ļ		ANTVKPHLY
				207	114	DEVERKEEOFIEGHKQIVNKWRDLLCSWKRK
443	1793	A	3578	287	114	I STIKK SVI ONNL *FSAASMRFQKVFF
					1000	HLFFSLFLAAMAMTGSTPCSSMSNHTKERVT
444	1794	A	3582	3335	1909	MTKVTLENFYSNLIAQHEEREMRQKKLEKV
			Į.			MEEEGLKDEEKRLRRSAHARKETEFLRLKRT
		İ			1	RLGLEDFESLKVIGRGAFGEVRLVQKKDTGH
		-		1		VYAMKILRKADMLEKEQVGHIRAERDILVEA
				1		A LAWKITKY GASSODAL M. ALL DURANGE DECOM
	1	1	1	1		DSLWVVKMFYSFQDKLNLYLIMEFLPGGDM
		1		1		MTLLMKKDTLTEEETQFYIAETVLAIDSIHQI
	1	-				GFIHRDIKPDNLLLDSKGHVKLSDFGLCTGLI
			1			KAHRTEFYRNLNHSLPSDFTFQNMNSKRKAI
		1				TWKRNRRQLAFSTVGTPDYLAPEVFMQTGY
						KI CDWWSI GVIMYEMLIGYPPFCSETPQETY
	1	1				KKVMNWKETLTFPPEVPISEKAKDLILRFCC
		ļ				WEHRIGAPGVEEIKSNSFFEGVDWEHIRERP
	1	Ì				AISIEIKSIDDTSNFDEFPESDILKPTVATSNHF
	1		1	1	1	TDYKNKDWVFINYTYKRFEGLTARGAIPSYN
						KAAK
					(1/0	RTRGIEKRFAYSFLQQLIRYVDEAHQYILEFL
445	1795	A	3584	1	6169	GGSRGKGEHFPYEQEIKFFAKVVLPLIDQYFI
				1	1	NHRLYFLSAASRPLCSGGHASNKEKEMVTS
1					1	NHKLYFLSAASKFLUSUUMASINAEREMIY ISI
4		-		1		FCKLGVLVRHRISLFGNDATSIVNCLHILGQT
1		ı			1	LDARTVMKTGLESVKSALRAFLDNAAEDLE
1			ĺ			KTMENLKQGQFTHTRNQPKGVTQIINYTTV
						LLPMLSSLFEHIGQHQFGEDLILEDVQVSCYI
						LI TSI VALGTSKSIYVERORSALGECLAAFAG
i	İ					FPVAFLETHLDKHNTYSIYNTKSSRERAALSL
	1	1	1	1	I	THE PROPERTY OF THE PROPERTY ASSOCIATION OF THE PROPERTY OF TH
		ı	l	ı		TNVEDVCPNIPSLEKLMEEIVELAESGIRYTC

						Aluin C-Curtaina
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	l=Isolcucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutarnine, R=Arginine, S=Serine,
uence		Ì	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
	}		1	sequence		nucleotide insertion
	ļ	ļ	<del> </del>	Sequence	<del> </del>	MPHVMEVILPMLCSYMSRWWEHGPENNPER
						AFMCCTALNSEHMNTLLGNILKIIYNNLGIDE
					}	GAWMKRLAVFSOPIINKVKPQLLKTHFLPLM
		1		j		FKLKKKAATVVSEEDHLKAEARGDMSEAEL
						LILDEFTTLARDLYAFYPLLIRFGDYNRAKWL
				1		KEPNPEAEELFRMVAEVFIYWSKSHNFKREE
		1	ł			QNFVVQNEINNMSFLITDTKSKMSKAAVSDQ
1			İ	1		ERKKMKRKGDRYSMQTSLIVAALKRLLPIGL
	1		1		1	NICAPGDQELIALAKNRFSLKDTEDEVRDIRS
		1				NIHLQGKLEDPAIRWQMALYKDLPNRTDDTS DPEKTVERVLDIANVLFHLEQKSKRVGRRHY
			1		}	CLVEHPQRSKKAVWHKLLSKQRKRAVVACF
			1			RMAPLYNLPRHRAVNLFLQGYEKSWIETEEH
				1		VEEDKLIEDLAKPGAEPPEEDEGTKRVDPLHQ
ì		ł		1		LILLFSRTALTEKCKLEEDFLYMAYADIMAKS
		1		1	1	CHDEEDDDGEEEVKSFEEKEMEKQKLLYQQ
	}	j	]	}	1	ARI HDRGAAEMVLOTISASKGETGPMVAA1
		1				LKI GIAILNGGNSTVOOKMLDYLKEKKDVGF
				1		FOST A GI MOSCSVLDLNAFERONKAEGLUM
				Į		VTEEGSGEKVI ODDEFTCDLFRFLOLLCEGH
	1		,	Į.		NSDFQNYLRTQTGNNTTVNIIISTVDYLLRVQ
1		- {	1	ł		ESISDFYWYYSGKDVIDEQGQRNFSKAIQVA
		1		ļ		KQVFNTLTEYIQGPCTGNQQSLAHSRLWDAV
	ļ	1	}		}	VGFLHVFAHMQMKLSQDSSQIELLKELMDLQ KDMVVMLLSMLEGNVVNGTIGKQMVDMLV
				1		ESSNNVEMILKFFDMFLKLKDLTSSDTFKEYD
	1			1		PDGKGVIFKRDFHKAMESHKHYTQSETEFLL
į						SCAETDENETLDYEEFVKRFHEPAKDIGFNVA
-					{	VLLTNLSEHMPNDTRLQTFLELAESVLNYFQP
)		}			ì	FI GRIFINGSAKRIERVYFEISESSKTQWEKPQ
}						VKESKROFIEDVVNEGGEKEKMELFVNFCED
	1	- 1				TIFFMOLAAOISESDLNERSANKEESEKERPEE
		ı		1		OGPRMAFESTI TVRŠALFALRYNILTLMKMLS
1	- 1	1	- 1 ·	l		I K SI K K OMKK VKKMTVKDM V TAFFSSY W SI
	ļ	1	Ì	(		FMTLLHFVASVFRGFFRIICSLLLGGSLVEGA
				1		KKIKVAELLANMPDPTQDEVRGDGEEGERKP
				}		LEAALPSEDLTDLKELTEESDLLSDIFGLDLKR
	1			1		EGGQYKLIPHNPNAGLSDLMSNPVPMPEVQE
		-				KFQEQKAKEEEKEEKEETKSEPEKAEGEDGE KEEKAKEDKGKQKLRQLHTHRYGEPEVPESA
		- [	1	ļ		FWKKIIAYQQKLLNYFARNFYNMRMLALFV
	1	ĺ	}			AFAINFILLFYKVSTSSVVEGKELPTRSSSENA
	1	1		1		KVTSLDSSSHRIIAVHYVLEESSGYMEPTVRIL
	1	1.	1		(	DIT HTVISFFCIIGYYCLKVPLVIFKREKEVARK
		1	}			I FEDGL VITEOPSEDDIKGOWDRLVINTQSFP
					!	NNVWDKFVKRKVMDKYGEFYGRDRISELLU
				1		MDKAALDESDAREKKKPKKDSSLSAVLNSID
				1		VKYOMWKLGVVFTDNSFLYLAWYMIMSVL
					-	GHYNNFFFAAHLLDIAMGFKTLRTILSSVIH
						NGKOLVLTVGLLAVVVYLYTVVAFNFFRKF
	}		}	1		VNKSEDGDTPDMKCDDMLTCYMFHMYVGV
		Ì	)	}		RAGGGIGDEIEDPAGDEYEIYRIIFDITFFFFVI
	ĺ	1		1		VIII A TIOGI TIDAFGELRDOOEOVKEDMETKC
	1					FICGIGNDYFDTVPHGFETHTLQEHNLANYLF
	1		1			FLMYLINKDETEHTGQESYVWKMYQERCWE
		1		1		FFPAGDCFRKOYEDOLN
446	1796	A	3592		355	AGLELLNSDDPPALASQSAGITGVTRTPSLFF*
446	1/90	I A	3392	1		DTVLLCCSGWSAVAPSRLTAALFS*AQAVCL
i		(	-	-	ļ	SLPRSWDYRRW/PPHPANFCIFCRDE/SLA/ML
	1		1	-		PRLVSNSWTQAILLPRPPKMLGLQV
		l				

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ıucl-	peptide		in	nucleotide	corresponding	1-Icoleucine K=I vsine L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	l	ĺ	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
		1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		]	}	peptide		nucleotide insertion
	Į			sequence		LFVGGGPlCPEGASGFAPGPAPAPRVGVDAEV
447	1797	A	3598	1202	1070	GR*V*GAAASQGA/GSLRPRPTGPGHPGAWL
7-17	1	ĺ	1		Ì	QVWGAAAVCAGPAM*/AVRAKRGPRAG*EP
	1	1		1	1	NSPWRSGVLAA\RAVGAGPWP*P*PGCS*ARG
	1	1		1	ì	NSPWRSGVLAAKAVUAGI WI I I GOOTAGA GRI I CVI
	1			ļ	}	PSSRSAPGLASGPAAPLLQGVHSSAGPLLCYI
		1	1	}		NGTLALGLKP**AWGWGEWRPKG
448	1798	A	3604	3115	557	FRRKGGGGPKDFGAGLKYNSRHEKVNGLEE
440	1790	1 '	300.			GVEFLPVNNVKKVEKHGPGRWVVLAAVLIG
	ì	1	}			LLLVLLGIGFLVWHLQYRDVRVQKVFNGYM
	1		}	· ·	<b>\</b>	RITNENFVDAYENSNSTEFVSLASKVKDALKL
	İ	]	}		ļ	LYSGVPFLGPYHKESAVTAFSEGSVIAYYWSE
•		1	-		ì	FSIPQHLVEEAERVMAEERVVMLPPRARSLKS
	Ì	1	l			FVVTSVVAFPTDSKTVQRTQDNSCSFGLHAR
•	ļ	1	i	1	1	GVELMRFTTPGFPDSPYPAHARCQWALRGD
	1		1		l l	ADSVLSLTFRSFDLASCDERGRHLV\TVYNT\L
	1		1			SPMEPHALLVQLCGTYPPSYNLTFHS\S\QNVL
		}				LITLITNTERRHPG\FEATFFQLPRMSSCGGRL
		1	1	ļ		RKAQGTFNSPYYPGHYPPNIDCTWNIEVPNN
	1			-		QHVKVRFKFFYLLEPGVPAGTCPKDYVEING
	1	1	İ	1		EKYCGERSQFVVTSNSNKITVRFHSDQSYTDT
	1		l	\		GFLAEYLSYDSSDPCPGQFTCRTGRCIRKELR
	}	ł	1	ļ	1	CDGWADCTDHSDELNCSCDAGHQFTCKNKF
	}	}	1	ļ	Ì	CKPLFWVCDSLNDCGDNSDEQGCSCP\AQTF
	1	l	1		1	RCSNGKCLSKSQQCNGKDDCGDGSDEASCP
	i		ł	Ì		KVNVVTCTKHTYRCLNGLCLSKGNPECDGK
	1	1		1		EDCSDGSDEKDCDCGLRSFTRQARVVGGTD
	1	Ì				ADEGEWPWQVSLHALGQGHICGASLISPNWL
	1	}	}		1	VSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS
		1		1		QRSAPGVQERRLKRIISHPFFNDFTFDYDIALL
	1		1		1	FIEKPAEYSSMVRPICLPDASHVFPAGKAIWV
ļ.			.		İ	TGWGHTQYGGTGALILQKGEIRVINQTTCEN
ł	1		1	[		LLPQQITPRMMCVGFLSGGVDSCQGDSGGPL
1						SSVEADGRIFQAGVVSWGDGCAQRNKPGVY
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			3618	2	613	FVSGSPWRMDGSTERLEARRPAGRLPWSSRQ
449	1799	A	3018	2	015	EMTRRPSLMAGROHGWSAQQSATVANPVPG
1	i i	1		ļ	}	ANPOLLPHELGEPEDVYIVKNKPVLLVCKAV
ì		(	í			PATOIFEK CNGEWVROVDHVIERSTDGSSGLI
1	1		1	}		TMEVRINVSROOVEKVFGLEEYWCQCVAWS
}		1		1	1	SSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSL
		)	Į	1	1	FOGIVI PCRPPEGIPPAE
i				+	2676	MEPSI GOGMDLTCPFGVSPACGAQASWSIFG
450	1800	A	3620	1	2070	ADAAFVPGTRGHSOOEAAMPHIPEDEEPPGE
}		İ				POAAOSPAGOOGPPTAGVSCSPTPTIVLIGDA
1		1				TSPECETOKNI ANRVHSPHKRLSHRHLKVSI
			1			ASLTSVDPAGHIIDLVNDQLPDISISEEDKKKN
1			1		1	LALLEEAKLVSERFLTRRGRKSRSSPGDSPSA
		1				VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS
1						SPHPGEPNVPKGLADRKQNDQRKVSQGRLAI
ł		1		İ	ĺ	RPPPVEKSKEIAIEQKENFDPLQYPETTPKGLA
1		Ì				PVTNSSGKMALNSPQPGPVESELGKQLLKTG
		1	İ	1		WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP
1		-				MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEI
Ì	<b>1</b>	1		ļ		PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAI
						PUPKLUK YLAKLI LAEBEKKI AUKAUUKLI
1		}	1			APGLKDFQIQVQPVRMQKLTKLREEHILMRN APGLKDFQIQVQPVRMQKLTKLREEHILMRN
	ì					QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPI
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						1 TEKEVENVFVOLSSAFRNDSYTLESRINQAL
						LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE HRETYQKLLEDIAVLHRLAARLSSRAEVVGA

						Alarine C-Cysteine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide sequence	Y=Tyrosine X=Unknown, *=Stop codon,
	ļ	l	İ	residue of	Sequence	/=possible nucleotide deletion, \=possible
	•	l		peptide		nucleotide insertion
	<u> </u>	<b></b>	<del> </del>	sequence		VROEKRMSKATEVMMOYVENLKRTYEKDH
		ļ		1		A FI MEFKKI ANONSSRSCGPSEDGVLKIAKS
	1	1		1		MSI TI GKNMPRRRVSVAVVPKFNALNLPGQ
		1	1	İ		TRESSSIPSI PALSESPNGKGSLPVTSALPALLE
	1		İ			NGKTNGDPDCEASAPALTLSCLEELSQEIKA
	i	İ	1	1		PMEERAYSKGFOEGLKKTKELQDLKEELELQ
		1	1			KSESPEEPEEVEETEEEEKDPRSSKLEELVHFL
	1	1		1		QVMYPKLCQHWQVIWMMAAVMLVLTVVL
		}		Ì		GLYNSYNSCAEQADGPLGRSTCSAAQKDSW
		ţ			ļ	WSSGLQHEQPTEQ
161	1801	+ <u>-</u> -	3623	504	198	QLIQHQTVHTGRKLYECKECGKAFNQGSTLI
451	1801	^	3023	1 30.		RHQRIHTGEKPYECKVCGKAFRVSSQLKQHQ
	ļ	1	l		1	RIHTGERPYQCKELKGRGAEMLAVLAVKEQ
		1				NRTPVNYGK
452	1802	HA-	3628	2	195	MTCLHSAKAFHY*SSCSFSCEEGFALIGPEVV
432	1802	1		1		QCTALGVWTAPAPVCIAVQCQHLEALNEGT MG*DYPFTAFAYGSSCKYECHTVYRVRGLD
						MG*DYPF1AFAYGSSCK1ECHTY IKYKOBB MLHSRGCYLWNGHFTT*EAISCEPLERPCH*S
		Ì		-	1	V*CSFSCEEGFALIGPEVVQCTALGVWTAPAP
	1					V*CSFSCEEGFALIGFE V VQCTALOV V II II II
	1	1				VCIAVQCQHLEALNEGTMG IQAKGLGIWHVPNKSPMQHWRIKGSLLRYRT
453	1803	A	3637	662	142	DTGFLQTLGHNLLGIYQKYPVKYGEGKCWT
155	1	1		1	1	DNGPVIPVVYDFGDAQKTASYYSPYGQREFT
		1		1		AGFVQFRVFNNERAANALCAGMRVTGCNTE
		1		}		HHCIGGGGYFPEASPQQCGDFSGFDWSGYGT
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1					362	TOVHPAMI GLDELGRSGCGHCTQADLRFGD
454	1804	A	3641	1	302	AAGRDPGODNDRNTAEPAFPPPPRVMAAAA
1	Ì	l l				ALRAPAOSSVTFEDVAVNFSLEEWSLLNEAU
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			3646	12	414	AAAGRGASGALTGEGGGEOGRRVGLGSRAH
455	1805	Α	3040	1	1	SILL GPTENSCOVSSOPPRVAGLGLPLKHEPS
	1	l	j	)	}	RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR
		1	1			
		1		1		PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE
L	<b>\</b>	ļ				SRVRAPSYDDIT
1 456	1806	\	3656	396	8	SRVRAPSYDDIT OVSENSYLTLYTKNNLKSMKDLNVNTEMIK
456	1806	A	3656	396	8	SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK
456	1806	A	3656	396	8	SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK  LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW  PA IK IK SECSI SDTIKKMKROTIVWEQTFIIHI
456	1806	A	3656	396	8	SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK
456	1806	A	3656	396		SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK
	1806	A	3656	396	1961	SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F SFAKI GGPTGMDLWOLLLTLALAGSSDAFSG
456						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F SEAKLGGPTGMDLWQLLTLALAGSSDAFSG SFATAAII SRAPWSLOSVNPGLKTNSSKEPKF
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF VTRRNTOEWTOEWKECPDYVSAGENSCYFN
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDDPIALNWTILNVSLTGIHADIOVRWEAPRN
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIOKGWMVI FYELOYKEVNETKWKMMDP
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GESSFVI YVTI.POMSOFTCEEDFYFPWLLIIIF
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNIKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVFFIELDIDEPDEKTEESDTDRLLSSDH
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLITLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVFKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYNDACPATOOPSVIOAEKNKPQPLPTEGAE
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTECSDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPLALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTIQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGQKNKAGMSQCDMHPEMVSLCQENF
						SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE

				D. Nov. d	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ĺ	in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
(		(	{	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
}	Ì	Į.	ĺ	residue of	sequence	/=possible nucleotide deletion, \=possible
1	i		1	peptide	Ì	/=possible nucleotide deterion, \-possible
	ļ	1		sequence		nucleotide insertion
	<u> </u>	<b></b>	1		1	PVPDYTSIHIVQSPQGLILNATALPLPDKEFLS
ł	1	}	ţ			SCGYVSTDQLNKIMP
458	1808	A	3663	154	462	TRAPASGRSGAGLALSANAPDSGGHPGATEG
430	1000	\ ^	3003			PAGSLAHASGSARGTWRVRGRGSHGWERTV
Ì		ì	į		ì	GAGGCANPVPALHSCASAPRGTGRVSALGPK
}	· ·	l	1	1	İ	TGSSPLSSPKG
	1000	<del> </del>	3664	902	135	LGKYNTSMALFDFVLHNSTGEIRYITEDDVIQ
459	1809	A	3004	702	133	SONALGKYNTSMALFESNSFEKTILESPYYVD
1			1			INOTIFYOVSLHTSDPNLVVFLDTCRASPTSD
1	1	1		Ì	ì	FASPTYDLIKSGCSRDETCK\VYPLFGHYGRF
1	1	j	1			QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRC
(		1	l		1	WQGCVSRSKRDISSYKWKTDSIIGPIRLKRDR
	1		1			SAINGNSGFQHETHAEETPNQPFNSVHLFSFM
İ		1	i			VLALNVVTVATITVRHFVNQRADYQ\YQKLQ
1	1		1	}	ł	
		1	ľ		<u> </u>	NY LGILMSPQVEAGEI*ALLTPPPGCMQFSPLTL/P
460	1810	A	3670	850	557	K*WVSPGLTP/PPPEVPSVFLVEPGLPHAGQA
1	1	İ	1	1		K*WVSPGLTP/PPPEVPSVFLVEPGLPHAGQA
	ì	1	1		1	GLDLL\TSGDPPASTSQSARTTDVSHRAQPLAI
		Ì	1		_	.S
461	1811	A	3671	2472	2099	IGVLAFETGSCSVTRLYCIGIIMPHCSLDLAGS\
461	1011	1.	1 30,1		Ì	TSAFRIAGTTSVHHHPQLTFFFFWIETGSHCV
İ		1				VQTGL*LLALSNPPALASQIAGISGMSHRAWP
1			l		<b>\</b>	GLVLYSLEFSLLCASQSLIMLFTCYNE
L	1010		3672	394	110	VKPVNGESKRD*GADTOTCEGEADEQLQT\N
462	1812	A	3072	374	1	CYYD/STKSFFYISCG*K\RKPTWAENRRLNA
j .			}		}	KMFGIPLHSNSDPWGYEEREVIGFHRSRVSRG
1	1	ł	į.			HGS
			0.550	348	$\frac{1}{1}$	ORNPESAGHPORPPTSGSOSELLAOPRLRPGR
463	1813	Α	3673	348	1	KSSFSRDQDVW*SQAVPKRQ*QRNPFSAGHP
1	}	1				QRPPTSGSQSELLAQPRLRPGRKSSFSRDQDV
i i	1	1			j	WPGQKPRPSQQQHQMCASPTLGQRSPFALEP
i	1	Ĭ	l l			VPAYHGGRDPFASARPSPVGIPKPRAAPAGG
		i				GWRRIRPKSSTK
1	1	}				PVIQRCSQPYGFSLLISFFLKCVSETSQQPPSR
464	1814	A	3676	2253	320	KVFQLLPSFPTLTRSKSHESQLGNRIDDVSSM
į -	1	1	1	1		KVFQLLPSFPTLTRSRSncsqcotttdbbvbom
			1			RFDLSHGSPQMVRRDIGLSVTHRFSTKSWLS
ļ			l		j	QVCHVCQKSMIFGVKCKHCRLKCHNKCTKE
ì		ì				APACRISFLPLTRLRRTESVPSDINNPVDRAAE
ļ		-	1		[	PHFGTLPKALTKKEHPPAMNHLDSSSNPSSTT
ì		ł	ı		İ	FSTPSSPAPFPTSSNPSSATTPP\NPSP\GQR\DSR
	ļ	ļ ·	}			FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE
	1	1	1	İ		AADGTRLDDOPKADVLEAHEAEAEEPEAGK
Į.	ł		ŀ			SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS
1	1	1	j	ì	1	VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR
		Į.	1			WHGEVAIRLLEMDGHNODHLKLFKKEVMN
						YRQTRHENVVLFMGACMNPPHLAIITSFCKG
					}	RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY
)		1	ļ	1	1	LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF
					[	\GISGVVP\EGRRENQLKLSHDWLCYLAPEIVR
1	1	- 1		i		EMTPGKDEDQLPFSKAADVYAFGTVWYELQ
	ĺ			1		ARDWPLKNQAAEASIWQIGSGEGMKRVLTS
	!	1		1	1	AKDWYLKNYMAEMSI WYIOSOEGINIAK VDIS
			1			VSLGKEVSENLSACWAFDLQERPS\FSLLMD
		1	1			MLEKLPKLNRRLSHPGHF*KSADINSSKVVPR
			}		1	FERFGLGVLESSNPKM
165	1815	A	3679	8	803	IPSPAWWNSTWADTFSLLLALAVALYLGYY
465	1912	ΙΛ.	3013	١		WACVLOTHRAFCASNTEDLETVVNHIKHRYP
	l l	- 1	1	1	1	OAPLLAVGISFGGILVLNHLAQARQAAGLVA
				1	1	ALTISACWDSFETTRSLETPLNSLLFNQPLTA
						GLCQLVERLSY/E*DLQARTIRQFDERYTSVA
L	1			l		1

	cro m	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	hod	ID NO:	beginning	nucleotide	D-Accordic Acid F=Cilutamic Acid,
10: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience		1	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	l l		peptide		/=possible nucleotide deletion, \=possible
		i		sequence		nucleotide insertion
	<b></b> _	ļ	<b></b>	Sequence		FGYQDCVTYYKAASPRTKIDAIRIPVLYLSAA
		ļ	ŀ			DDDFGTVCAIPKOAAOHSPYVALLIJAKUUNI
		l		1		GFLEGLLPWQHWYMSRLLHQYAKAIFQDPE
		1		1	ì	GLPDLRALLPSEDRNS
		<del>                                     </del>	3684	3	307	SSQYIVQSKTKIFL*AAREKQ/RHTCRRFSIRLS
466	1816	A	3084	1		ANISSQTGEARGQWPSVFKVLKEKKLSTKKS
	1	1	ļ			FGQK*GR\RKTFPDKQK/LREFDTTRPTIQEML
		ľ		1		TOVI OG
			2.07	2465	837	ELPTPLIAAHQLYNYVADHASSYHMKPLRMA
467	1817	A	3687	2403	( 05 /	PROCEEDING AT VSAWHSSGSYLDSEGLKHQ
	İ				[	DDEDVSI I VCHCAAPFEEOGEAERHVLKLQF
		1				TRANSPER FOR TADMERICAL PREPER
	1	}	1			ADGCCAGCOCFASGI II APGPAPLEPPLAAEVU
		-	1	1		MARARI ACI VRI AGGHCRRDTLWKKLFLLE
	ì	-			}	DECEMBER OF STREET
		1		ļ		IDDOLDCELSMTVSWYOSLIKVLLSRFPQSCK
	l l	-			1	L REOSDIL CTOM VVI NOKETDCF VLVFLUSH
	}	1		4		I CALCALLA LA
		-	.1		1	IND ESYMMACETI WTRLL*GSGLDH*MSLFL
		1	}		Ì	LEGWAYOLACOROD*PALLGPRASQILSDIAG
	ĺ	ı	1			EVTMS*GSAAPAWOOEPPSPNTHSH*PIQUSK
	1	-	1	ļ	1	LECOPPOPI GPFWGTPFGPPGRVSGVHIGWQ
	Ì	ł	Ì		}	TDDD A PI PESCPI \PLTTVSHLCPLSLKVF1SHL
	Ì	1		ļ		DITACHSHRDDTWVPIPALPLKHLKPPSSPFA
	1	- 1	l l			LGPWVSHPLMRWVQKLSHLHSNPGTGFSMG
	l l		i	i		CKUOBN
			3691	960	499	QTCRKDKRAIYPHFQNE*MNEIKAI*SGTGGI
468	1818	A	3091	300	1 ',	OCCUSONDS A FFFFI. FLLETEFCS AAVI Y Q W D
		1			Į	DELSMOPPPPGFKOFTCLSLLSSWNIKKUFFF
	l	1			}	PGNE/*FLVKTGFPHVGQTGFELLT35DLAFEA
	ì		-	}	1	SQNGGITGMSPCAWPFFFFFFGLC
			3714	4747	495	MAYSWQTDPNPNESHEKQYEHQEFLFVNQP
469	1819	Α	3/14	1777	1	TISSSOVSI GFDOIVDEISGKIPHYESELDEN IFF
				i		VDTADE WINSTGHSLNEAHOISLNEF I SKOKEL
		- 1			•	SWHQVSKAPAIGFSPSVLPKPQNTNKECSWG
		1				SDIGKHHGADDSRFSILAPSFISLDKINLEKEL
	ı	- 1	1	1		ENENHNYHIGFESSIPPTNSSFSSDFMPKEENK
		- 1		1	1	RSGHVNIVEPSLMLLKGSLQPGMWESTWQK
		- 1	ĺ	l l		NIESIGCSIQLVEVPQSSNTSLASFCNKVKKIR
				l l	ì	EDVHAADVNFNSGKIWSTITAFPYQLFSKIK
	ļ	1	ł	i		ENTURED NISTOPI HEMPCANYLVKULIAEILA
ļ		1	1	İ		ECTATION I PENHII SVWGSEEFLONDHULUS
1			1		1	TIVE ACOUNT STOLE HIS OF SKEAP CRESKED AND A STOLE OF THE CONTRACT OF THE CONT
			1	1	1	DUGOCVI NOLI EFMHLWKYSKUCLLILIKA I
1		ŀ		1	1	PERI KALI KAUENAANIIEEAKKIOSAFOOAT
		-				TV OTTO A VAIGI SI II ORKGENEY USSELSANG
ł .	1		[			I TEXATTEL STSTYOLINVYCNSFY ADPUPVIN
1						DDCTEVI NDGI PSHI SFIVYAAHNUEL WYE
]			}	1	İ	INTEDICTIVES PRESMITVKLEGIACA I NNANLI
1		Ì		1	1	AWTO DI COVERGII GSMI FSMI LUSEPPVEN
1		Ì		1		TTPGVWDVSOPSPVTLOIDFPATGWEYMIKTL
		1	1	1		CEEND ON FEPI KECIKHIARLOUKU I PLLLOI
1						FUKDVI WEYRFYCNNENCSLPLVLGSAPGW
1						DEDTUGEMENTI RRWTFSOPLEALGLLISSER
	1					DORTORVAVOOLDNILINDELLEYLPQLVQA
			1	1		VERNALI ESPI VOLLI HRSLOSIOVARICE I WI
	1					
						I VALAGNG A VEK SWYOKI LAALUFUAUKALI
						I VALAGNG A VEK SWYOKI LAALUFUAUKALI
						LKNAENEAYFKSWYQKLLAALQFCAGKALI DEFSKEQKLIKILGDIGERVKSASDHQRQEVI
						I VALAGNG A VEK SWYOKI LAALUFUAUKALI

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Glycine, H-Illstidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
1		ļ.	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		<b>\</b>	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	(	1	1			Y=Tyrosine, X=Unknown, *=Stop codon,
1	i			residue of	sequence	/=possible nucleotide deletion, \=possible
Ì	1	1	\	peptide	1	
ļ		1		sequence		nucleotide insertion
	+	1				GDDLRQDMLVLQLIQVMDNIWLQEGLDMQ
)					ł	MIJYRCLSTGKDQRLVQMVPDAVTLAKIHRH
1		ì	1		ļ	SGLIGPLKENTIKKWFSQHNHLKADYEKALR
ì		1	1	i		NEFYSCAGWCVVTFILGVCDRHNDNIMLTKS
				Į		GHMFHIDEGKELGHAOTEGGIKRDRAPFIETS
		ļ	,	1	}	EMEYFITEGG\KNPQHFQDFV\ELCCRAYNIIR
	[	1	1	i	1	KHSQLLLINLLIEMMLYAGILPELSGNQDLKY
	1	ł	1		{	VYNNLRPQDTDLEATSHFTKKIKESLECFPVK
ì		1	1			VYNNLKPODIDLEATSHITKKIKESEBETI VI
1	1	1				LNNLIHTLAQMSAISPAKSTSQTFPQESCLLST
}		-				TRSIERATILGFSKKSSNLYLIQVTHSNNETSL
				1	1	TEKSFEQFSKLHSQLQKQFASLTLPEFPHWW
i					1	HI PETNSDHRRFRDLNHYMEQILNVSHEVIN
1		1		1		SDCVLSFFLSEAGOOTVEESSPVYLGEKFPDK
1		1				KPKVOLVISYEDVKLTILVKHMKNIHLPDGSA
1	1	· ·	-		1 .	PSAHVEFYLLPYPSEVRRRKTKSVPKCTDPTY
İ		1	1	1		NEIVVYDEVTELQGHVLMLIVKSKTVFVGAI
ł	· l	1	1			NIRLCSVPLDKEKWYPLGNSII*PLLLFSSFGM
j	1	1		1	ł	NIKECSVFEDKER WIT BOROW I BEEF SET
						KSLEKDEFVGGMLLSNPIW
470	1820	A	3718	430	75	SHGSISILNLHQGCVFLPSLPAQGLRCYRCLA
4/0	1620	1 ' '	3		į	VLEGASCSVVSCPFLDGVCVSQKVSV/CWQ*/
	ì		1		1	CPWGARAEGRLSAVVDSQISCCKGDLCNAV
1	ĺ			1		VLAAGSPWALCVQLLLSLGSVFLWALL
		_\	2502	891	494	L POST NISVPOAGVOWRDSSLOAPPPRFTPLS
471	1821	Α	3723	891	424	CLSLPSSWDYRRLPPCLANFLYF**RRGFTML
İ				1		ARMVLIS*PRDPPASASQ\STEITGGSHRAQHP
-	1	- (	1	1		TDSRDHSERSVKKSHEVISELRMKVIKCKVAF
}	1	1		1		
ł		1				SKNPI GFIET*NFCVSKDTSKKLS/RLPTKWKNVFAN
472	1822	A	3734	443	251	GFIET*NFCVSKDTSKRES/REI TRVIREYTYEL
17/2	10000		1	1	l	*ISDKGLVSRICQELLRHLDAEQVSSTAGLSL
453	1823	A	3746	3	500	THASGGARSGAGWAGRGVRAGTEAGRGGIF
473	1023	^	3740	-		LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ
	1		1			DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE
						PPPPVROEPSPKPNNKTPAILYTYSGLKNKKA
l		]				AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV
1		-		ļ		KFAENRAK
1		1_			<del></del>	RPLFAREGGIYAVLVCMQEYKTSVLVQQAG
474	1824	A	3753	2	5262	LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ
1		ļ		1	1	LAALKINLA VASSELI II VI UKUSHIOLI DAQ
}	1				1	MTREIFASIDSATRPGSESLLLTVPAAVILMLN
		- 1		{	1	TEGCSSAARNGLLLLNLLLCNHHTLGDQUTQ
	j	)		}	1	ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR
ſ	Į.		<b>\</b>	ļ	i	VSEPPGSP\ERAALETPIIOGODGSPELLIRSLV
1	Ì	ì		1	1	GGPSAFLLLDLERVLCREGSPGGAVRPLLKRL
<b>,</b>		i	1	ļ	}	OOFTOPFLLLLRTLDAPGPNKTLLLSVLRVII
i	Í	ì	- 1			RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE
	ľ	- 1	1			IVQELTCFLHRLASMHKDYAVVLCCLGAKEI
}	j		ì			LSKVLDKHSAQLLLGCELRDLVTECEKYAQL
		1	<b>\</b>			LOK VLDKHOAQLLLUCELKDLY I DCDK I AQL
						YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP
1			1	1		FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN
			1		}	PHRASKLTDHNPKTYWESNGSTGSHYITLHM
		-				HRGVLVRQLTLLVASEDSSYMPARVVVFGG
- {	1	1				DSTSCIGTEL NTVNVMPSASRVILLENLNRFW
		}			1	PHOIRIKRCOOGGIDTRVRGVEVLGPKPTFWP
1	1				)	LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL
		1		1		LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL
		1			ţ	LULUTELLI VON TENDA ECVE AL CWLI
		1				GKTCWEALVSPLVQNITSPDAEGVSALGWLL
				1		DQYLEQRETSRNPLSRAASFASRVRRLCHLL
	1	1				VHVEPPPGPSPEPSTRPFSKNSKGRDRSPAPSP
					1	VLPSSSLRNITQCWLSVVQEQVSRFLAAAWR
				1	}	APDFVPRYCKLYEHLQRAGSELFGPRAAFML
J	i i	1	1	l		

	- C - C - C - C - C - C - C - C - C - C	- A	CCO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	<b>\</b>	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	İ	\	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
]	ł	ł	1 1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	ł	. !	residue of	sequence	/=possible nucleotide deletion, \=possible
	-			peptide		
ĺ				sequence		nucleotide insertion
	<del> </del>	<del>                                     </del>			]	ALRSGFSGALLQQSFLTAAHMSEQFARYIDQ
		1	1		j .	QIQGGLIGGAPGVEMLGQLQRHLEPIMVLSG
		1	1			LELATTFEHFYQHYMADRLLSFGSSWLEGAV
1			ì			LEQIGLCFPNRLPQLMLQSLSTSEELQRQFHLF
						QLQRLDKLFLEQEDEEEKRL*EEEEEEEEA
1	ì		1		1	EKELFIEDPSPAISILVLSPRCWPVSPLCYLYHP
		1	1			RKCLPTEFCDALDRFSSFYSQSQNHPVLDMG
}	1	}	ļ	Ì	1	PHRRLOWTWLGRAELOFGKQILHVSTVQMW
	1		1	}		LLLKFNQTEEVSVETLLKDSDLSPELLLQALV
ĺ						PLTSGNGPLTLHEGQDFPHGGVLRLHEPGPQ
		1		1		RSGEALWLIPPQAYLNVEKDEGRTLEQKRNL
			l l	1	1	LSCLLVRILKAHGEKGLHIDQLVCLVLEAWQ
			1			KGPNPPGTLGHTVAGGVACTSTDVLSCILHLL
		1	1		1	GQGYVKRRDDRPQILMYAAPEPMGPCRGQA
1						DVPFCGSQSETSKPSPEAVATLASLQLPAGRT
1					1	DALLOS OF THE OTHER OF THE THE THE THE THE THE THE THE THE THE
1				1		MSPQEVEGLMKQTVRQVQETLNLEPDVAQH
1		1	ŀ	Ì		LLAHSHWGAEQLLQSYSEDPEPLLLAAGLCV
ŀ		Į.	j		1	HQAQAVPVRPDHCPVCVSPLGCDDDLPSLCC
1	1		-			MHYCCKSCWNEYLTTRIEQNLVLNCTCPIAD
1	į		1		1	CPAQPTGAFIRAIVSSPEVISKYEKALLRGYVE
1		l	1			SCSNLTWCTNPQGCDRILCRQGLGCGTTCSK
	ł	ì	}	1	j	CGWASCFNCSFPEAHYPASCGHMSQWVDDG
ł	i		1			GYYDGMSVEAQSKHLAKLISKRCPSCQAPIE
	İ		1			KNEGCLHMTCAKCNHGFCWRCLKSWKPNH
1	ì		1			KDYYNCSAMVSKAAROEKRFQDYNERCTFH
			1			HOAREFAVNLRNRVSAIHEVPPPRSFTFLNDA
1						COGLEOARKVLAYACVYSFYSQDAEYMDVV
]				1		EQQTENLELHTNALQILLEETLLRCRDLASSL
-		1		Ì		RLLRADCLSTGMELLRRIQERLLAILQHSAQD
1		}				FRVGLQSPSVEAWEAKGPNMPGSQPQASSGP
İ	į.		1	Ì		EAEEEEDDEDDVPEWQQDEFDEELDNDSFS
1		1	· [			YDESENLDQETFFFGDEEEDEDEAYD
1						GTSRNQHSPKTHA*RSS/WPQPPPLFLPPLQPQ
475	1825	A	3754	1093	96	ATGRRRRTRTQQRTAALLTDGTTKTGAAW
1	ł		}	,		SRRPSLCWPSRTTGAPGAK*AVLVRSATPTTN
						SKRPSLCWPSKI I GAFGAR A CVERSCOFPPP
1					1	PPNPQSPTGAAGKLRAPGNRAG/SEPSSQEPPP
İ	1	l	1		1	DGTR\RPASITGVAQSPATRATPSLPCLHVPAP
					1	SRGQTLGVRTTGRASRLTVDRSRLSWPGRSA
	1			1	1	RSGGGRWRPNAPRGRWPRAP*SWEPGSWTE
					1	PWRWPFPAAESPPHRCIYCTNHVSPAGPARPS
1	]					HVYIIRATINSISHPLCRAQSSPWEAAGVWRR
	1			1		PAQPAPTSDVNINLLRKPRVKRHDLIYQFLGN
						TLWEEGRORPPETLOPAR
426	1826	$-\frac{1}{A}$	3758	901	521	FFFGNGVSPCPQAGV*WHDLDSLQNLPPGFK
476	1826	A	3130	701		RESYLSLPSSW\DYRHVPPRQANFCIF/M*RRG
		1		1		FTMLARMVSIS*PRDLPALASQSAGITGVSHH
				1		APPOMDFTFALLCFAPKGCLPRQKEGGTLNLI
				1042	575	GVISAHCNLRL/CHLPGSSNSPASASQVAGTIG
477	1827	Α	3761	843	575	ARTTPS*IFVFLVETGFHHVSQDGLDLL/NFVI
		1		1		RPRRPLKVLGLQACTRARLPSPLKEL
						HLLSFHLWSASLDCLEQLSQERHVKGMLLGP
478	1828	A	3763	267	1240	HLLSFHLWSASLUCLEQLSQEAR ANGINEDOF
1		ļ. <sup>-</sup>				PPVNESTKPSPSPWKLTPPMCSIPPVFPPKSGS
	1					PTTSWS/PSGHSKLEVERAQTGPFCLHIYCP*P
1				ł	i	GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY
	1					WTGHSFASQAWLRQVPEVSKHLQCPSAESLL
				1		TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG
	1					PDEHPODTDARDADGEAREREP/RRPSFAA*P
ļ			}		1	VWGOP\ESPLPEASSAPPGPTLGTLPEVETIRA
	[	1				CSMPOELP*SPRTROPEPDFYCVKWIPWKGE
1				}		OTPIITOSTNGPLPSPCHHEHPLSSVEGEAPPA
1	1	1	i i	ŀ	_	V.1.11.40.11.01.21.11.01.11.11.11.11.11.11.11.11.11.11.11

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uenœ		İ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	ļ	1	peptide	Soquence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<u> </u>	<del> </del>	<b>├</b> ──	sequence		EGSDHIG
	1000	<b></b>	3766	2	2152	YSPIRLLEVCVPLPKIFIKRQAPLKVSLLQDLK
479	1829	Α	3700			DFFQKVSQVYVAIDERLASLKTDTFSKTREEK
	]		1			MEDIFAOKEMEEGEFKNWIEKMQARLMSSS
	ļ		1			VDTPQQLQSVFESLIAKKQSLCEVLQAWNNR
	1			1	1	LQDLFQQEKGRKRPSVPPSPGRLRQGEESKIS
			-		t	AMDASPRNISPGLQNGEKEDRFLTTLSSQSST
				1		SSTHLQLPTPPEVMSEQSVGGPPELDTASSSE
	1	l	(	1		DVFDGHLLGSTDSQVKEKSTMKAIFANLLPG
						NSYNPIPFPFDPDKHYLMYEHERVPIAVCEKE
	1	1				PSSILAFALSCKEYRNALEELSKATQWNSAEE
				ļ		GLPTNSTSDSRPKSSSPIRLPEMSGGQTNRTTE
	}		ł			TEPOPTKKASGMLSFFRGTAGKSPDLSSQKRE
	į.	ļ		ŀ		TLRGADSAYYQVGQTGKEGTENQGVEPQDE
Ì	1	1	1	ŀ		VDGGDTQKKQLINPHVELQFSDANAKFYCRL YYAGEFHKMREVILDSSEEDFIRSLSHSSPWQ
1	1	1	1		Ĭ	ARGGKSGAAFYATEDDRFILKQMPRLEVQSF
[				}		LDFAPHYFNYITNAVQQKRPTALAKILGVYRI
	ļ					GYKNSQNNTEKKLDLLVMENLFYGRKMAQ
	1					VFDLKGSLRNRNVKTDTGKESCDVVLLDENL
		}				LKMVRDNPLYIRSHSKAVLRTSIHSDSHFLSS
}			ŀ			HLIIDYSLLVGRDDTSNELVVGIIDYIRTFTWD
	1					KKLEMVVKSTGILGGQG*MPTVVSPELYRTR
1						FCEAMDNYFLMVPDHCTGLGLNC
				251	3	OGCGSAGTLIHY**ECKMVQLLWKTV*QFLI
480	1830	A	3777	251	3	KLNI/KDPAITLDVYPNEVKNYVRTKTYTQMF
		İ	1	ļ		I/ANFIMAKSWKOPTHPSVRT
	1001	<del></del>	3779	333	3	FAAIROPEPNILDVNOIFKDLAMIIHDQGDLID
481	1831	A	3119	1 333	1	STEANAESSEVLVERAPGOLORPANYYQKKSK
l			Ì			KKMCLVVLVQTAIILICERIM*VVYTTKWSPPI
ŀ		1		1		VLPVSCFQGQKFN
482	1832	A	3780	2	371	TGGRQGKNDHTSITEKPSRDFNRHLITQNI*M
482	1032	1	3,00	-	1	PNQDMKSSSNSLIIRKVQIKPTILYHHIFTRKA
İ		1				KMKTTDKTKYR*GFKAITTLIHCSQDCKLQ*S
						/L*ENHFMIFPKAEQHITYDTTIPFLR
483	1833	A	3787	43	448	LMKDLSPYVMETHYILNRLNER/RSMWRHIIG KLPNTKDQEKILKAIRGRREVIQGS/RQQYRR
100						PAAFSAAEKARRLWCS/VFNIERRNL/CEYPTK
1		l		i		LSFNIKGEMTFSDKTEFTTNRPSLKMLLKDRI
1	İ	-		İ		QEEGKMF*KEKCFKRKE
1		1				FFFFETESRSVAQAGVQWCNLGSLQALPPGF
484	1834	A	3798	1	727	SHSPASASRVAGTTGTRH*ARLIFYIFSRDGVS
			]	1		PC*PGWS*SPDLVIRPP\RLPKCWDYRREPPRP
1			-	1		A*FFVFLVE\QGFTMLARMVSIS*PQ/CDLPAS
			[	1		VSQNAGITGVSHCAWPCLHFCFFGFFFEMESC
-		ļ				SVAQAEVQWHDLRSLQAPPPGFTPFSCLSLPG
1		- 1	l l	i	1	SWDYRRPPPRPANF\CIFSRDGVSPC*PGWSRS
						PDLVIRPPRPPKVLGLQA
		_ _		<del></del>	239	FFFFEMECLTVSOAGVQWYNLHSLQPLPPGF
485	1835	A	3802	1	239	KOFSC\LSLPSSWD*RVPTSRPAKF/CVIF*DGV
-		}		1	1	SHCOPGWSAVVQPPLH
L				270	98	RYD*SSOSENIP\OKEFLLKYP*CTATLGMRN
486	1836	A	3811	378	96	MSIMKKKSIFSAEFYKVSLPSLLL\HLLAIEWG
					1	FHIEIOLTIHOHFLNYELESDFVHIVEYM
L					320	FDPDWTRAAGIRHEKKPKALAYRRENSPGDL
487	1837	A	3814	771	320	PPPPLPPPEEEASWAL/GAEGSRQHVLPGAGA
						OWGEESGPGRAPGSPAGAPPR*RGLAP\NSRP
		-		- }		SFLSRGOGTSTCSTAGSNSSRGSSSSRGSRGPG
1	1	1	1	i	1	1
Į.				\ \	I	RSRSRSQSRSQSQRPGQKRREEPR

PCT/US01/03800 WO 01/57188

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I-Isoleucine K=I vsine L=Leucine,
eotide	seq-	}	USSN	location	to last amino	M=Methionine N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	C-Glutamine R-Arginine, S-Serine,
uence		}	914	ng to first amino acid	of peptide	T-Threonine V=Valine W=!ryptopnan,
				residue of	sequence	V-Tyrosine X=I inknown, *=Stop codon,
		1		peptide	Soquesia	/=possible nucleotide deletion, \=possible
ì		1		sequence		lectide insertion
	1020	A	3818	3cquones	781	FRACLLELIPYAPTLSWTACPPAMAGPRGLLP
488	1838	A	3616	1	1	LCLLAFCLAGFSFVRGQVLFKGCDVKTTFVT LCLLAFCLAGFSFVRGQVLFKGCDVKTTFVT
			ļ		1	HVPCTSCAAIKKQTCPSGWLRELPDQITQDCR YEVQLGGSMVSMSGCRRKCRKQVVQKACCP
						GYWGSRCHECPGGAETPCNGHGTCLDGMDR
l	1	1		ļ		NGTCVCQENFRGSACQECQDPNRFGPDCQSV
}		1		İ	Í	1 COCUMOVCNHGPRGDGSCLCFAGTTGFACD
}			ļ	1		QELPVWQELGFPQNNPRLRKAPNCKCLPG*H
			ŀ			I DNICT LATENPORP
				934	669	T PERSONNES PSYTRIFCS GAISAHLRLLUSS NSP
489	1839	Α	3822	934	1005	ASAS*VAGTIGACHHAQLIFVFLVEIGFHTIVG
						LODGI DI LAN MIHPPRPPK VLGPUA
105	1070	+	3825	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW  BECEVI PRE APELAPVI.SGA
490	1840	I A	3023	1	1	GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA ASRPEASGDCRAGRETAMATLEKLMKAFESL
		1				ASRPEASODCRAURE TAINT BOTTOM TO THE REPORT OF THE REPORT O
ł		1			1	DODDDDDOI POPPPOA()PLLPUPUPTFFFFFFF
						CDAVACEDI LIRPKKELSALKKURYNICULIC
		-			1	- LEMINA OCUDNOPEROKLI GIAMELELLUSUUA
		}		}		L DODADAMADECI NK VIK ALMUSNUFALQUUL I
٠.		İ	Í	ł		A VERICANICADEST RAAL WEETABLE AND VALVE I
		į .		ì		CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP
				l		KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG
1	i				]	LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV
			Ì		}	L VOTEL VICEROUTRKEMEVSPSAEOUVQ 1 122 L
		i				THE THEOLOGICAL PLANT OF THE PROPERTY OF THE P
		- 1				1 OT TAVGGIGOLTAAKEESUUKSKSUSI VEEL
			-	ļ	1	ACCCGGCGPVI SRK()KGKVLLGEEEALLDDG
İ		1				TEDSTIVESSALTASVKDEISGELAASSGVS1FG
-		ļ	Į			SAGHDIITEQPRSQHTLQADSVDLASCDLTSS SAGHDIITEQPRSQHTLQADSVDLASCDLTSS
		-		Ì	1	ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG
			į.		ļ	TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA
						FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF
ļ		Ì		1		1 AU DUE ATERCHOENK PCKIKUDIGQSIDDDS
ļ		- 1		•		ADI VIICVETT SASFILI GGKNYLYFDAD YAY I
ŀ		-	1			CVV AT AT SCVGAAVALHPESEESKLIK VELD
				1		TTEVPEEOVUSDII NYIDHGDPOVKGATALLC
		1	1	l		CTI ICSII SPSRFHVGDWMGTIKILIGNIFSL
		1	1			ADCIPLLRKTLKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTLRNSSYWLVRTEL
		1		1		LETLAEIDFRLVSFLEAKAENLHRGAHHYTGL
1		1		1		TVI OEDVI NNVVIH LGDEDPRVRHVAAASL
Ì	}	1		1		THE ARK EVECTOGOADPVVAVARDUSS VID I
		1		1		VII MUETOPPSHFSVSTITRIYKGYNLLF3IID
						ATTACKNI CRVIA AVSHELITS I I KALIFUCE
		1		1	ļ	ALCIL STAFPVCIWSLGWHCGVPPLSASDESK
						VCCTVCMATMILTI LSSAWFPLDLSAHQDAL
		1	1	{		TI A CART I A A S A PK ST R S S W A S E E E A N PA A I A
		1				QEEVWPALGDRALVPMVEQLFSHLLKVINIC
						AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS
						GKEKEPGEQASVPLSPKKUSEASAASKUSTI GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA
1		(		1		I STANKET DI ONSTEKEGGELRSALDYLSQILEL
		ļ				TI ODICKOVEEILGYLKSCESKERMMAI VC
		[			İ	UCOLI VTI EGTNI ASOFDGLSSNYSKSYUKA
		ļ				ODI CCCCI/DDGI VHVCFMAPY I HI I UALADA
						LOT DATACIOA EO ENDTSGWEDVLUK V 31 QUAL
			1	1		NLTSVTKNRADKNAIHNHIRLFEPLVIKALKQ
			l			

				D-4:	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
IO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	1	in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location		M=Methionine, N=Asparagine, P=Proline,
eq-	uence	ļ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ		1	peptide		nucleotide insertion
				sequence		YTTTCVQLQKQVLDLLAQLVQLRVNYCLL
						DSDQVFIGFVLKQFEYIEVGQFRESEAIIPNIFF
	l			Į	1	FLVLLSYERYHSKQUGIPKUQLCDGIMASGR
	1				l .	FLVLLSYERYHSKQUGIFKIQECDGMMIGGK
		İ				KAVTHAIPALQPIVHDLFVLRGTNKADAGKE
	]	1				LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ
				1	1	CHKENEDKWKRLSRQIADIILPMLAKQQMHI
	1			1	*	DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF
	1			4		VTPNTMASVSTVQLWISGILAILRVLISQSTED
						IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE
				1		EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT
	1		1	Ì		KQLKVEMSEQQHTFYCQELGTLLMCLIHIFKS
	1		1	1		GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR
		]	1	1		ARSMITTHPALVLLWCQILLLVNHTDYRWW
		1	l	1		AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA
		1				AKLGMCNREIVRRGALILFCDYVCQNLHDSE
	-			1	{	HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS
		1			1	AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI
		1	1			HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL
	1	1	1			ACRRVEMLLAANLQSSMAQLPMEELNRIQEY
		ì	1	ļ		LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS
						PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK
		i		j		SQCWTRSDSALLEGAELVNRIPAEDMNAFM
				1		MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA
	1	-	ļ			AREVTLARVSGTVQQLPAVHHVFQPELPAEP
	İ			1		AAYWSKLNDLFGDAALYQSLPTLARALAQY
		1			1	LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL
	· '					SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL
		}		1	{	WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG
		İ	· I		1	EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI
		ļ	ļ			TAACEMVAEMVESLQSVLALGHKRNSGVPA
			ļ		ļ	FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG
						WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYR
		1		ļ		INTLGWTSRTQFEETWATLLGVLVTQPLVME
				Ì		QEESPPEEDTERTQINVLAVQAITSLVLSAMT
		1				VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK
			Ì			LSIRGIVEQEIQAMVSKRENIATHHLYQAWD
						PVPSLSPATTGALISHEKLLLQINPERELGSMS
	1	1		1		YKLGQVSIHSVWLGNSITPLREEEWDEEEEEE
!		1				ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
	l	<b>\</b>	1			LELYSRWILPSSSARRTPAILISEVVRSLLVVS
					Ì	DLFTERNQFELMYVTLTELRRVHPSEDEILAQ
		1				YLVPATCKAAAVLGMDKAVAEPVSRLLESTL
ļ				1		RSSHLPSRVGALHGVLYVLECDLLDDTAKQL
1	1	ł	1	{	!	IPVISDYLLSNLKGIAHCVNIHSQQHVLVMCA
1		[	1		1	TAFYLIENYPLDVGPEFSASIIQMCGVMLSGS
ŀ		1		Ì		EESTPSIIYHCALRGLERLLLSEQLSRLDAESL
1		1	1	1	1	VKLSVDRVNVHSPHRAMAALGLMLTCMYT
1		1		1		GKEKVSPGRTSDPNPAAPDSESVIVAMERVS
	.	1	i	1	1	VLFDRIRKGFPCEARVVARILPQFLDDFFPPQ
1				1		DIMNKVIGEFLSNOOPYPOFMATVVYKVFQT
1		-				THSTGOSSMVRDWVMLSLSNFTQRAPVAMA
				1		TWSLSCFFVSASTSPWVAAILPHVISRMGKLE
		)	}	}		OVDVNLFCLVATDFYRHQIEEELDRRAFQSV
		{	}	1		I EVVAAPGSPYHRLLTCLRNVHKVTTC
<u> </u>					302	SNPPASASRVAGITGVHQHAWLIFVFLVEMER
491	1841	Α	3826	469	302	LITHUGOAVI KLLISGDLPVSASOSA
471	1	_1				VAPSPMIMPDLYFYRDPEEIEKEE*AAAEK\EE
491	_1		1 2026	392	88	1/11 01 1/11/11 2011
491	1842	A	3836	1 3/2	1	FOSEWTAVV/P/EFTATOSEVADWFKDMQVP
	1842	Α	3830	372		FQSEWTAVV/PÆFTATQSEVADWFKDMQVP SVPIOOFPTEDWST*PTMNDWSATSTAQTTE
	1842	A	3836	372		FQSEWTAVV/P/EFTATQSEVADWFKDMQVP SVPIQQFPTEDWST*PTMNDWSATSTAQTTE WVRITTEWP

_				5 3:44	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Acpartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine K=I.vsine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i			amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	[		residue of	sequence	/=possible nucleotide deletion, \=possible
		l		peptide		nucleotide insertion
		1		sequence	100	TPSDMNRAFETDTQSIGEKNRSPSEPDYFERK
493	1843	A	3838	19	380	KFKRS*EKAHIRYKIDQPEDIPLK\EFLCKHSK
.,,	1	Į	1			CTATLSMRNMSLMKKKCSFSEEF\LAFFPSLL
	1	1	1			VCHLLAIKLGFYIEIHLTTFNNTF
		}	İ			FFFLRRSL/DSVAQAEAQWLVELGLLQAPPPGF
494	1844	A	3845	2	352	KPISLP\GLPSSWDYGRPPPCPANFCIF/M*RRG
7/7	10	1			İ	KPISLP/GLPSSWDTGRFFFCFATTCH/MTGC
	1	ļ	1			FTVLARMVLIS*PCDPPTLASQGTAITGMSYH
	1			Ì	Ì	ARPQDIDFLYAHQGRCWFRLL
100	1845	A	3847	1774	40	DIFFRRAKEGMGQDEAQFSVEMPLTGKAYL
495	1843	1 ^	30.7			WADKYRPRKPRFFNRVHTGFEWNKYNQTHY
	1	1	l		}	DFDNPPPKIVQGYKFNIFYPDLIDKRSTPEYFL
	}	1				EACADNKDFAILRFHAGPPYEDIAFKIVNREW
	1		1			EYSHRHGFRCQFANGIFQLWFHFKRYRYRR*
		1	Ì	1		RPWGTAGRCPRGHSKGASVKLVVTPGPLSGL
		}	1	1		CONCETCHI RPHI SFARPOFPPI*KGGHH*AC
		1			Į.	UCET PRHWDRI A*GPDATEGALGASTEREG
		1	ł			GOOPPADLTVOADTLHRPSARLGGAHRACPK
			1			PRPHRVI WRWARGAWAWRCQAREKQEIQG
	1	1	1	l	}	OPCHITCHPL GREAEPAAAGAAPALAHKPPF
			1	ļ	1	APTGSTE/PGPCWRPIRHCRRDPLWIPILCKD
	į	1	1			WPPTHPVLAGGVHFPAAG/IGGCVEVPVSVN
ļ		1	-			VMCTKSH*AVLPPPPSTGPGGQGLPEGWGLE
		{	{			VCEGI PPGIPPPGLLTGPW\SMRPVTPSFAHIK
ì		Ì	1			TVAPSHSPESGOEGRGPHGCHSPGR\SGP\AGK
ļ	ı	1	1			I VI OHPTGTSPTEAKRKVPPGPPEGHP1SPV1
	1	1	1			SPRPPTAPPRHPASSGNSSVCFSKKTCRWEKK
	1	1	Ì		1	SFVLMELAYWQDRMFF
	1	- }				AKSPLPLG*IQWR/NLGSLKLRLPGFK*FTCLG
496	1846	A	3849	830	442	LLSSWDYRSLPPRPVNFCILVELGFHHVDQAG
""		1	}		1	LKLLTSSALPALASQSAEITGMSHRIWPLPLLR
ļ		1				RPPVIRIRAPPQRLPFNLITSLKALSPNMATF
	)	- 1				ALRKTRADGIARTGAQPAASWKGTNNYPWR
497	1847	A	3859	2	393	LEMAGRPGSQEQSKDRGTGSLPPPSQRPLGPS
1 77	1	1	ı	Ì		PEGAGPSPPPPGIPRGGGSSSSEGP/PQLLFVPR
	1	1		}		RFPAPKKGLPSDTPHSKAPPTPHLILGGEDSQ
1	1	[	l l		i	
		1		1		VPIL VPIL ALVACAG
400	1848	+	3860	253	634	KNASTVYSSQGDPKSFFFLLRWSLALVAQAG
498	1040	^	3003			EQ*RDLSSLQPPPPGFK*FSCLSLPSSWD\YRCP
l		1		1		I DOT ANEX FI VETGEHHVGOADLALL ISOUR
1		}		1	İ	PTSASESAGITGVSHRAWPRIHFLYWKTFFL
		<del></del>	3863	423	263	APSOISVAFLYAA/DKLFEKEI*KKIPFIIAS/DKI
499	1849	Α	3803	723		VICINI TKEVKYLYTENYII LMKEIKIDIDKW
		l			1	VDII V*WIGKINI*KMSTPPKAIYRFNAIPIKIP
]		1	1	-	1	MTEETEIEKSIIKFIWNHKKPPNTOSNIEQKE*S
1		-	1			FCSILLWVFGGFLWFHMNFMIDFSISVKNVIGI
1	-	-				LUCIALNI
		Ì			15246	LPRGCLWCLQRSPTPARPQPSRPARSPLPLFP
500	1850	A	3865	2	15246	DLRPWASDLDIMGDAEGEDEVQFLRTDDEV
	1	1				VLQCSATVLKEQLKLCLAAEGFGNRLCFLEP
	1	1	1	1		TSNAQNVPPDLAICCFVLEQSLSVRALQEML
1				}		ANTVEAGVESSQGGHRTLLYGHAILLRHAH
		1		1		SRMYLSCLTTSRSMTDKLAFDVGLQEDATGE
	1			1	}	SKWATPCT112K2M17MT4LALDAGEDY105
			J	1		
						ACWWTMHPASKQRSEGEKVRVGDDIILVSVS
						CEDVI HI STASGELOVDASFMOTLWNMNPIC
						SERYLHLSTASGELQVDASFMQTLWNMNPIC
						SERYLHLSTASGELQVDASFMQTLWNMNPIC SRCEEGFVTGGHVLRLFHGHMDECLTISPADS DDORRI VYYEGGAVCTHARSLWRLEPLRIS
						SERYLHLSTASGELQVDASFMQTLWNMNPIC SRCEEGFVTGGHVLRLFHGHMDECLTISPADS DDQRRLVYYEGGAVCTHARSLWRLEPLRIS WSGSHLRWGOPLRVRHVTTGQYLALTEDQG
						SERYLHLSTASGELQVDASFMQTLWNMNPIC SRCEEGFVTGGHVLRLFHGHMDECLTISPADS DDQRRLVYYEGGAVCTHARSLWRLEPLRIS WSGSHLRWGQPLRVRHVTTGQYLALTEDQG
						SERYLHLSTASGELQVDASFMQTLWNMNPIC SRCEEGFVTGGHVLRLFHGHMDECLTISPADS DDORRI VYYEGGAVCTHARSLWRLEPLRIS

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moteotide of peptide contide to contract the contract of peptide sequence of peptide s		, -		- 1		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
cortsponding to distant or cortsponding to state amino acid residue of peptide sequence    914	-	P.				location	F=Phenylalanine, G=Glycine, H=Histidine,
### 1949		1				corresponding	I=Isoleucine, K=Lysine, L=Leucine,
uence    14   mainto acid residue of peptide residue of peptide peptide sequence   mainto acid residue of peptide sequence   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue   mainto acid residue			·				M=Methionine, N=Asparagine, P=Proline,
mento acid residue of peptide sequence		uence			•	-	O=Glutamine, R=Arginine, S=Serine,
residue of peptide sequence  y=Tyrosine, X=Unknown, *=Stop codon, }-possible nucleotide detaion, \textitation   Possible nucleotide insertion    APPEKAIR.GVIA.KKAMLHQEGHMDDALSL. TRCQQEESQAARMINISTINGLYNOFIKSLDSTS   GKPGSGOPAGTALPIEGVILS.GQLII.YTEPPS   EDLQHEEQGSLLSILRINGSLGEEGMLSMV   LNCDRLINVYITAAHFAFAGEEAASWKE!	uence	Ì		914			T=Threonine, V=Valine, W=Tryptophan,
pepide nucloidé insertion APDRALRI.GVI.KKKAMLHQEGHMDDALSI. TRCQGESQAARMIRTSNIQ.TNOFKSLDSFS GKRGSGPPAGTALPIEGVI.SLQD.II/FEPPS EDU, HEERCQSKLASI.RNOSL, FORGEM. SMV LNCIDRLN-VYTTA-HFA BEFAGEEAAESWKEI. VNLLYELLASI.RORSNECALFSTNILDW.U'S KLDRLEASSGILEVI.YCVI.ESPEVLNIQENHI KSISILLDEHGRINEVLDVI.CSLCVCKGWAV RSNODLITENLLPGRELLLQTNILNYVTSIRPN IF UGRACETTOYSK WYFSWMDEWTPFILTQ ATHLR NOWALTEGYTPYPGAGEGWGGNGV GDDLYSYGEGGHU.WTGHWARWYTSPGOHL LAPEDVISCCLDI.SVPSISFRINGCPYQGYFESF NLDGLFFFVVSFSAGVKVRFLLGGREFKF LPPPGYAPCHEAVLPRELHILEPKEYRREOP RGPHLWOFSRCLSHTDYPCPPDTVOYLOPH LERIREKLAENHELWALTREIGOWTYGPVRD DNKLHFCLYDFISLEPERNYSLAGWASSEL KTILLALGCHVGMADEKAEDNILKITKLPKITY MMSNOYKYAPLDLSHVRLTPAGTILLOPKA NGHNWARDRVGGWSYSAVQDIPARRHPR LVPYRLIDEATKRSNBSLCQAVRITLAGFY NIEPPOGPSOVENOSKCDRVBIRAEKSYTV OSGRWYFEEAVTTGBRRWGWARPELRPDV ELGADELAYYPNGIRGGRWIGGREFGRW OFGDVVGCMIDLISTRIITITINGEVLAWISDSG ETAFREIEIGDGFFPANWGRWFUNSDSG ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFPANWGRWFUNSDS ETAFREIEIGDGFFFANWGRWFUNSD	i			1			Y=Tyrosine, X=Unknown, *=Stop codon,
nucloside insertion  Sequence  APPEKALRIGVILKKAMLHQEGHMDDALSI. TRCQGESQAARMISTNGLYNOFIKSLDSYS GKPGGSGPAGTALPIEGVILSLQOLITYEPPS EDLQHEEKQSKLRSIRNOSLOGEGMI.SMV LNCDRIANVTTAAHFAFAGEGAASSWKEI VNLLYELLASIRGNRSNCALFSTNLDWLVS KLDELFASSGLEVILYCULESPEVLNIGENH KSIISLDEHGRNHKVLDVLCSLCVCNGVAV RSNODLITENLLFRGEHLLIGTNLNYVTSIRN IFVGRAEGTTOYSKWYFEVMOEVTPFLTAQ ATHERVOWALTEGVTYPPOAGEGWGNOV GDDLYSYGPOGHH.WTGHVARPVTSPGOHL LAPEDVISCLDLSSYSIFRINGGVOGGNOV GDDLYSYGPOGHH.WTGHVARPVTSPGOHL LAPEDVISCLDLSSYSIFRINGGVOGYGFS NLDGLFFFVVSSAGVKVRELLGGBHGEFKF LPPPQY APCIEAVLPRELHLEFEKEYREGOP ROPHLVGPSRCLSHTDFYPCPVDTVQIVLPPH LERREKLAENHELWALTRIEGGWTYGFVRE DNKKLHPCLVDFHSLEFEERNYLLQMSGETL XTLALGCHVMADBEKAEDNLKKTLLFYTY MMSNOYKPAPLDLSHVELTPAQTTLVDRLAE NGHNVWADBEVGGGWSYSAVQDIPAGRAPPH LVPYRILDEATKRSNRDSLCQAVRTLLGYGY VIEPPPQGESYSVENGEWSFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWSFACHWIFTAGT VIEPPQTAGENEY STAREFT GROWNERS STAREFEIGHTEFIERSFORPW QGGDVVGCMDLTENTIITTLNGEVLMSDSGS ETAFREIERIGGGFPVESCREWFWSRDGTVDTFPCLR LITHRTWGSONSLVEMTLABGRAFTAFT CTAGATFAPPGLQFPFVSRDGTVDTFPCLR LITHRTWGSONSLVEMTLABLSPVQFHOHFR CTAGATFALPPGLQFPFVBLEHPFVSRVDGTVDTFPCLR LITHRTWGSONSLVEMTLABLSPVQFHOHFR CTAGATFALPPGLQFPFADEARAAEPDPDVE NLRRSAGGWSEAENGKEGTAKEGAREGARE AKKVAMMTOPFATFTLFRLHFDVVPADNDD PEILINTTTTYYSVSVAFAGGESCVWAGWVT PDYHOHDMSFDLSKVRVVTTVMODEQGVV NSILKFFALGGLQGGGFFSHODMALMPSWSR MPHHELOVETRAGEGRIGWAVQCOGSHTDL VIGCLVDLATGIMFTANGKESNTFFQVEN NLLRRSAGGWSEAENGGFTSROWAGNETHAL SAVACALGNRNVAHALCSHVDQAQLHALE DAHLPGFRAGYYDLLISHILSSACRSRSMI. SEYLVPLTFPTATLTPPGRFTEMOFFRHIGLF GGGVTTSLRPPHHFSPCTVAALPAGAABAP ARLSPAHDATSTARTARTSFFPCTVAALPAGAABAP ARLSPAHDATSTARTARTARTSFFPCTPNALICFGGEEEDE EKEEDEETTAGREGEEEDEEETEGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEEEDEE EKEEDEETTAGREGEE		ľ				sequence	/=possible purleotide deletion. \=possible
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TRCOQUESO, AARMIHSTNGLYOFISLLOSP'S  CKPRGSOPPAGTALPIEGVILSLO, LIVTEPPS'  EDLOHEEKQSKLRSLRNROSLF, GEGMLSW'L  NULDELASSIGLEVLYOVLLESPEVLNIQENH'L  KSILDLEASSIGLEVLYOVLLESPEVLNIQENH'L  KSISLLDKHGRNHKVLDVLCSLCVCNGWA'V  SNODLITENLLFORELLLOTNLINVYTSIR'N  IF VGRAEGTTQYSK WYFEWM/DEVTPFILAG  ATHLRYOWALTEGYTPYPGAGEGWGRWO'V  GDDLYSYGFOGLILWTGHVARYYTSIFGOHL  LAPEDVISCCLDLSYSISRINGCEVOGYFESF  NLDGLFFPVYSFSAGVKVRFLLGGRHGEFKF  PPPGYAPCHAEVLYPRSHLHLEGGHGEFKF  PPPGYAPCHAEVLYPRSHLHLEGGHGEFKF  PPPGYAPCHAEVLYPRSHLHLEGGHGEFKF  PPPGYAPCHAEVLYPRSHLHLEGGHGEFKF  PPPGYAPCHAEVLYPRSHLHLEGGHGEFKF  PPPGYAPCHAEVLYPRSHLHLEGGHGEFKF  ROPHLVOFSRCLSHTDFVPCPVDTVQVLYPH  LEIRIRKLAENIEL WALTRIEGGWTGFVAR  DNKRHPICLVDFHSLPEPRNYNLOMSGETL  KTLLALGCHYGMADERAEDNLKKTLFXTY  MMSNGYKPAPLDLSHYRLTPAQTTLVDRLAE  NGHNWARDRVGGWSYSAVODPARRNP  LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY  VIEPPDOEPSOVENGSCRNVHFFAGYTTLVDRLAE  NGHNWARDRVGGWSYSAVODPARRNP  LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY  NEPPDOEPSOVENGSCRNVHFFAGYFTLOGEPGRPW  QFGDUVGGMIDLTENTIIFTLNGEVLMSDSG  STAFREIEIGGFLFVCSLGFGGYGHALGGO  VSSLRFFAICGLQEGFEFFAHNQRWYTTFPCLR  LTHRTWGSONSLVEMLFLLSLFVOFHOHR  CTAGATFLAPFOLGPAPEDEARAAPPOPDYE  NLRSAGGWSEARNGKEGTTAKEGAFGGTPC  AGGEAQPARAENEKDATTEKNKGFLKAG  KKVAMMTQPAITPTLFRLIPHDVYPADNDDD  PILILITTTYYSVRYAGOPESCOPGISHTDL  VIGCLVDLATGLMTFLANGKESNTFFQUEN  PDYHOHDMSFDLKKVNVTVTMGDEGGWN  NSLKCSNCYMVWGGDVSFGOQGRISHTDL  VIGCLVDLATGLMTFLANGKESNTFFQUEN  TLIFPAVFVLPTHONVOGELGKOKNIMPLSA  AMPGESRKNPAPCOPPRLEMMLMPYSWS  MYHHFLQVETRRAGEGLGWAVGGOPHLAML  ALHPEENRCMDLELSERLDLQRFHSHTLL  YRAVCALGNNRWYMGGOPSTOQOGRISHTDL  VIGCLVDLATGLMTFLANGKESNTFFQUEN  TLIFPAVFVLPTHONVOGELGKOKKNIMPLSA  AMPGESRKNPAPCOPPRLEMMLMPYSWS  MYHHFLQVETRRAGEGLGWAVQOEPLTMM  ALHPEENRCMDLELSERLDLQRFHSHTLL  PARVELAARAECKJUNGGFFFALAE  GVGYTTSLRPHHTSSPCCYGLANGGOPHA  RDPUGASVSPGCPVVLKLVSKLEKE  PEERSAESSFRSLOLLOKRISHVVKKEEK  FENERSAESSFRSLOLLOKRISHVVKKEEK  FENERSAESSFRSLOLLOKRISHYLKKKEE  PEERSAESSFRSLOLLOKRISHYLKKKEE  PEERSAESSFRSLOLLOKSHVVXKEEK  PEERSAESSFRSLOLLOKSHVVXKEEK  PEERSAESSFRSLOLLOKSHVVXKEEK  PEERSALESSKPRSLOLLOKSHVVXKEEK  PEERSAESSFRSLOLLO		l	İ		sequence		ADDREAL DI CVI KKK AMI HOEGHMDDALSI.
GKPRGSOPPAGTALPIEGVILSLODLITYEPS  EDLOHEKGSKLRASBLRNROSLOPEGMLSMV LNCIDRLNVYTTAAHFAEFAGEAAESWKEI  VNLLYELLASLIRGNSNCALPSTNLOWLVS KLDRLEASSGILEVLYCVLESFEVLNIQENH KSISLLDKHGRINKVLDVLCSLCVCNGVAV RSNODLITENLLPGRELLLOTNLINVYTISRN HVGRAEGTTGYSK WYFEWMDEVFIFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGGNOC GDDLYSVGPGOLILWTGHVARPYTSFGOHL LAPEDVISCLDLSVPSISSRINGCPVGGVESFS NLDGLFPVVSTSGAGWKPELLGGRHGEFKF LPPPGVAPCHEAVLPRERLHLEPKEYRREGH LAPEDVISCLDLSVPSISSRINGCPVGGVESFS NLDGLFPVVSTSGAGWKPRHLGGRHGEFKF LPPPGVAPCHEAVLPRERLHLEPKEYRREGH ROPHLVGPSRCLSHIDEVPCPVDVIQVLPPH LERIRKLAENHEL WALTRIEGGWTYGPVRD DIKKRLHPCLVDPHSLPPENRYNLOWGSEIL XTLLALGGNGMADEKAEDNLKKTKLPKTY MMSNGWKPAPLD ISHTDEVPCPVDVIQVLPPH LERIRKLAENHEL WALTRIEGGWTYGPVRD DIKKRLHPCLVDPHSLPPENRYNLOWGSEIL XTLLALGGNGMADEKAEDNLKKTKLPKTY MMSNGWKPAPLD ISHTDEVPCPVDVIQVLPPH LERIRKKAENHEL WALTRIEGGWTYGPVRD DIKKRLHPCLVDPHSLPPENRYNLOWGSEIL XTLLALGGNGMADEKAEDNLKKTKLPKTY MMSNGWKPAPLD ISHTDEVPCPVDVIQVLPPH LERIRKKAENHEL WALTRIEGGWTYGPVRD DIKKRLAPCLUDPHEL PHDVFLYBGWFGWFGTAEKSYTV QGGWYSAVQOBDARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPVTAGGWGYSAVQODPARRHPR UPTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG						1	TROOFESOA ARMIUSTNOI VNOFIKSI DSFS
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LINCIDRLINVYTTAAHFAEFAGEAAESWKIV VNLIYELLASLIKORRSNCALFSTNLOWLVS KLDRLEASSGILEVLYCVLIESFEVLNIQENH KSISLLDKEGRINKVLDVLCSLCVCNGVAV RSNODLITENLLFORELLLOTNLINVYTSIRYN PVGRAEGTTOYSK WYFEWMDEVTPFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGGNOV GDLYSVGFOGLILWTGHVARPYSGOHL LAPEDVISCCLDLSVPSISFRINGCPVGGVESF NLDGLFPVVSFSKGAVKPFLLGGRHGEFKF LPPPGVAPCHEAVLPRERLHLEPREYPREGP ROPHLVGPSRCLSHIDDVPCPVDTVQVLPPH LERIREKLAENHEL WALTRIEGGWTVGPVRD DINKRLHPCLVDPHSLEPPENNYLDGWGGTL KTILALGCHVGMADEKAEDNLKIKLEKTY MMSNGYKAPALD SHYNTLPAGTLYDRIAL HGHNVWARDRVGGGWYSAVQDPARRIPR LVPVRLLDEATKRSNDSLCQAVTLGOWGGTL KTILALGCHVGMADEKAEDNLKIKLEKTY MSNGYKAPALD SHYNTLPAGTLAYGY VNEWALDEATKRSNDSLCQAVTLGOWGGTL KTILALGCHVGMADEKAEDNLKIKLERTY GGRAVYFEFEAVTGGMSVGGWGGCTLANG HGPPOGEFSQVENGRCDRVRIFRAEKSYTV GSRAVYFEFEAVTGGMSVGMSCLMSSOS GFARAELEGGGFLANGNAGAT VFNGHGRGRAFTARVSTORD VSLAFFACGLGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	l	1	ĺ	1			GKPKGSGPPAGTALFIEGVILSEQUEITTEITS
VNILYELLASLIRGNRSNCALFSTRILDWIVS KIDRLEASSGILEVLYCVLESPEVLNIQENHI KSIISLIDKHGRNHKVLDVLCSLCVCNGVAV RSNQDLITENLICYGELLLGYDNLNYVTSIRN IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ ATHLRVGWALTGHYARPYTSFGOHL LAPEDVISCCLDLSVPSISFRAIGCPVGGYESF GDDLYSYGFDGHLWTGHVARPYTSFGOHL LAPEDVISCCLDLSVPSISFRAIGCPVGGYESF NDGLFPFVVSFSAGVKVRFLLGGRHGEFKF IPPPQYAPCHEAVLPERELHERFKERGPPG RGPHLVGPSRCLSHTDFVPCPVDTVQNUPPH LERIREKLAENHELWALTREEKYREGP RGPHLVGPSRCLSHTDFVPCPVDTVQNUPPH LERIREKLAENHELWALTREEKYREGP RGPHLVGPSRCLSHTDFVPCPVDTVQNUPPH LERIREKLAENHELWALTREEKYREGPTGHEN DNKRLHPCLVDFHSLEFPERYYNLOMSGETL KTLLALGCHVGMADEKAEDNLKKTKLDVDRLAE NGHNVWARDRVGGGWSYSAVQDBARRNPR LVPYRLIDEATRKSNROBSLCGAVRTLLGYGY NIEPPDGEPSQVENGSRCDRVRIFFAERSTYV QSGRWYFEFEAVTTGEMRYGAVARFLLGYGY NIEPPDGEPSQVENGSRCDRVRIFFAERSTYV GSGRWYFEFEAVTTGEMRYGVARFLERPV QFGDVVGCMIDLTENTIFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNGEPFGRPW QFGDVVGCMIDLTENTIFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNGLQD VSSLRFALGCIGGGFFFAMMQRPVTTWFS KGLPOFFEVPLEIPHVEVSRVDGTVDTFPGLR LTHRTWGSNDSLVEMLFLLSLSPVOFHOHFR CTAGATPLAPPGLQCPFAEDEARAAEPPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTTY AGGEAQPARAENEKDATTEKNKKRGFLKKA KKVAMMTQPPATDTPLRIPHDVVPADNRDD PEILNITTTYYSVRVFAGGEPSCVWAGWVT PDYHQLDMSFDLSKVRVVTVMGGEQGNV HSSLKCSNCYMWGGGFVSPOQQGRISHDD VGGLVDLATGLMFTANGKERTFFQVEFN TKLFFAVFUPTHONVIOFELGKGKNIMPLSA AMFGSERKNPAPOCPPELEMMMPNSWSR MPNHFI QVETRRAGERI GWAVQCGEPLTMM ALHIEEDRICAGIMFTANGKERTFRYEVFR TKLFFAVFUPTHONVIOFELGKGKNIMPLSA AMFGSERKNPAPOCPPELEMAMMPNSWSR MPNHFI QVETRRAGERI GWAVQCGEPLTMM ALHIEEDRCMODIL ELSRICLORMSHTALL YAAVALGNRVAHALCSHVOQAQLIHALE DAHLPGPLRAGYVPLLISHIE AGRERGSRSMM, SEYMPLTFI QVETRRAGERI GWAVQCGEPLTMM ALHIEEDRCMODIL ELSRICLORMSHTALL YAAVALGNRVAHALCSHVOQAQLIHALE DAHLPGPLRAGYVPLKLVSTLLVMGTGGDE DVGQLKMIPPEVFTKEDEEELGEEDEE ELEGELORMSLIPPSVLQMCRAGRSFCHAG GGEPEETTINGSRMSLLERGGLBCHER GEERSAAESKPRSLQCLUKHVRWAGEDF VQSPELVRAMRSLHRRQYDGLGELLTARPCOCH GEEEPFEETTINGSLHLGGLGGLGLARAPCH GOUGHTMALLGGLDL GEEEPFEETTINGSLHLGGLGGLGLARAPCH GOUGHTMALACGGLDL GEEEPFEETTINGSLHLGGLGGLGLARAPCH GUGHTMALACGGLDL GEEEPFEETTINGSRMSLLEGGLGGLGLARAPCH GUGHTMAL		l	1	L			EDLQHEEKQSKLKSLKNKQSLFQEEGWLSWIV
KLDRLEASSGILEVLYCVLIESPEVLNIQENH KSIISLLDKHGRINKVLDVLYCVCNGVAV RSNQDLITENILPGREILLOTNLINYVTSIRN IFVGRABGTTYGYSKWYPEWWDEVTPFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGGNOV GDDLYSYGPGLHLWTGHVARPYTSPGQHI LAPEDVISCLDLSVPSISFRINGCPVQCYPESP NLDGLFPFVVSFSAGVKVFFLLGGRHGEFKF IPPPGYAPCHEAVLPRERLHEPKEYRREGP RGPHLVGPSRCLSHTDFVPCPVDTVQVTPGVRD NCRLHPGLVDFHSLEPERNYNLQMSGEIL KTLLALGCHVGMADEKAEDNIKKTLPKTY MMSNGYKPAPLDLSHVRLTPAQTTLYDRLAB NGHNVWARDRVGQGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLGYGY NIEPPDQEPSQVENQSRCDRYMFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRDV ELGABELAYVFGHRGGRWWARPELRDV ELGABELAYVFGHRGGRWHGSEPFGRPW QPGDVVGCMIDLTENTIFTLNGEVLNSDGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFFACGLQEGFBFAINMQRVTTWFS KGLPQFEVPLEHPHVENSYRDGTVDTPPCLR LTHRTWGSONSLVEMIFLRLSLPVOFIDHFR CTAGATPLAPPGLQPPALDPAALPAAAEDPDVE NIRRSAGGWSAENKEGTAKEGAPGGTPQ AGGAQPAAAENEKDATTERLPDDVVPADNRDD PEILNTTTTYYSVRVFAGQEPSCVWAGWOTY PDYNGHDMSPLSKVRVTVTMGDGGQNID HSSLKCSNCYMVWGGFVSGPGQVGHLNLL LYGCLVLATGLIMFTANKEKSRTFFCVEFN TKLFFAVFULPTHQNVTIVFGLGRGKWMLSA AMFQSERKNPAPQCPPTLERDMLSRNYTVTMGDGGGNID VIGCTVLATGLIMFTANKERSNTFFQVEFN TKLFFAVFULPTHQNVTIVFGLGRGKNMLSA AMFQSERKNPAPQCPPTLEMMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCGEPLTMM ALHIPEENERGMDLELSERLDAMMLSANFALAR LYRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGTYPLLSFRLGRGKFRIFILL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGTYPLTPETRATLFPPGRSTSTENGHRRMIGLP GVGTYTTSLRPPHISSPCTVAAAPAAGAAEAP ARLSPAPLEALRAKALARLGEAVRDGGOHA RDPVGASVEFOPVPLKLIVALIVAGIGGDE DVKQLIKMIPFVPTEEEEEDEEEEEGEEDEE EKEEDEETAQEKEEGEKEEE EKEEDEETAGEKEEGEKEEE EKEEDEETAGEKEEGEKEEE EKEEDEETAGERGERGAGREGGEN EKEEDEETAGERGERGERGERGE LEGGLUMKLPSVRLQAGLLAHALGEAVRDGGOHA RDPVGASVEFOPVPLLLVALVALRAGGLUD GEEEFFEETTITGSRLMSLLEGRUNGLLGFULDAGLICGUL GEEFFEETTITGSRLMSLLEGRUNGLLGFULDAGLICGUL GEEFFEETTITGSRLMSLLEGRUNGLGGLURAGPE PUNDONGSRINNKVYVQDELGGLLLAAPLACGGUL GEEFFEETTITGSRLMSLLEGRUNGLGGLURAGPE PUNDONGSRINNKVYVQDELGGLLTAAPLACGGUL GEEFFEETTITGSRLMSLLEGRUNGLGGLURAPPE PUNDONGSRUNGNNKVYVQDELGGLLTAAPLACGGUL GEEFFEETTITGSRLMSLLEGGUNGLGGLURAPPE PUNDONGSRUNGNNKVYVQDELGGLLTAAPLACGGUNG				1			LNCIDRLNVYTTAAHFAEFAGEEAAESWAEI
KSIISLLDKHGRNHKYLDVLCSLCVCNGVAV RNNQDLITENLLPGRELLLQTPILNTYVTSIRNY IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGGNGV GDDLYSYGFDGLHLWTGHVARPVTSFGQHL LAFEDVISCCLDLSVPSISFRINGCPVQGVFESF NLDGLFFPVVSFSAGVKVRFLLGGRHGEFKF LPPPGVAFCHEAVLFREIHLEPKEYRREGP RGPHLVGPSRGLSHTDFYPCTVDTVQTVLPPH LERIREKLAENIHELWALTRIEQGWTYGFVRD DNKRLHPCLVDFHSLPEERFYNLQMSGETL KTLLALGCHVGMADEKAEDNLKKTKLKTYY MMSGYKPAPLDLSHVRLTPAQTTLVDRLAE NGRNVWARDRVGQGWSYSAVQDDRARNPR LVPYRLDEATRASNRDSLGQAVRTLLGYGY NIEPPOGEPSQVENGSRCDRVRIFRAEKSTYV QSGRWYFEFEAVTTGEMRVGAVFLLGYGY NIEPPOGEPSQVENGSRCDRVRIFRAEKSTYV QSGRWYFEFEAVTTGEMRVGAFRELMDY GCGAWYFEFEAVTTGEMRVGAFRELMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLALGQD VSSLRFFAICGLQGGFPFAINMQRRYTTWFS KGLPQFEVVPLEHPHYEVSRYDGTVDTPPCLR LTHRTWGSONSLVEMLERLSLPVQFIGHFR CTAGATPLAFPGLQPAEDEARAAEPDPDYE NLRRSAGGWSEAENKEGTAKEGAFGTPQ AGGEAQPARAENEKDATTESKKRGFLKA KKVAMMTQPPATPTLPRLPHIDVVPADNRDD PEILNTTTYYTSVRVFAGGERSCWMGRWN HSSLKCSNCYMWGGDFVSFOQQGRISHTDL VIGCLVDILATGLMFTANGKESNTFFQVEN TKLFPAVFULPHHONIOPELGRCN HSSLKCSNCYMWGGDFVSFOQQGRISHTDL VIGCLVDILATGLMFTANGKESNTFFQVEN TKLFPAVFULPHHONIOPELGRCNN MAHLEENRCMDLELSRLDQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLIHALE DAHLPGPLRAGGYPLLGRLGGWANGGGHA ALIFEERCMDLELSRLDQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLIHALE DAHLPGPLRAGGYPLULSRLGGARSKNINL SEVIPLTPETRAITLFPPGRSTBNGHRFRLIP GVGTYTSLRPPHFSPFCTVAALPAAGAAEAP ARLSPAPLEARRACHALCSHVDQAQLIHALE DAHLPGPLRAGGYPLULSRLGGARSKRING SEVIPLTPETRAITLFPGRSTBNGHRFRLIP GVGTYTSLRPPHFSPFCTVAALPAAGAAEAP ARLSPAPLEARRACHALGEAVBGOQHA RDPYGASSEFGOPPVLKLVGGGPN LSGLLQMKLPESVLQMCHLLEFFCDELQ HRVESLAAPAERVYDKLQANGRSFYGLLKA FSNTAAETARRTREFRSPPGGORGNHLQFKOG TDEEDCPLPEERGDLUFHCDLAHCGILD GEEFPEETTILGSRLMSLLEKVLGGCNBLLARCGLU GEEFPEETTILGSRLMSLLEKVLGGCNBLLARCGLU GEEFPEETTILGSRLMSLEKVLKKKEEK PEEERSAESKPRSLQCLVSHMVVRAQDF VQSPELVRAMRSLLHRRYQDGIGGLLARALPACDF UNDSIGNINNKVYYOURGLGELLARALPACDF UNDSIGNINNKVYYOURGLGELLARALPACDF UNDSIGNINNKVYYOURGLGELLARALPACDF UNDSIGNINNKVYYOURGLGELLARALPACDF UNDSIGNINNKVYYOURGLGELLARALPACDF			1	1			VNLLYELLASLIRGNRSNCALFSTNLDWLVS
RSNODLITENILLPGRELLLQTNLINYVTSIRPN IFVGRABGTTVGYSKWYFEWVDEVTPFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGGNGV GDDLYSYGFGGHLWTGHVARPYTSFGGHL LAPEDVISCCLDLSVPSISFRINGCPVGGVFESF NLDGLFPFVYSFAGVKWRFLLGGRHGEFKF NLDGLFPFVYSFAGVKWRFLLGGRHGEFKF RPFNLVGPSRCLSHTDFYPGYTVQVLPPH LERIREKLAENIHELWALTRIEGGWTYGFVRD NKRLHPCLYDFHSLPEPRNYNLOMSGETL KITLLALGCHVGMADEKAEDNLKKTKLPKTY MMSNGYKPAPLDLSHVRLTFAQTTLYDALAE NGRINVWARDRVGGWSYSAVQDIDARRNYR LVPYRLLDEATKRSNADSLCQAVRTLLGYGY NIEPPDQEPSGVENOSRCDRWRFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELERDV ELGADELAYVFGHRGGRWHGSEFFGRW QPGDVVGCMIDLTENTIFTLNGEVLMSDGS ETAFREIEIGDGFLPVCSLGFGQVGHLNLGQD VSSLSFFAICGLQEGFBFAINMQRVYTTWFS KGLPGFEVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLR.SLPVOFHOHRE CTAGATPLAPPGLQPFADEARAAEPDPDYE NLRRSAGGWSEAENKEGTAKEGAPGGTPQ AGGADPARAENEKDATTERAKKRGLKAG KKVAMMTOPPATPTLPRLPHDVVPADNRDD PEILNTTTYYYSVRVFAGGBEVGWHGNAD KKVAMMTOPPATPTLPRLPHDVVPADNRDD PEILNTTTYYYSVRVFAGGBEVGWHGLAG KKVAMMTOPPATPTLPRLPHDVVPADNRDD PEILNTTTYYYSVRVFAGGBEVGWHGLAG KKVAMMTOPPATPTLPRLPHDVVPADNRDD NSSLKCSNCYMVWGGDFVSFQQGRISHTDL VIGCLVDLATGLIMFTANGKESNTFPQVEPN TKLFFAVFVLPTHQNVIOFFELGRGKNIMBLAS AMMOSERKNPAPQCPPRLEMGMLMPVSWSR MPNHELQVETRRAGERLGWAVQCQEHTMM ALHIPEDNECMDILLESERLDLQRFHSHTIRL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYTDLLISHLEGNLGRHSHTLLL YRAVCALGNNRVAHALCSHVDQAQLHALE DAHLPGPLRAGYTDLLISHLEGNLGRHSHTLLL YRAVCALGNNRVAHALCSHVDQAQLHALE DAHLPGPLRAGYTDLLISHLEGNLGRHSHTLLL YRAVCALGNNRVAHALCSHVDQAQLHALE DAHLPGPLRAGGYTPLISHLEGARSKSML SEVIPLTPETRATLFPPGRSTENGHPRKIGLP GVGYTTSLRPPHHSPPCTVALPAGGABAP ANI SPAPLEALRDKALRMLGEAVROGGOHA RDPYGASSPFOPVPVLKLVIMGIGGDE DVKQLKMIEPFVTTEEEEDEEDEEEGEEDEE EKEEDEETAGEKEEDEELEEGEEDEE EKEEDEETAGEKEEDEELEEGEEDEE EKEEDEETAGEKEEDEELEEGEEDEE EKEEDEETAGEKEEDEELOEGEEDEE EKEEDEETAGEKEEDELOFFUNKLVANGEKE PEERSAAFEKSPRSLQLVSHMVVWAQEDF VQSPSEVRAMRTELHRRYQTGGLILKAAPG TDEEDCPLPEEIRQDLLDFHQDLLAHLGGLDL GEEFFEETTILGSRIMSLLEKQVGGLGELLRAAPG FINTMADGSERKINDMNKVKYOPPELLAGLGGLUNGGRE PIN MINGIGGNINNKVYCHOPPLLAGLGGLUNGGRE	i		1				KLDRLEASSGILEVLYCVLIESPEVLNIIQENHI
IFVGRAEGITQYSKWYFEVMODEVTPLIAQ ATHLRYGWALTEGYTTPYGAGEGWGGNGV GDDLYSYGFDGLHLWTGHVARPYTSPGHL LAPEDVISCCLDLSVPSISRINGCPVGGVFESF NLDGLFFPVSFSAGVKVRFLLGGRIGEKF 1PPPGYAPCHEAVLPREAL LEPIKEYRREGP RGPHLVGPSRCLSHTDFVPCPVDTVQLPH LERREKLAENHEILWALTRIEGGWTYGPVRD DNKRLHFPCLVDFHSLEPFERNYNLQMSGETL KTLLALGCHVGMADEKAEDNLKKTLLPKTY MMSNGYKPAPLDLSHVRLTPAQTTLVORLAE NGHNVWARDRVGGGWSYSAVQDDFARNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENOSRCDRVRIFTAGKTLVTY QSGRWYFEFEAVTTGERMFWOWARPELRPDV ELGADELAYYFNGHRGGRWHLGSEFGRPW QPGDVVGGMDLTENTIITLMGEVLMSDSGS ETAFRIEIGGGELPVCSLGFGQVGHLNLGQD VSSLRFALGCLOGFGEPFBANMGRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPFCLR LTHRTWGSQNSLVEMIFLRLSLPVQFHIGHR CTAGATPLAPPGLOPPAEDARAAAPDDPYE NLRRSAGGWSEAENGKEGTAKEGAFGTPQ AGGGAQPARAENKDATTKKNKRGFLKA KKVAMMTQPATPTLPRLPHDVYADNRDD PEILINTTTYYSVRVFAGGPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGGDQGNV HSSLKCSNCYMVWGGDFVSFGQQGRISTIDL VIGCLVDLATGLMTFLANGKESNTFFQVEFN KLEPAAFVLYTHONVIGEGQGNVA HSSLKCSNCYMVWGGDFVSFGQQGRISTIDL VIGCLVDLATGLMTFLANGKESNTFFQVEFN KLEPAAFVLYTHONVIGEGGKNIMPLSA AMFQSEKNRAPQCPPRLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSEKNRAPQCPPRLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSERNRAPGCPPPLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSERNRAPGCPPFLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSERNRAPGCPPFVLKLVLSLLL DAHLPGFLAGGYDLLISHILLSAGRSRSML SEYIVPLTPETRAGTLFPGRSTENGHPHGGLP GVGVTTSLRAGYTPTLEFREEDEBEEGEEDEE EKEEDEETAAGEKFEERAAGEKEEG LEEGLLQMKLPESVKLQMCHLLEYFCQCELQ HRVESLAAFARYVDKLQANGRSYGCLLKA FSMTAAETARRTREFERSPFGQNIMLLQFKDG TDEEDCPLFEERGDLLDFHQDLLAAFGGQLA GEEEPFEETTLGSRLMAKLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDD VGSPELVRAMFSLLHERQDLLDFHQDLLAAFGGQLA GEEEPFEETTLGSRLMAKLLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDD VGSPELVRAMFSLLHERQDLLDFHQDLLAAFGGGLA GEEEPFEETTLGSRLMAKLLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDD VGSPELVRAMFSLLHERQGLAAFGRAFGEREAGEREDE DE ENDMOSIGNIMNNNKYVFYDFLLAGGIGLL		į.	İ	1	ļ	1	KSIISLLDKHGRNHKVLDVLCSLCVCNGVAV
IFVGRAEGITQYSKWYFEVMODEVTPLIAQ ATHLRYGWALTEGYTTPYGAGEGWGGNGV GDDLYSYGFDGLHLWTGHVARPYTSPGHL LAPEDVISCCLDLSVPSISRINGCPVGGVFESF NLDGLFFPVSFSAGVKVRFLLGGRIGEKF 1PPPGYAPCHEAVLPREAL LEPIKEYRREGP RGPHLVGPSRCLSHTDFVPCPVDTVQLPH LERREKLAENHEILWALTRIEGGWTYGPVRD DNKRLHFPCLVDFHSLEPFERNYNLQMSGETL KTLLALGCHVGMADEKAEDNLKKTLLPKTY MMSNGYKPAPLDLSHVRLTPAQTTLVORLAE NGHNVWARDRVGGGWSYSAVQDDFARNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENOSRCDRVRIFTAGKTLVTY QSGRWYFEFEAVTTGERMFWOWARPELRPDV ELGADELAYYFNGHRGGRWHLGSEFGRPW QPGDVVGGMDLTENTIITLMGEVLMSDSGS ETAFRIEIGGGELPVCSLGFGQVGHLNLGQD VSSLRFALGCLOGFGEPFBANMGRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPFCLR LTHRTWGSQNSLVEMIFLRLSLPVQFHIGHR CTAGATPLAPPGLOPPAEDARAAAPDDPYE NLRRSAGGWSEAENGKEGTAKEGAFGTPQ AGGGAQPARAENKDATTKKNKRGFLKA KKVAMMTQPATPTLPRLPHDVYADNRDD PEILINTTTYYSVRVFAGGPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGGDQGNV HSSLKCSNCYMVWGGDFVSFGQQGRISTIDL VIGCLVDLATGLMTFLANGKESNTFFQVEFN KLEPAAFVLYTHONVIGEGQGNVA HSSLKCSNCYMVWGGDFVSFGQQGRISTIDL VIGCLVDLATGLMTFLANGKESNTFFQVEFN KLEPAAFVLYTHONVIGEGGKNIMPLSA AMFQSEKNRAPQCPPRLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSEKNRAPQCPPRLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSERNRAPGCPPPLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSERNRAPGCPPFLEMQMLMPVSWSR MPNIFILQVETRAGEBELGKGKNIMPLSA AMFQSERNRAPGCPPFVLKLVLSLLL DAHLPGFLAGGYDLLISHILLSAGRSRSML SEYIVPLTPETRAGTLFPGRSTENGHPHGGLP GVGVTTSLRAGYTPTLEFREEDEBEEGEEDEE EKEEDEETAAGEKFEERAAGEKEEG LEEGLLQMKLPESVKLQMCHLLEYFCQCELQ HRVESLAAFARYVDKLQANGRSYGCLLKA FSMTAAETARRTREFERSPFGQNIMLLQFKDG TDEEDCPLFEERGDLLDFHQDLLAAFGGQLA GEEEPFEETTLGSRLMAKLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDD VGSPELVRAMFSLLHERQDLLDFHQDLLAAFGGQLA GEEEPFEETTLGSRLMAKLLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDD VGSPELVRAMFSLLHERQDLLDFHQDLLAAFGGGLA GEEEPFEETTLGSRLMAKLLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDD VGSPELVRAMFSLLHERQGLAAFGRAFGEREAGEREDE DE ENDMOSIGNIMNNNKYVFYDFLLAGGIGLL	1	1	1			1	RSNQDLITENLLPGRELLLQTNLINYVTSIRPN
ATHLRYGWALTEGYTPYPOAGEGWGNOV GDDLYSYGFOGLIH.WTGYPGGHL LAPEDVISCCLDLSVPSISRINGCPVGVYESF NLDGLFFPVYSSAGAVE WRFLLGGRHGEFKF LPPPGYAPCHEAVLPRERLHLEPIKEYREGO RGPHLWGPSRCLSHTDFVPCPVDTVQIVLPH LERIREKLAENHEL WALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLPFERNYNLGMSGETL KTLLALGGHGGMADEKAEDNLKKTKLPKTY MMSNGYKPAPLDLSHVRLTPAQTIT.VORLAE NGHNVWARDRVQGGWSYAQVDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENGSRCDWIRFAEKSYTV QSGRWYFEFEAVTIGEMRVGWARPELRPDV GSGRWYFEFEAVTIGEMRVGWARPELRPDV GSGRWYFEFEAVTIGEMRVGWARPELRPDV ELGADELAYVFNOHRGGPKHLGSEPFGRPW QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS ETAFREIEIGIGGFLVCSLGFGQVGHLNLGQD VSSLRFAICEICLGGFEFFAINMGRPUTURFS KGLPGFEPVPLEHPHYEVSRVDGTVDTPPCLR LITHRTWGSONSLVEMLFLRSLEVQHHQHRR CTAGATPLAPPGLQPPAEDEARAAEDPDPYE NLRRSAGGWSEANGKSGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGLFKA KKVAMMTOPPATPLTLRHDDVVPADNRDD PEILINTITTYYYSVRVAGQEPSCVWAGWTY PDYHQHBMSFDLSK VRVVTVTYMGDEQONV HSSLKCSNCYMVWGGDFVSFGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFRQVEPN SKLCSNCYMVWGGDFVSFGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFRQVEPN KLEPAVFVLPHQNVLQFELGKQKNIMPLSA AMFQSEKNPAPQCPPRLEMQMLMCPSWSR MPNIFLQVETRRAGERLGANGTSTRALL YRAVCALGONFRAAGLESSERSML SEYIVPLTPETRAITLPPGRSTENGHPRHGLP GVGVTTSLRPPHFFSPFCTVAALPAAGAAEA ARLSPAIPLEALRNAALMGEAVROGQGIA RDPVGASVEFGFVPVLKLVSTLLVMGFGGE DVKQULKMIEPSVFTEEEEEDEEEGEEDEE EKEEDEEETAQEKEDEKEFEEAAGEGKEGG LEGGLLQMKLPESVFLOEKLULL HRVESLAFARRYDDLLGANGRSYGLLKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCHLFEIRGDLLDHQDLLAHGIDL GGEEEPETEETTUGSRUMLLGRYCDGLU HRVESLAFARRYDDLLQANGRSYGLLKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCHLFEIRGDLLDHQDLLAHGIDL GGEEEPETEETTUGSRUMLLGRYCDGELQ HRVESLAFARRYDVBLLGANGRSYGLLKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TOEEDCHLFEIRGDLLDHQDLLAHGIGLD GGEEEPETEETTUGSRUMLLGRYCDGELG PELMMOSIGNIMNNKYPLAGLGELKRALPRA YTISPSVEDTMSLLECLGGIRSLLIVVAMOYED FUNMOSIGNIMNNKYPTYDFLAGGHLAGHEL DAMLMGGINMNNKYPTYDLAMACGHEE		•		}		}	IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ
GDDLYSYGFOGHLWTGHVARPYTSFGQHL LAPEDVISCCLDLSVPSISRINGCYOGVFESF NLDGLFFPVVSFSAGVKVRFLLGGRIGEKGF LPPGY APCHEAVLPRENLHLEGRIGEKGF LPPGY APCHEAVLPRENLHLEGRIGEKGF RGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPH LERIREKLAENHELE WALTRIEGGWYGPVED DNKRLHFCLVDFHSLPPERNYNLQMSGETL KTLLALGCHVGMADEKAEDNLKKTLPKTY MMSNGYKPAPLDLSHVALTPAQTTLVDRLAE NGHNVWARDRVGGWSYSAVQDIPARNPR LVPYRLLDEATKRSNRDSLAVAVDIPARRHPL LVPYRLLDEATKRSNRDSLAVAVDIPARRHPL LVPYRLLDEATKRSNRDSLAVAVDIPARRHPL LVPYRLLDEATKRSNRDSLAVAVDIPARRHPL LVPYRLLDEATKRSNRDSLAVAVDIPARRHPL VGSGRWYFEFEAVTIGEMRVGWARPELRPDV ELGADELAVYFNGHRGGRWHLGSEPFGRPW QPGDVVGCMIDLTENTIHTILNGEVHANDSGS ETAFREIEIGGFLPVCSLGFGQVGHLNLGQD VSSLRFFAICCLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVAUGTVDTPPCLR LTHRTWGSONSLVEMLFIRLSLFVQFHOHRR CTAGATPLAPPGLQPPAEDEARAAGEPDPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENSKDATTEKNSKREFLFKA KKVAMMTIQPATPTLTRHDVVADNRDD PEILNTTTYYYSVRYFAGQEFSCVWAGWVT PDYHQHHDMSFDLSKKVRVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSFGQGGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEN TKLFPAVFVLPTHQNVIQFELGKGKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERIG WAVQCQEPLTMM ALHIPENRCMDLELSERLDLQRFHSHTRLL YRAVCALGNINRVAHALGTWAQCGLFLMM ALHIPERRCMDLELSERLDLQRFHSHTRLL YRAVCALGNINRVAHALGTWAQCGLFLMA ALHIPERRAGMPULLSHELSEACRSRSML SEYIPLTFETRATILFPPGTVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVROGQHA ARDFYGASVEPGFFPVLKLVSTLLVMGIFGDE DVGQLKMEPFSVFTEEEEEDEEEGEEDEE EKEEDEEET AGEKEDEEKEEEAAGGKEGG LEGGLLQMKLPFSVFLGEGEBEEDEDEE EKEEDEEET AGEKEDEEKEEEAAGGKEGG LEGGLLQMKLPFSVFLGEGEBEEDEEDEE EKEEDEEET AGEKEDEEKEEEAAAGGKEGG LEGGLLQMKLPFSVFLGEGEBEEDEEDEE EKEEDEEET AGEKEDEEKEEEAAAGGKEGG LEGGLLQMKLPFSVFLGEGEBEEDEE EKEEDEEET AGEKEDEEKEEEAAAGGKEGG LEGGLLQMKLPFSVFLGEGEBEEDEEDEE EKEEDEEET TLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQLLVSHMVYRWAQEDF VGSPELVRAMFSLLHRQVGGLGELLRALPRA YTISPSVEDTMSLLECLGQIRSLLIVQMGPGE FINLMOSIGNIMNNVKYPLQUELAURHAUGHEE		1		1			ATHLRVGWALTEGYTPYPGAGEGWGGNGV
LAFEDVISCCLDISYPSISRINGCP/QQVFESF NLDGLIFFEVYSSAGVEVRFLLGRHGEFKF LPPPQYAPCHEAVLPRERLHLEPIKEYRREGP RGPHLVGPSRCLSHITDYCPVDTVQIVLPH LERIREKLAENHEL WALTRIEGGWTYGPVRD DNRKHPCLVDFHSLPEPERNYNLQMSGETI KTILALGGHVGMADEKAENNLKKTKLPKTY MMSNGYKPAPLDLSHVRLIFAGTITLVBILAE NGHNVWARDRVGQGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVSTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFFAEKSYTV QSGRWYFEFEAVTIGEMRVGWARFLERDV GLADELAYPNGHRGGGWHLGSEPFGRPW QPGDVVGCMIDLTENTIITINGEVLMSDSGS ETAFREIEIGDGPLPVCSLGGWYGHLMGDD VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYSVSRVDGTVDTPPCLR LTHRTWGSORSNLVEMLFRLSLEVQFHQHRR CTAGATPLAPPGLQPPAEDEARAAEPPDPYE NLRRSAGGWSEAENIKGRAKGAPGTPQ AGGEAQPARAENEKDATTEKNKKRGLEKA KKVAMMTQPATPTLERAHENDVVPADNRDD PEILNTTTYYYSVRVFAGGEPSCVWAGWTI PDYHQHDMSPDLSKYRVYTVMGGDGONV HSSLKCSNCYMVWGGDFVSPGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFQVEPN TKLPFAVFVLYTHONVIQGELGKQKNIMPLSA AMFQSEKNPAPCCPPRLEMQMLMPVSWSR MPNIFLQVETRRAGERLGMAVQCQEPLTMM ALHIPEENRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVOQCPLTMM ALHIPEENRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEENRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRFHSHTLLL YRAVCALGNINVAHALGEMAVQCQCPLTMM ALHIPEERRCMDILELSERLDLQRAGAAEAP ARLSPAIPLEALRIKALRRAGGAVPGOQCHA RDDYGASVERGFFPVPLKLLVSTLLVMGFFGDE DVGQILKMIEPFVFTEEEEDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEE	1	1				1	GDDLYSYGFDGLHLWTGHVARPVTSPGQHL
NLDGLFFPVSFSAGVKVRFLLGRHGEFKF LPPGYAPCHEAVLFPERLHLEPIKEYRREGP RGPHLVGPSECLSHTDFVPCPVDTVQIVLPPH LERIREKLAENHEL WALTRIEGGWTYGPVRD DNKRLHPCLVDFHSLPEPERNYNLQMSGETI KTILALGCHVGMADEKAEDNIKKTKLPKTY MMSNGYKPAPLDLSHVRLTPAQTITLVDRLAE NGHNVWARDRVGQGWSYSAVQDIPARNDR LVPYRLLDEATKRSNBSLCQAVRTLLGYGY NIEPPDQEFSQVENQSRCDRVBIFAEKSYTV QSGRWYFEFEAVTIGEMRVGWAPRELRPDV ELGADELAYVFNGHRGQRWHLGSEPFGRPW QPGDVVGGMIDLTENTIFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLGEGFBFFAINWARPVTTWFS KGLPQFEFVLEHIPHVSSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRISLEVQFHQHFR CTAGATPLAPPGLQPFALPEDEARAAEPPDYE NLRRSAGGWSAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDTATKNKKRGFLEKA KKVAMMTQPATPTLPRLPHDVVPADNRDD PEILNTTTYYSVRVFAGGEPSCWAGWVT PDYHQHDMSFDLSKVRVVTVTMGBEQGNV HSSLKCSNCYMVWGGDFVSPGQGGRISHTIDL VIGGLVDLATGLMFTKNKKRGFLEKA AMFQSERKNPAPCPELMGMLMPSVSSR MFNHFLQVETRRAGERLGWAVQCQEFLTMM ALHIPENRCMDILELSRLDLGHPSSCRSRSML SEYIVPLTETRATTLENGMLMPSVSSR MFNHFLQVETRRAGERLGWAVQCQEFLTMM ALHIPENRCMDILELSRLDLGHPSHTLRL LYRAVFALPHFPGRSTEMGHPRHGLP GVGVTTSLRPPHFSPPCTVALPAGAGAAEAP ARLSPAIPLEALRAKLAGHVEGQHA BALPGPLRAGYYDLLISHLESACRSRRSML SEYIVPLTETRATTLFPGRSTEMGHPRHGLP GVGVTTSLRPPHFSPPCTVALPAGAGAAEAP ARLSPAIPLEALROKALOSHVQAQLHHALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SEYIVPLTETRATTLFPGRSTEMGHPRHGLP GVGVTTSLRPPHFSPPCTVALPAGAGAAEAP ARLSPAIPLEALROKALGHEVAGQHA RDPVGASVEFGFVPVLKLVSTLLVMGFGGE DVKQLKNIEPEVTTEEETEEDBEEDEEEGEEDEE EKEEDEEETAQEKEEDERGEEEGEEEDEE EKEEDEETTAGRKLGGANAACAEAP ARLSPAIPLEALROKALGHEVAGAAGAEAP ARLSPAIPLEALROKALGHAUGANGRSTGLIKA FSMTAAETARRTREFRSPPCQCDNMLLQFKDG TDEEDCPLPEEITGLOSLMALLSKVLVKKKEEK PEEERSAEESKRRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPA YTISPSSVEDTMSLLECLGQRSLLIVQMGPGE	1			1	1		LAPEDVISCCLDLSVPSISFRINGCPVQGVFESF
LPPGYAPCHEAVLPRERLHLEPIKEYRREGP RGPHLVOFSRCISHTD/PCPVDTVOYLVPH LERIREKLAENHEL WALTRIEGGWTYGPVRD DNKRLHPCLVDFHSLPEPERNYNLQMSGETL KTILALGCHYGMADEK AEDNILKTKLPKTY MMSNGYKPAPLDLSHVRLTPAQITILVDRLAE NGHNWARDRVGGGWAYNTLLGYGY NISPOPGPSQVENOSRCDRVBIFAREKSTV QSGRWYFEFAVTTGEMRVGWARPELRPDV ELGADELAYVPNGHRGGRWHLGSEPFGRPW QPGDVVGCMIDLTENTHITINGEVLMSDSGS ETAFREIEIGDGFLPVCSLGFGQVGHLNLGQD VSSLRFFAICGL,GGEFFARNWGRPVTTVFS KGLPOFEPVPLEHPHVEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPVQFHOHRR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRRSAGGWSBAENGKEGTAKEGAPGGTPQ AGGEAQPARENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEILINTTTYYYSVRVAGGPSCVWAGWVT PDYHOHDMSFDLSKVRVVTVTMGDEGGNV HSSLKCSNCYMVWGGDFVSFGQQGRISTIDL VIGGLVDLATGLMTFTANGKESNTFPQVEPN TKLFPAVFVLPTHQNVIQPELGKKNIMPLSA AMFQSERNPAPQCPPRLEMGMLMFVSWSR MFNHFLQVETRRAGERLGWAVQQCFLTMM ALHPEENRCMDLELSEDLORFHSHTILL YRAVCALGNNRVAHALCSHYDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SEYIVELTETRATLEPFGRSTENGHPRHGLP GVGVTTSLRPPHHFSPPCFVAALPAAGAAEAP ARLSFAPILEALDRALRMLGEAVRDGQGHA RDPVGASVEFGCPVPVLKLVSTLLVMGFGGDE DVKQILKMIEPEVPTEEDEEEDGEEGEEGEEDEE EKEEDEEETAQEKEDEKEEEAAEGEKEEG LEEGLLQMKLPSSVKLQWCHLLETYFCQEL HEVELLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFSPPGCDINMLLQFKDG TDEEDCPL PEEIRQDLIPHQDLLAHCGIQLD GEEEPFEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKFRSLQELVSHNVVRWAQEDF VQSPELVRAMFSLLHERVYDRGJGGLELRALPRA YTISPSSVEDTMISLLECLGQRISLLIVQMGPGE	1	1		1		1	NLDGLFFPVVSFSAGVKVRFLLGGRHGEFKF
RGPHLVGPSRCLSHTDFYPCPVTYOTVLVPHPL LERIRKLAENIHEL WALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLPEPRNYNLGMSGETL KTLLALGCHVGMADEKAEDNIKKTKLPKTY MMSNGYKPAPLDLSHVRLTPAQTITLVDRLAE NGHNVWARDRVGQGWSYSAVQDIPARRNPR LVPYRLIDEATKRSNRSLCQAVRTLIG GYGY MIEPPDGEFSQVENOSRCDRVRIFRAEKSTYV QSGRWYFFEFAVTTGEMRVGWARPELRPDV ELGADELAYVFNGHRGGWHLGSEFGRPW QPGDVVGCMIDLTENTHIFTLNGEVLMSDSGS ETAFREIEGGGFLPVCSLGPGQVGHLNLOQD VSSLRFFAICGLGEGFEFFANWQRPVTTWFS KGLPQFEPVPLEHPHYVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAEPDPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPATPTLPHDVVPADNRDD PEILINTTTYYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGPVSPGQQGRISHTDL VIGGLVDLATGLMFTANGKESTFFQVEPN TKLFPAVFLPTHGVNIOFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMGMLMPVSWSR MFNHFLQVETRRGERG GWAVQCQEPLTMM ALHPEENRCMDLELSERLDLQRHSHTILL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLSHLESEALDLGRHSHTILL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLISHLESEACNGERSIML SEYIVPLTPETRATILFPPGRSTENGHPRHGLP GVGVTTSLRPHFSPPCFVAALPAAGAAEAP ARLSFAPLEALROKALRMLGEAVRDGQHA RDPVGASVEFGFVPVLKLVSTLLVMGFGDE DVKQLKMIMPEVFTEEGEEDDEEEGEEDEE EKEEDEET AGEKEDEEKEEELADGFKEG LEEGLLQNKLMIPEVFTEEGEEDDEEEGEEDEE EKEEDEET AGEKEDEEKEEEELADGFKEG LEEGLLQNKLMIPEVFTEEGEEDDEEEGEEDEE EKEEDEET AGEKEDEEKEEEEAAEGKEEG LEEGLLQNKLMIPEVFTEEGEEDDEEEGEEDEE EKEEDEET AGEKEDEEKEEEEAAEGKEEG LEEGLLQNKLMIPEVFTEEGEEDDEEEGEEDEE EKEEDEET AGEKEDEEKEEEAAEGKEEG LEEGLLQNKLMIPEVFTEEGEEDDEEEGEEDEED EKEEDLEFENTALTHAGGULD GEEEPFEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGIGELLRALPRA YTTSPSSVEDTMSLLEEVQVIPPILMRAALGMHE	ļ		1	}			LPPPGYAPCHEAVLPRERLHLEPIKEYRREGP
LERIREKLAENIHELWALTRIEGGWTYGPVAGETL NTLALGGHVGMADEKAEDNIKKIKLPKTY MMSNGYKPAPLDLSHVRLITPAQTIL VYDRLAE MGHNIWARDRVGGGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLQAVRILLGYGY NIEPPOGEPSQVENOSRCDRVRIFRAEKSTIV QSGRWYFEFEAVTIGEMRVGWAPFELRPDV ELGADELAYVPNGHRGGWHLGSEPFGPW QPGDVVGCMIDLIENTHITLINGEVLMSDSGS ETAREHEIGDFLPVCSLGPRGVGHLNLGQD VSSLRIFAICGL,GEGFEFAINMGRPVTTWFS KGLPOFEPVPLEHPHVEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPVOFHGHFR CTAGATPLAPPGLOPPAEDEARAEPDPDYE NLRRSAGGWSEAENGKEGTAKEGATAGEAPPDYE NLRRSAGGWSEAENGKEGTAKEGATAGEAPGDPDYE NLRRSAGGWSEAENGKEGTAKEGATAGEAPGDPDYE NLRRSAGGWSEAENGKGTAKEGATAGEAVGHOFH MSIKCSSCNYMWGGDFVSPGQOGRISHDL VIGCLVDLATGLMTFTANGKESTIFFQVEPN TKLPPAVFLYFHONVIGFLGKKINMPLSA AMFQSERNPAPQCPPRLEMGMLMPVSWSR MPNHFLQVETRRAGERLGWAVCQCEPLTMM ALHPEENRCMDLELSERLDLQRHSHTILL YRAVCALGNNRVAHALCSHYDQAQLLHALE DAHLPGPLRAGYYDLLISHLESRCLDLQRHSHTILL YRAVCALGNNRVAHALCSHYDQAQLLHALE DAHLPGPLRAGYYDLLISHLESRCADGGHA RDPVGASVEFGVPVLKLVSTLLVMGFGDE DVKQILKMEPEVFTEEFEDDEEEGGEEGEEELDEE EKEEDEETAQEKEDEKEEEAAGGEKEG LEEGLLQMKLPESVKLQWCHLLFYFCDQELQ HRVESLAAFARTYVDKLQANQKSRYGLLIKA FSMTAAETARRTREFFSPPGCODINILLQFKDG TDEDCOPL PEEIRQULDFHQDLLAHCGIQLD GEEEPFEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVYRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMISLLECLGQROSLLIRALPRA YTISPSSVEDTMISLLECLGQRYGLHALGHEE				1			RGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPH
DINKRLHPCLVDFHSLPEFERNYNLOMSGETL KTLALGCHVGMACKADNIKKTLPKTY MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE NGHNVWARDRVGQGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRDRWIFRAEKSYTV OSGRWYFEFEAVTGEMRVGWARPELRPDV ELGADELAYVFNOHRGGRWHLGSEPFGRPW QPGDVVGCMIDLTENTIITLINGEVLMSDSGS ETAFREIEIGDGFLEVCSLGPQQVGHLNLGQD VSSLRFFAIGGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPYSSRVDGTVDTPFCLR LTHRTWGSONSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPPDPYE NLRRSAGGWSEAENGKBGTAKEGAPGGTPQ AGGEAQPARAENEKDATTERNKKRGFLFKA KVAMMTOPPATPLAPPHDVYPADNRDD PEILNTTTYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEGONV HSSLKCSNCYMVWGDFVSPQQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLFHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCGPLTMM ALHIPEENRCMDLELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYVDLISHILESCRSRSSMLL SEYLYPLTPETRATILFPPGRSTENGHPRHGLP GVGVTTSLRPPHIFSPPGTVAALPAAGAAEP ARLSPAPLEALRDKALRMLGEAVRDGGQHA RDPVGASVEFQFVPVVLKLNSTLLVMGIFGDE DVKQILKMIEPSVFLYSHLISHILESCRSRSSRSMLL SEYLYPLTPETRATILFPPGRSTENGHPRHGLP GVGVTTSLRPPHESPECTVAALPAAGAAEP ARLSPAPLEALRDKALRMLGEAVRDGGQHA RDPVGASVEFQFVPVVLKLNSTLLVMGIFGDE DVKQILKMIEPSVFLYSHLAGVAGAGAEP  LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERTVDKLQMANGRSPYGLIKA FSMTAAETAARTREFRSPPQEQINMLLQFKDG TDEEDGPLPFERGIQLFFHQLAFKDG DTEEDGPLPFERGIGLFEEDGEEEDEE EKEEDEETTLGSRLMSLLEKVRLVKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VCNPELVRAMFSLLHRQYDGLGELLZALPRA YTISPSSVEDTMSLLLECGGRSLLIVQMGPQE		i.					LERIREKLAENIHELWALTRIEQGWTYGPVRD
KTLLALGCHVGMADEKAEDNILKKTKLPKTY MMSNGYRPAPALDLSVALTPAQTILVORLAE NGHNVWARDRVGQGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPOGPSQVENQSRCDRVRIFRAEKSYTV OSGRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVFNGHGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFALICGLOGEFEPFAINMQRPVTTWFS KGLPOFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVOPHQHER CTAGATPLAPPGLOPPAEDEARAAEPDPDYE NILRSAGGWSEAENGKBGTTAKEGAPGGTPQ AGGEAQPARAENEKDATTENNKKRGFLFKA KKVAMMTOPPATPTLPRLPHIDVVPADNRDD PEILINTTTYYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSPDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQQQGRISHTDL VIGCLVDLATGLMTFANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPHHFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDILELSERLDLORFHSHTLRL YRAVCALGNNRVAHALCSHVDQALLHALE DAHLPGPRAGGYDLLISHLESACRSRSMI. SEYIVPLTPETRAITLFPGRSTENGHPRHGLP GYGVTTTSLRPPHHFSPPCTVALIPAAGAAEAP ARLSPAPLEALROKALRMLGEAVRDGGOHA RDPVGASVEFQFVPVLKLLVSTLLVMGFGGE DVKQILKMIEPEVTTEEEEEDEEEGEEEDEE EKEEDEETTAGKKEDLAKARAGGERGEEEDE EKEEDEETTAGKKEDLAKARAGGERGEEEDE EKEEDEETTAGKKEDLAKARAGGERGEEEDE EKEEDEETTAGRKEDLAKARAGCERGE LEEGIL QMKLIPESVLLVMGFGGDE DVKQILKMIEPEVTTEEEEEEDEEEGEEEDEE EKEEDEETTAGRKEDLAKARAGCEKEG LEEGIL QMKLIPESVLLVMGFGGDE HVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETAARTREFRSPPCQINMLLQFKDG TDEEDCPLFEERIGDLLDFHQDULAHCGIQLD GEEEEPFEETTIGSRLMSLLEKVRLVKKKEEK PEERSAEESKPRSLQELVSHMVVRWAQEDF VOSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLELCGGRISLLIVQMGPGE	1	-				ł	DNKRLHPCLVDFHSLPEPERNYNLQMSGETL
MMSNGYKPAPLDLSHYKLIPAQTILYDRIALE NCHNWARDRVQGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTIGEMRVGWARPELRPDV ELGADELAYVFNGHRGGRWHLGSEPFGRPW OPGDVVGCMIDLTRIITINGEVLMSDSGS ETAFREIEIDGFLPVCSLFGGGVGHLNLGOD VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVLEHPHYEVSRVDGTVDTPFCLR LTHRTWGSONSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPAEDEARAAEPDEDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENSKDATTEKNKKRGFLFKA KKVAMMTOPPATPLTPRLPHDVVPADNRDD PEIILNTTTYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVVVTVTMGDEGGNV HSSLKCSNCYMVWGGDFVSPGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPHHFLQVETRRAGERLGWAVQCOFELTIMM ALHPEENRCMDILELSERLDLQRFHSHTLRL YRAVCALGNIRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYVDLLISHHLESACRSRRSML SEYLYPLTPETRAITLFPPGRSTENGHPRHGLP GVGVTTSLRPPHFISPPCTVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGGHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVGQILKMIEPSFTFCTVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGGHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPSFTEREEEEDEEEGEEDEDEE EKEEDEETTAGSKEDEEKEEERAAGGKEEG LEEGLLQMKLPESVKLJOMCHLLEYPCDQELD HWVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPGQISMLLQFKDG DEEEDPLFEETIGGRLMSLLEKVRLVKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VONDPLEVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLLECGGRSSLLIVQMGPQE		}	ł		•		KTLLALGCHVGMADEKAEDNLKKTKLPKTY
NGHNVWARDRVGGWYSAVQDPARRNPR LVPYRLIDBATKRSNRDSLCQAVRTILGYGY NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTIGEMWGWARPELRPDV ELGADELAYVPGHRGQRWHLGSEPFGRPW QPGDVVGGMIDLTENTIIFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLOPPAEDEARAAEPPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPTLPHDVVPADNRDD PEILINTTTYYSVRVFAQGEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEDGNV HSSLKCSNCYMVWGGDFVSPGQQGRISHTDL VIGCLVDLATGLAMFTANGKESNTFFQVEPN TKLFPAVFLPTHQNVVJGELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRAGERLGWAVQCQEPLTMM ALHIPEENRCMDLLELSERLDLQRFHSHTLRL YRAVCALGNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRSMIL SEYIVPLTPETRATILFPPGRSTENGHPRHGLP GVGVTTSLRPHHFSPPCTVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGGHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQLKMIEPEVFTEEDEEEDEEEGEEEDEE EKEEDEEETAQEKDEEKEEEAAAEGEKEEG LEEGLLQMKLPESVRLQMCHLLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLIKA FSMTAAETTARTREFFSPPQEQINMLLQFKDG TDEEDCPLFEEIRQDLLDFHQDLLAHCGIQLD GEEEPPEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLLEKVRLVKKKEEK PEEERSAEESKPRSLLEYFODGELGLRALPRA YTISPSSVEDTMSLLEKCLGQIRSLLIVVRWEKEEK PEEERSAEESKPRSLLGCLVSHMVVRWAGEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLEKCLGQIRSLLIVQMGPQE		ł					MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE
LVPYRLLDEATKRSNRDSLCQAVRTIFAAEKSYTV VIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVFNGHRGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTIIFILINGEVLMSDSGS ETAFREIGIGGFLPVCSLGPGQVGHLNLGQD VSSLRFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFIRLSLPVQFHQHFR CTAGATPLAPPGLPPAPEDEARAAEPDPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDAITEKNKKRGFLFKA KKVAMMTQPATPTLPRLPHDVYPADNRDD PEILINTTTYYYSVRVFAGQEPSCVWAGWVT PPYHQHDMSFDLSKVRVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSFGQQGRISHTDL VIGGLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSEKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCGPLTMM ALHIPEENRCMDLELSERLDLQCFELTMM ALHIPEENRCMDLELSERLDLQCFELTMM SEVIVLTPETRATILEPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPCFVAALPAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGQGHA RDPVGASVEFGQTVPVLKLVSTLLVMGIFGDE DVKQILKMIEPEVYTEEEEEDEEEGGEEDEEE EKEEDEEETAQEKEDEEKEEEAAFGEKEEG LEEGLLQMKLPSVKLQMCHILLEYPCDQELQ HRVESLAAFAERYVDKLQANGRSRYGLIKA FSMTAAETARRTREFRSPPQEQINMLOFKDG TDEEDCPLFEEIRQDLLDFHQDLLAHCGIQLD GEEEEPPEETTLGSRIMSLLEKVRLVKKKEEK PEEERSAEESKPSLQELVSHMVVRWAGEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLEKCLGQIRSLLIVVJMGPQE		j					NGHNVWARDRVGOGWSYSAVQDIPARRNPR
NIEPPDQEPSQVENQSRCDRVIEFAEKSYTV QSGRWYFEFAVTTGEMRVGWARPELRPDV ELGADELAYVPNGHRGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTIITILNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLOEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPFATPTLPRLPHEVVPADNRDD PEIILNTTTYYSVRVPAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQQQGRISHTDL VIGCLVDLATGIMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPWSWSR MPNHFLQVETRRAGERLGWAVQCOEPLTMM ALHTPENRCMDLELSERLDLQRFHSHTLRL YRAVCALGNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESRADLQRFHSHTLRL YRAVCALGNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SEYIVPLTPETRAITLFPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPPCTVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGQHA RDPVGASVSFQFVPVLKLVSTLLVMGIFGDE DVKQLKMIEPEVFTEEEEEDEEEGEEEDEE EKEEDEETAQEKEDEKEEEAAAGEKEEG LEEGLLQMKLPSVKLQMCHLLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAACTARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRGDLLDFHQDLLAHCGIQLD GEEEEPEEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNILMOSIGRIMNNKEYFQOHPNLMALGMHE		1				1	LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY
QSGRWYFEFEAVTTEGMRVGWARPELRPDV ELGADYFNOHRGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS ETAFREIEIGDGFLPVYCSLGPGQVGHLNLGQD VSSLRFFAICGLQEGFEPFARMQRPYTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEIILNTTTYYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVYTVMGDEGNV HSSLKCSNCYMVWGGDFVSPQQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFULPHONVIOPELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHPEENRCMDILELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SEYIVPLTPETRAITLFPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPCFVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGQHA RDPVGASVEFGFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPEVFTEEEEEDDEEEEGEEEDEE EKEEDEETAQEKEDEEKEEEAAAEGKEG LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERVYDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLOFKDG TDEEDCPLPEEIRQDLDFHQDLLAHCGIQLD GEEEPPEETTLGSKLMSLLEKVRLVKKKEEK PEEERSAEESKPSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNILMOSIGGNIMNNKYFYOHFNLMRALGMHE	1	1	Ì	1		1	NIEPPDOEPSOVENOSRCDRVRIFRAEKSYTV
ELGADELAYVFNGHRGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTIITLINGEVLMSDSGS ETAFREIGIDGFLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLQEGFEFARIMQRPVTTWFS KGLPQFEVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRRAGGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPFATPTLPRLPHDVVPADNRDD PEIILNTTTYVSVRVPAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGPFSCPWGQGRISHTDL VIGGLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDILELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SEYIVPLTPETRAITLFPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPCFVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGQHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPEVTTEEEEEDDEEEEGEEEDEE EKEEDEEETAGEKEEEEEAAAGEKEEG LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERTVÜDKLQANGKSRYGLLIKA FSMTAAGTARTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEEPEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPSLQELVSHMVYRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENI MIOSIGNIMNNKYFQOHPNLMRALGMHE			1			1	OSGRWYFFFFAVTTGEMRVGWARPELRPDV
QGGDVGCMIDLTENTIIFTLNGEVLMSDSGS ETAFREIGIDGFLPVCSLEGGQVGHLNLGQD VSSLRFFALGCLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSDNSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEIILNTTTYYYSVRVFAQQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHPEENRCMDLELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRSML SEYIVPLTPETRAITLEPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPPCFVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGEAVRDGGQHA RDPVGASVEPGFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPEVYTEEEEEDEEEEGEEEDEE EKEEDEETAQEKEDEEKEEEAAGEKEGG LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARTTREFRSPPQEQDNMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEPPEETTLGSRLMSLLEKVRLVKKKEEK PEEERSALESKRSLOELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQKGPGE ENIMOSIGNIMNTKYFYOHPNLMRALGMHE				1			FL GADELAYVENGHRGORWHLGSEPFGRPW
ETAFREIEIGDGFLPVCSLGPGGVGHLNLGQD VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRSAGGWSEAENGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTERNKKRGFLFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEILINTTTYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPGQQGISHTDL VIGGLVDLATGLMFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHPEENRCMDILELSERLDLQRFHSHTLRL YRAVCALGNINRVAHALCSHVDQAQLLHALE DAHLFGPLRAGYYDLLISIHLESACRSRRSML SEYIVPLTPETRAITLFPPGRSTENGHPRHGLP GVGVTTSLRPPHHSPPCFVAALPAGAAEAP ARLSFAIPLEALRDKALRMLGEAVRDGQHA RDPVGASVEFOFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPEVFTEEEEEDEEEGEEDEEE EKEEDEEET AQEKEDEEKEEEAAGEKKEG LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFFSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHGGIQLD GEEEEPEETTLGSRLMSLLEKVRLVKKKEEK PEEERSALEESKPRSLOELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDIMSLLECLGQIRSLLIVQMGPQE ENIMOSIGNIMNINKYFYOPIPNLMRALGAHER	Ì	l l	ļ	}			OPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS
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RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPEVFTEEEEEEDEEEGEEEDEE EKEEDEEETAQEKEDEEKEEEAAEGEKEEG LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEPEEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNNKVFYOHPNLMRALGMHE		1		1	1	1	GVGVTTSLRPPHHFSPPCFVAALPAAGAAEAP
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EKEEDEETAQEKEDEEKEEEAAEGEKEEG LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEPEEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNNKVFYOHPNLMRALGMHE		i			1		RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE
LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEEPEEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNNKVFYOHPNLMRALGMHE	1			1	1	1	DVKQILKMIEPEVFTEEEEEEDEEEGEEEDEE
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TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEEPEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNNKVFYOHPNLMRALGMHE				-		1	FSMTAAFTARRTREFRSPPOEOINMLLOFKDG
GEEEEPEETTLGSRLMSLLEKVRLVKKKEEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNNKVFYOHPNLMRALGMHE			1				TOFFOCPLPEEIRODLLDFHODLLAHCGIQLD
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VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNKVFYOHPNLMRALGMHE	j		į				PEEERSAEESKPRSLQELVSHMVVRWAQEDF
YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE FNI MIOSIGNIMNKVFYOHPNLMRALGMHE					1	}	VOSPELVRAMESLLHROYDGLGELLRALPRA
FNI MIOSIGNIMNNK VFYOHPNLMRALGMHE					1		VTISPSSVEDTMSLLECLGOIRSLLIVOMGPOE
TVMEVMVNVLGGGESKEIRFPKMVTSCCRFL			1				ENI MIOSIGNIMNIK VEYOHPNI MRALGMHE
1 VINE VIVI VE COOLDIALIS TRAVECCO Z					1		TVMEVMVNVI GGGESKEIRFPKMVTSCCRFL
			. ]				1 AIMT AIMT AIM A POOCEDING THE LAND AND A

					D. Hard and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	Į.	residue of	sequence	/=possible nucleotide deletion, \=possible
}		1	1	peptide	{	nucleotide insertion
	1	İ	1	sequence	<u> </u>	CYFCRISRQNQRSMFDHLSYLLENSGIGLGM
<u> </u>	<del> </del>	<del> </del>	1			QGSTPLDVAAASVIDNNELALALQEQDLEKV
1	1	1				VSYLAGCGLQSCPMLVAKGYPDIGWKPCGG
1		1	1		l	ERYLDFLRFAVFVNGESVEENANVVVRLLIR
j	1	j	ļ	1	1	ERYLDFLRFAVFVNOESVEDIVANV VIGEBAR
Ī	1	1	1			KPECFGPALRGEGGSGLLAAIEEAIRISEDPAR
	1	1	İ	1	ì	DGPGIRRDRRREHFGEEPPEENRVHLGHAIMS
		1	ĺ			FYAALIDLLGRCAPEMHLIQAGKGEALRIRAI
		1	1		1	LRSLVPLEDLVGIISLPLQIPTLGKDGALVQPK
	Ţ	1	]		1	MSASFVPDHKASMVLFLDRVYGIENQDFLLH
1	1	1		1		VLDVGFLPDMRAAASLDTATFSTTEMALAV
1		1		1		NRYLCLAVLPLITKCAPLFAGTEHRAIMVDS
		1				MLHTVYRLSRGRSLTKAQRDVIEDCLMSLCR
	1	-		1		YIRPSMLQHLLRRLVFDVPILNEFAKMPLKLL
1		1	1	1	1	TNHYERCWKYYCLPTGWANFGVTSEEELHL
				1	1	TRKLFWGIFDSLAHKKYDPELYRMAMPCLC
		1	1	1		ALAGALPPDYVDASYSSKAEKKATVDAEGNF
			Į.			DPRPVETLNVIIPEKLDSFINKFAEYTHEKWAF
						DKIQNNWSYGENIDEELKTHPMLRPYKTFSE
1						KDKEIYRWPIKESLKAMIAWEWTIEKAREGE
1		-	1	İ		EEKTEKKKTAKISQSAQTYDPREGYNPQPPDL
}	}		1	1		SAVTLSRELQAMAEQLAENYHNTWGRKKKQ
			į.	l	ļ	ELEAKGGGTHPLLVPYDTLTAKEKARDREKA
			ŀ			QELLKFLQMNGYAVTRGLKDMELDSSSIEKR
		Ì		İ		FAFGFLQQLLRWMDISQEFIAHLEAVVSSGRV
			ì			EKSPHEQEIKFFAKILLPLINQYFTNHCLYFLS
			Ì	1		TPAKVLGSGGHASNKEKEMITSLFCKLAALV
	1					RHRVSLFGTDAPAVVNCLHILARSLDARTVM
	İ			Į	1	KSGPEIVKAGLRSFFESASEDIEKMVENLRLG
		ľ				KVSQARTQVKGVGQNLTYTTVALLPVLTTLF
	1	ł	1	Ì	1	QHIAQHQFGDDVILDDVQVSCYRTLCSIYSLG
		- 1	ł	1		TTKNTYVEKLRPALGECLARLAAAMPVAFLE
		1	1			PQLNEYNACSVYTTKSPRERAILGLPNSVEEM
		1		]		CPDIPVLERLMADIGGLAESGARYTEMPHVIE
			ļ	l l		ITLPMLCSYLPRWWERGPEAPPSALPAGAPPP
			Ì		Ĭ	CTAVTSDHLNSLLGNILRIIVNNLGIDEASWM
1		1	Ì			KRLAVFAQPIVSRARPELLQSHFIPTIGRLRKR
	1	-				AGKVVSEEEQLALEAKAEAQEGELLVRDEFS
		İ				VLCRDLYALYPLLIRYVDNNRAQWLTEPNPS
						A FEI FRAVGEIFIYWSKSHNFKREEUNFYYU
-		1	1			NEINNMSFLTADNKSKMAKAGDIQSGSDQE
			j		I	RTKKKRRGDRYSVQTSLIVATLKKMLPIGLN
1		1	1		1	MCAPTDODI ITLAKTRYALKDTDEEVKEPUH
1	] '		1	1		I NEW UT OCK VEGSPSLRWOMALYRGVPGREE
1				ĺ		DADDPEKIVRRVOEVSAVLYYLDQTEHPYKS
				1		VKAVWHKI LSKORRRAVVACFRMIPLYNLI
	}	1		- 1		TUD A CNIMEL ESYK A A WILTEDHSFEDRMIDL
	1	1				I SKAGEOFFFFFFFVEEKKPDPLHQLVLHFSK.
	1			1		AT TEKSKI DEDYLYMAYADIMAKSCHLEEG
						CENCEARREVEVSFFEKOMEKORLLYQQAK
İ	1	1	ł			TTTD CAAEMVI OMISACKGETGAMVSSILKL
1						CIGIT MCGNAFVOOKMLDYLKDKKEVUFFU
						LIDALMOTCSVLDLNAFERONKAEGLUMVNE
}	-	l	1	1		DCTVINDONGFKVMADDEFTODLFRFLQLLU
	}	-				ECHNINDEONYL RTOTGNTTTINIIC IV DYLL
		1		1		DI OFGISDFYWYYSGKDVIEEOGKKNI SKAW
			1		1	CVAROVENSI TEYIOGPCTGNOQSLAHSKLW
	ľ	1	I			
						DAVICEI HVEAHMMMKLAODSSQLELLKEL
						DAVVGFLHVFAHMMMKLAQDSSQIELLKEL LDLOKDMVVMLLSLLEGNVVNGMIARQMV
						DAVVGFLHVFAHMMMKLAQDSSQIELLKEL LDLQKDMVVMLLSLLEGNVVNGMIARQMV
						DAVICEI HVEAHMMMKLAODSSQLELLKEL

			CEA	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	ì	1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ	1	Ì	residue of	sequence	/=possible nucleotide deletion, \=possible
		}	1	peptide		nucleotide insertion
	1		1	sequence		OFLLSCSEADENEMINCEEFANRFQEPARDIG
			T			FNVAVLLTNLSEHVPHDPRLHNFLELAESILE
					1	YFRPYLGRIEIMGASRRIERIYFEISETNRAQW
		i	1		1	YFRPYLORIEIMOASRCIER IT EISE ITTEL TO
	1	1	į	Į		EMPQVKESKRQFIFDVVNEGGEAEKMELFVS
	1		1			FCEDTIFEMQIAAQISEPEGEPETDEDEGAGA
	Į.		1	1	Ì	AEAGAEGAEGAAGLEGTAATAAAGATARV
	1		ł	}	1	VAAAGRALRGLSYRSLRRRVRRLRRLTAREA
	1	1	ļ			ATAVAALLWAAVTRAGAAGAGAAAGALGL
	1	}			ļ	LWGSLFGGGLVEGAKKVTVTELLAGMPDPT
1		ļ		1		SDEVHGEQPAGPGGDADGEGASEGAGDAAE
ļ	1		1			GAGDEEEAVHEAGPGGADGAVAVTDGGPFR
Į.						PEGAGGLGDMGDTTPAEPPTPEGSPILKRKLG
		1		1		VDGVEEELPPEPEPEPEPELEPEKADAENGEK
			1			EEVPEPTPEPPKKOAPPSPPPKKEEAGGEFWG
			-			ELEVORVKFLNYLSRNFYTLRFLALFLAFAIN
		1		Į.	1	FILLFYKVSDSPPGEDDMEGSAAGDVSGAGS
	1	1		1		GGSSGWGLGAGEEAEGDEDENMVYYFLEES
1	1	-	1			TGYMEPALRCLSLLHTLVAFLCIIGYNCLKVP
		İ	1			LVIFKREKELARKLEFDGLYITEQPEDDDVKG
	1		ľ		1	OWDRLVLNTPSFPSNYWDKFVKRKVLDKHG
1		}		ł		DIYGRERIAELLGMDLATLEITAHNERKPNPP
						PGLLTWLMSIDVKYOIWKFGVIFTDNSFLYLG
	ì	1				WYMVMSLLGHYNNFFFAAHLLDIAMGVK1L
				1		PTIL SSVTHNGKOLVMTVGLLAVVVYLYTVV
	i	ł	İ			AFNFFRKFYNKSEDEDEPDMKCDDMMTCYL
		}			ł	FHMYVGVRAGGGIGDEIEDPAGDEYELYRVV
		-	ļ			FDITFFFFVIVILLAIIQGLIIDAFGELRDQQEQV
1		İ			·	KEDMETKCFICGIGSDYFDTTPHGFETHTLEE
	-		1			HNLANYMFFLMYLINKDETEHTGQESYVWK
	ļ		- 1			MYOERCWDFFPAGDCFRKQYEDQLS
				1.5	665	VIVATYCOLIFDKGAKTIO*PFQQIAL/CKRMK
501	1851	A	3869	467	002	LGPCFTPCGKINSEWIRELSVRVKTIKHLEIGV
		1	1			N
						SGMQWRDLTPLQPLPPRFKQFSCLSLPGSWD
502	1852	A	3888	1042	724	YRHAP\PLLTNF\*FLVEMGFCYVGQAGRKLL
	1	l	J	}		ASSDQSALASQSAGITGISTAPGPPFFFLNFEA
{		1	i			GSCSVAQAGVQ
			_	_i		EVDSQSGVQ*QAPGSLQLQTPGLK/VSCLLSR
503	1853	A	3891	1773	1193	QDYRSSLPHLASCCYYYYYY/VFL*RRGLTTL
		1	1			VQGGLKLLPSSNPFASAP*TAGITGMSHCAGP
		i		1		HFNF*MFRKISCIRE*F*HTRIYDIPFLILFFKET
		1		1		HENE WERKISCIKE TO THE TOUT COUNTY
			1	İ	1	WVLLCYPGWPQIPGLKPSSCLRLLSSWDHRC
		-				APPCPASFFIFHVDRVSPPCPGLVSITFKMLLL
1			1			L TROPAGE A FRA
504	1854	В	3896	279	70	MVSKSKSILMSYNHVELTFSDMKKMPEAFRR
504	1034	P	3070	1		TQKHTTYLIPYQVIFWSTGKDAMRSFMMPFY
		J		1	1	QKEYYENQ*
<u></u>	_		2000	2	1396	EPGVPTKKTWFDKPDFNRTNSPGFQKKVQFG
505	1855	Α	3899	-	1370	NENTKLELRKVPPELNNISKLNEHFSRFGTLV
		1			-	NI.OVAYNGDPEGALIQFATYEEAKKAISSTEA
				1		VI NINRFIK VYWHREGSTOOLOTTSPKVMQPL
						VOOPILPVVKOSVKERLGPVPSSTIEPAEAQS
1	1	- 1				ASSDLPQVLST\LLA*QKQCIIQLL/WKAAQKT
-						LLVSTSAVDNNEAQKKKQEALKLQQDVRKR
						KOEILEKHIETOKMLISKLEKNKTMKSEDKAE
			-			IMKTLEVLTKNITKLKDEVKAASPGRCLPKSI
1	1	1				KTKTQMQKELLDTELDLYKKMQAGEEVTEL
			1	ì		KIKIQMQKELLDIELDLIKKIQAGED IED
				Ì	ĺ	RRKYTELQLEAAKRGILSSGRGRGIHSRGRGA VHGRGRGRGRGRGVPGHAVVDHRPRALEIS

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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Assertic Acid F=Glutamic Acid,
O of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	1	in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
1	uence	ļ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
eq-	balee		914	ng to first	acid residue	Q=Glutamine, K=Arginine, 3-3ct inc,
ence			-1-	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ		1			/=possible nucleotide deletion, \=possible
		]	1	peptide		nucleotide insertion
	1		ļ	sequence	ļ	ACTES DE DI L' PHEAOYGEIED COLDUS SILHA
			T -		ļ	VITEKTRAEAEAAAVHGAREKGQDLKLAWN
	1	1	1		ļ	KPVTNISAVETEEVEPDEEEQREIIIA
	1	1	1	1		DAELSGTLSLVLTQCCKRIKDTVQKLASDHK
	1856	A	3911	1952	919	DAELSGILSLVLIQCCKRRDIVQIDGCWOA
06	1830	1 ^	3211			DIHSSVSRVGKAIDKNFDSDISSVGIDGCWQA
	ŀ	ì	1	1		DSQRLLNEVMVEHFFRQGMLDVAEELCQES
	1	ì				GI SVDPSOKEPEVELNRILEALKVKVLRPALE
					]	WAVENDEMI IAONSSLEFKLHRLYFISLLMO
	1	ļ	}		1	CTTNODE ALOY AKNEOPE ALNHUKUIQ V LIVI
		{				L COLVET DOCIENSPYVHILLDANUWADICUITI
	ì	ł	l			RDACALLGLSVESPLSVSFSAGCVALPALINIK
	1	1			1	KDACALLULS VESTLS VSFSAGO VEST NEXT NEXT NEXT NEXT NEXT NEXT NEXT NEX
	1	1				AVIEQROCTGVWNQKDELPIEVDLG*KSAGY
		1		1	1	USIFACDII ROOTTONNPPMKLVCOMISKUM
	1	1	1	[	1	I NIV MENICSKI KCPYCPMEUSPUDANQUII
		_			<del>                                      </del>	CUDECD A PCICPID A PPPI PRPSKGLGHPU I AUA
507	1857	A	3936	439	18	PGSGARCHPPSTCSPSWASPG*GAKASPALPK
,,,	1				1	SHGVTLLCKAQAHLCRGEDSKDASGSTSQA
	ĺ		•			WEPG*GAWGMPRCQGPALGSCFCPPGTTVQ
		ł	1			WEPG-GAWGMFRCQGFAEGGGG
		İ	1			RPAKQRDKRNRHLGR
		<del></del>	3944	120	412	WCPAGTLDFPGPQEMVLLEIEVMNQLNHRNI
508	1858	Α	3944	120	1	TOT VA A TETPHETVI FME (YECPK*W*GLGGGG)
	Í	1	1	1	<b>1</b>	TRHGASRGGVCAHSIEGGELFERIVDEDYHL
	I	1	1	İ		LEV
	1	1	1			TELTPERPEKGROVI SVLLMMI*KCRVIFVKI
509	1859	A	3949	31	392	MVFFLQNFC/RIILNVA\WTGD*PNTL*KEQRO
309	1037	1 **			J.	MVFFLUNFURIENVALVELIKNRYID/ERN
	ł	1	1		•	ITFSDSKS*YKATKIKTMWYCHKNRYID/ERN
	1	- 1	1		ŀ	RIEIPEINPCICDKIIFRKLSMTTQ
				1013	885	FSETRACCPRLEHSGRIEAHCSLNIPGSSDPPT
510	1860	A	3954	1013	003	LACCVAATTG
		<u> </u>			1054	DDAWADR SPITIWAPTSGRHPCRAALPWS155
511	1861	A	3956	1	1034	DWODSEKOPPPPAHRGPADSLSTAAGAAELS
		ì				AEGAGK SRGSGEODWVNRPK I VKDILLALI
		1	1	1		QHGHSGPFESKFKKEPALTAVARTARKRKPS
	1	}			}	PEPEGEVGPPK\TTERPSRGCPHPQRGSRSP*I
		1	1		ļ	PEPEGEVGPPK/TTEKPSKOCITH QAGOANDISP
		ì		l		LHPLLCLRHHPLPHLIPTGPHRLKRPRM\P\SP
			-		1	MAALILVADNAGGSHASKDANQVHSTTRN
	1	1				CNICDDCDCSMNORRI.GPREVGGOGAGNIGO
	l l	1		1		EDITIDASI POSSI ATSAPLCU LUHERUEDI
		1				FUCCBENDSHIKECEPCSROSIKOOGASOE VI
	1	l		1	1	PSGEKCPLVGSNVPWAFMQGEIATILAGDV
		1	-	ì		MAKEDDE
	1		1	1	L	VKKERDS  VKKERDS  VKKERDS
		<del></del>	3957	1086	3	QDRARLDCSSATSAHCNLRLPGS*DSPASAS
512	1862	Α	1 2531	1300	1	I VACTTOTHHHTWI.ILGSSVOIGFURVOQA
		l		1	1	I TELL TECHOPPISASESAGIMGMONUV WE'S W
	1	ļ		1		T CUTLINA PROGRAGGE ARGTPGPEQSEW NUSC
1	1	1	l	j		UI*DDCOVDS*LMTOL/FWGRHUYNPIMARO
!	1	1	(	1		LRHREACSLPLPGEGEPGLQPSS\*SQNPCSS
ļ			l	1		FHHGL*AWLWCPELLLQGQARRH*RSPPS/F
			- 1	1		FHHULTAWLWCFELLLQUQAIGGI ROLL AND AL
1	1	l			l	CPATLSLTAWSQTKRLRSQFLLLPWL*RAL*
1	l					- I DD/CHWDSRRSI GDPLLPRSUG*KUG1*A511
1		1	1	1		CVE*DTECHI VANAGVOWRDLUSLUPPUR
1	1	1				K\RFSRLSPPSSYTHRYVPSHLAESCISSRDR
1		1				PSRPDRSRNSNSLSR
!		1		1	1	LOKLDKOKIJIJOPUK CV CIVDBCCVI
L			3961	3038	476	VALTTSMCCNKQVIVIDKIKSASIADRCGAL
513	1863	A	3901	3036	1	VCDUII SIDGTSMEYCTLAEATUFLANT IDG
1	l			i		VIVI EII DHHOTRI ALKGPDHVKIQRSDRQL
ı	ı	1	1			TUDOW A SNHSSLHTNHHYNTYHPDHCK V PA
1		i		1		TOO WAS A VICE PER TEMS A VSI SSI
			1		1	TEDV A DODNEDDAT VASAFAFTAMAAT 102002
			Ì			TFPKAPPPNSPPALVSSSFSPTSMSAYSLSSL MGTLPRSLYSTSPRGTMMRRRLKKKDFKSS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	(	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	}	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
ence		Ì	914	ng to first	acid residue of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		İ	peptide	sequence	/=possible nucleotide deletion, \=possible
	1	1		sequence		nucleotide insertion
	ļ	<del> </del>	<del> </del>	sequence		SLASSTVGLAGQVVHTETTEVVLTADPVTGF
			İ			GIOLOGSVFATETLSSPPLISYIEADSPAERCG
		1			1	VLQIGDRVMAINGIPTEDSTFEEASQLLRDSSI
		}				TSKVTLEIEFDVAESVIPSSGTFHVKLPKKHN
	Ì	1				VELGITISSPSSRKPGDPLVISDIKKGSVAHRT
		1		1	1	GTLELGDKLLAIDNIRLDNCSMEDAVQILQQC EDLVKLKIRKDEDNSDEQESSGAIIYTVELKR
	1				}	YGGPLG\ITISGTEEP\FDL*IISSLTKGGLAERT
	1			1	1	GAIHIGDRIL\AINSSSLKGKPLSEAIHLLQMAG
	ì	1			1	ETVTLKIKKQTDAQSASSPKKFPISSHLSDLGD
		l				VEEDSSPAQKPGKLSDMYPSHGCPSVDSAVD
			į			SWDGSA\IDTS\YGTEGT\SFOASGY\NFNTYD
	1	1				WRSPKORGS\LSPVT\KPRSQTYPDVGLSYED
		ļ		1		WDRSTASGFAGAA\DSAETEQEENFWSQALE
			1	1		DLETCGQSGILRELEATIMSGSTMSLNHEAPT
						PRSPAGSDRPSFQERSSSRPHYSQTTRSNTLPS DVGRKSVTLRKMKQEIKEIMSPTPVELHKVT
					1	LYKDSDMEDFGFSVADGLLEKGVYVKNIRPA
		1				GPGDLGGLKPYDRLLQVNHVRTRDFDCCLV
		1				VPLIAESGNKLDLVISRNPLASQKSIDQQSLPG
	1	1	]			D*SEONSAFFOOPSHGGNLETREPTNTL
	1000		3967	833	800	LEKOGVSGMATKRLARQLGLIRRKSIAPANG
514	1864	A	3907	033	000	NI GRSKSKOLFDYLIVIDFESTCWNDGKHHH
	}	]		}		SQEIIEFPAVLLNTSTGQIDSEFQAYVQPQEHPI
		1				LSEFCMELTGIKQAQVDEGVPLKICLSQFCK
		ļ				WIHKIQQQKNIIFATGISEPS/DF*SKIMCICYL
	j			l		VR*RISYTY*SKHKSKGC CRFWGISTHCDTCDPLSPQTTEG**EGDLWSL
515	1865	A	3969	492	182	DLLGPEFLARKPLFKTKTYQSTF*SISKNE/FTC
1		1			{	PNFIIEEGTDLIF/*QVKHNPCHRLTPEEGTVQL
						NRADS
			3977	12	1357	KMI C/OKESNYIRLKRAKMDKSMFVKIKTLGI
516	1866	Α	39//	2	1557	GAFGEVCLARKVDTKALYATKTLRKKDVLL
ĺ		1		\		RNQVAHVKAERDILAEADNEWVVRLYYSFQ
		-		j		DKDNLYFVMDYIPGGDMMSLLIRMGIFPESL
1		1				ARFYIAELTCAVESVHKMGFIHRDIKPDNILID
		1			}	RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA
		1		1		RODSMOFSNEWGOPSSCRCGDRLRFLEIGGGG ROHORCLAHSLVGTPNYIAPEVLLRTGYTQL
				1		CDWWSVGVILFEMLVGQPPFLAQTPLETQM
}	}	}			1	KVINWOTSLHIPPOAKLSPEASDLIIKLCRGPE
}				1		DRI GKNGADEIKAHPIF*NOFDFSQ*PEDSRS
		Į.				AFK OFP*NHTTPTDTSNFDP\VDPDKLWSDDN
	}	ł		İ	1	FEENVNDTLNGWYKNGKHPEHAFYEFTFRRI
		- 1				FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDL
		1				QNTGSEIKNRDLVYV
517	1867	- A	3980	1358	1022	FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY
311	1007	1 '				VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD
1			İ	]		*RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA
						QAIFQPQPPKVLGLQV SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F
518	1868	A	3986	974	666	SPEMESHPTIQAGVQWHALSSLQFLFTGFK T SCFSLPE*LGYRHVPPCLANSVFSVEMGVFLH
						VGQAGLELLTSGDLPALASQSAGITG\SHRAR
		Į				PENGFENIF
					126	NOGLRHVGLCRTCLVNQMFASSILGKSHHHS
519	1869	A	3994	751	126	LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC
1					}	DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS
		- 1				ORGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV
1						HLFSSEMGE\NRPMVG\ARHVYSNAALLSFTP
			1	1	1	

			· · · · · · · · · · · · · · · · · · ·	5 1 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid F=Glutamic Acid,
10: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I=Isoleucine K=Lysine L=Leucine,
otide	seq-	ļ	USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience		į	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		{		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	,	į .	1	peptide	,	/=possible nucleotide deletion, \=possible
	1			sequence	i .	nucleotide insertion
	<del> </del>	<del>                                     </del>	<del> </del>			LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI
		İ				AHVFADLLLITLPSYYIPFC
520	1870	A	3999	882	698	QSFRLSLLSSWDYRHM*PRLANF*TVFCRDR/
320	10,0	''		İ		SLALLPRLVSNSWPQAILPPRPPKVLGLQT FFF*ETVSCSAS*AGVRSHDNSSLQPPSPG\SSN
521	1871	A	4011	1346	1178	PPTSASHVAGATGTHHHAWLLSV
J2.		İ				QGIALLTRMGESVKHVTGGYKLRTRPLEFAA
522	1872	A	4015	2	377	IGDYLDTFALKLGTIDRIAQRIIKEEIEYLVELR
J-2						EYGPVYSTWSALEGELAEPLEGVSACIGNCST
		1				AL *ELTODMTEDELEVLREYILYSDSMK
						ERVIHNQIQQAQRSPHIFNARRSS/PRPNIVELP
523	1873	Α	4018	341	19	KVKEVCKTSKS/GQVIYKGVSIRLRANFLAEP
					1	L*NRREWDEAIKVLKEKQ\FLSKMVYPANLSF
		Ì	-			CNECDITSEPAK
				1.000	743	FET DWSL /DSVAOAGVKWCNLGSLQAPPPGF
524	1874	A	4020	1067	143	TPESCI SLPSSWDYRHPPPRLAN*LINFLCF**
	1					RQGFTVLARMVLIS*PHDLPASASQSAGITGL
						CUCCIVPTSSIIS
				701	351	OF PVIFFEL RRSHSVAOAGMOWHDHSLLQPL
525	1875	A	4021	781	331	DDDI KO/E/SHI SPPSIWDYRRVPPCLVNF3IFF
	1				<b>\</b>	I VETOSCOPCI OLI GSSNPPASASOSAGLAGISH
						QGQPE*SFDIRFACVIAALRETFQCLCSASRVN
	Ì	- [				I NIZ IIND PTHPVESSE
		<del></del>	4024	80	341	TPSSTSRGTEEOOSSKMAWORREEKEHLNYK
526	1876	Α	4024	80	1 3 1.	RSSAEDGWKADKP/VDG*TPGEDHLP1PSPFQ
1					-	T HTH SSESOL HHSVK SPPSLSFRLM
	1877	A	4026	593	230	DFYLYPERKKRGQMMTAVSLTTRPQESVAFE
527	18//	^	4020	1 3 3 3		DVAVYFTTKEWAIMG\PAERALYRDVMLEN
						YGGCGPL*CHPTSKPALVFS\LEQGKESCFSPA
	- [					TGSSLSRNDWRAGWIGYLELRRYTYLS
528	1878	A	4028	1160	242	GTSELLCIQRWNWGPAFPPRPGLALAPTLQLL
320	10,0	1.	1020		Ì	VEMGSAKSVPVTPARPPPHNKHLARVADPRS
l	.			1	1	PSAGILRTPIQVESSPQPGLPAGEQLEGLKHAQ
						DSDPRSPTLGIARTPMKTSSGDPPSPLVKQLSE
			İ			VFETEDSKSNLPPEPVLPPEAPLSSELDLPLGT QLSVEEQMPPWNQTEFPSKQVFSKEEARQPT
i		ì	1	1	1	ETPVASQSSDKPSRDPETPRSS\GSMRNRWKP
i i	1	ł				NSSKVL\GKSPLHPSCQDDNSPGTLTLRQGKA
1	1	l			1	AFKPLSENVSELK\EGA\LGTGR\LLKTEGRA
		ļ		İ		WEQGQD\HDKENQHFPLVES
						KDMVLIMEMQSMITMKCPQYL*E*RKIPDITE
529	1879	A	4039	2	366	CW*GCGSTGILIFC/WS*PL*KTI*QPR*FKQI*7
1		1				ILTIIYSIM*EHTFHNAGV*LSDIYPRFMKGYV
						HTEICT*MFIAVLFVVVKTWKQF
						LLEVNGNTIVTVFTKAQNKKNKGSRSILFKQI
530	1880	A	4057	358	3	RKYGSRINLLKSKHDKNICTENYKT*MKEIEA
		1				/DTDKWKDILCSWIRRIHMKDILCSWIGRTHV
}	Ì	ł	1			VKISILPKVNYRFYLISIKIIMAI
1						TOGTEEIYKISSCEWVQASFSTPLITLHDFKIY
531	1881	A	4061	50	278	HKATVIKMVWYWHRQ*KFSKN/RIESSEIEPH
1						IYDQFIFDKGEKIIQEKGNSFFNN/MCWKNWI
						T*KR
		1				NDLLENFKFWE*FKE*LENINGTVTEKETGG
532	1882	A	4069	19	368	YKELSSPKYSGTRQFYGQTISNFPGKIISMYY
				)	[	KLFQNTE/TEGRHPISLYEFRITLITIPNKDNIY
ļ						QIWMPVSLMNIVTLKCPT
	j	1				PIRKFTKVAG*KSNTPK*LAFLHINNEQFENK
533	1883	A	4076	1	355	ITNUPFIIASKRIK YSGISLTKEMKDLYTETLL
1 223	1 -000	1				KIKEDTNKWKDI/SCFWVGR/LNIVKMPK/VI
				1	1	I K IK HIJI NK WKIJI/JUF W Y ULVULILI I LUTI I L

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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	amino acid	1 F 1	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	}	residue of	sequence	/=possible nucleotide deletion, \=possible
		ļ	Ì	peptide	İ	nucleotide insertion
			<u> </u>	sequence	ļ	IFNAIPIKMPMMCMAKIEKNSS
					1021	IIDSSTRRMESERSPLYRQLIDLGYLSSSHWNC
534	1884	Α	4088	3	1931	GAPGQDTKAQSMLVEQSEKLRHLSTFSHQVL
						QTRLVDAAKALNLVHCHCLDIFINQAFDMQR
,	1	{			ļ	DLQITPKRLEYTRKKENELYESLMNIANRKQE
		,				EMKDMIVETLNTMKEELLDDATNMEFKDVI
l ,		1				VPENGEPVGTREIKCCIRQIQELIISRLNQAVA
·		1		1		NKLISSVDYLRESFVGTLERCLQSLEKSQDVS
		1	1	}		VHITSNYLKQILNAAYHVEVTFHSGSSVTRM
		1	1	ľ		LWEQIKQIIQRITWVSPPAITLEWKRKVAQEAI
ĺ					1	ESLSASKLAKSICSQFRTRLNSSHEAFAASLRQ
ĺ					İ	LEAGHSGRLEKTEDLWLRVRKDHAPRLARLS
(						LESRSLQDVLLHRKPKLGQELGRGQYGVVYL
[	ĺ					CDNWGGHFPCALKSVVPPDEKHWNDLALEF
			1			HYMRSLPKHERLVDLHGSVIDYNYGGGSSIA
1						VLLIMERLHRDLYTGLKAGLTLETRLQIALDV
1	1					VEGIRFLHSOGLVHRDIKLKNVLLDKQNRAKI
		Ì				TDLGFCKPEAMMSGSIVGTPIHMAPELFTGK
l'		1				YDNSVDVYAFGILFWYICSGSVKLPEAFERCA
	31	1				SKDHLWNNVRRGARPERLPVFDEECWQLME
]		1	1.	}		ACWDGDPLKRPLLGIVQPMLQGIMNRLCKS\
ļ						NSEOPNRGLDDST
535	1885	A	4090	2	417	ALMPHEANYEEIFLKTDKDMDGFESGLEVRE
333	1007	1^	1000	1		IFLKTR/GLPSTLLAHIWALCDSKDCGKLSKD
		1				HFALAFHLIT\QKLIKGIDPPLVLTPEKISPSNR
1				İ	1	ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK
		1				HNRKRIWLRA
536	1886	A	4102	569	829	DHQK*KNIPCSWIGRINIVKMSILPKAIYRFSAI
330	1000		1			PIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK
}	}	1		1		EQNLEESHYLDFK*YYRAV
537	1887	A	4104	54	281	SIDCEHLIRRMLVLDPSKRLTIAQIKEHKWML
337	100.					IEVPVQRPVLYPQEQENEPSIGEFNEQVLRLM
1		}		1	·	HSLGIDQQKTIE
538	1888	1 A	4109	141	314	IRHIPLKIRSVVSHLKCFYKFILTFFFAGCSQPL
550						VPRENITAWMNAIGLIITALPVS
539	1889	A	4111	268	1	ASRPWGHSYP*FNQQEVDTLKRPIASSEI*MM
***				ļ		I*KFAT\KKSPGPYRFTAEFSHTFKEDLVPILW
	1			_		PLFPKIYREGTLPHSFYEASITL
540	1890	A	4142	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE
		1				AALGDFLGLHRRTQQPAVDRLLSDASAQWR
		1				VRGHGGVRESGRAPQQPGRRRGRRPRKRPR
		}	1			GRWRREGCGAGGRGVCVAAWSQRSIAGNN DYRLFHKMSNSHPLRPFTAVGEIDHVHILSEH
1	1				1	IGALLIGEEYGDVTFVVEKKRFPAHRVILAAR
		1				IGALLIGEEYGDVIFVVERRRPPAHRVILAAR   CQYFRALLYGGMRESQPEAEIPLQDTTAEAFT
		1		1	1	CQYFRALLYGGMRESQPEAEIPLQDTTAEAFT MLLKYIYTGRATLTDEKEEVLLDFLSLAHKY
						GFPELEDSTSEYLCTILNIQNVCMTFDVASLY
		1	1			SLPKLTCMCCMFMDRNAQEVLSSEGFLSLSK
	i	İ				TALLNIVLRDSFAAPEKDIFLALLNWCKHNSK
		1				ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSP
		}		ì		DAILDAIKVRSESRDMDLNYRGMLIPEENIAT
		1				MKYGAQVVKGELKSALLDGDTQNYDLDHG
	1					FSRHPIDDDCRSGIEIKLGQPSIINHVRILLWDR
	i	1				DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS
1			1	1	1	DOVO 19 ILIE A OMPTED MAK AIDIIO LICKS
1			1		ļ	UNDER VEDAR VCR VIR IVGTUNI VNK IFHI VAF
						WQKLYFPARVCRYIRIVGTHNTVNKIFHIVAF
						ECMFTNKTFTLEKGLIVPMENVATIADCASVI
						ECMFTNKTFILEKGLIVPMENVATIADCASVI EGVSRSRNALLNGDTKNYDWDSGYTCHQLG
541	1891	A	4146	282	778	ECMFTNKTFTLEKGLIVPMENVATIADCASVI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		i	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		}		peptide		nucleotide insertion
				sequence		HAESENFAFWQDMKWKNKFWGKSLEIVPVG
		1	}		ĺ	TVNVSLPRFGDHFEWNKVTSCIHNVLSGQRW
		1				IEHYGEVLIRNTQDSSCHCKITFCKAKYWSSN
				Į.		VHEVQGAVLSRSGRVLHRLFGKWHEGLYRG
			1			PTPGGQCIWKP
		<u> </u>	1	1	433	SVDAYVCNDIVFSYRTTITLLEGA*LTHRYVA
542	1892	Α	4147	44	433	QDPKQGQLRSLHLTCDSAPAGSQGTWSTSCR
						INHLIFRGGAQITFLATFDDSPKAVLGDRLLLT
		1	1			ANVSSENNTPRTSKTTFQLELSVKDAVYTVV
		1				SSH
		ļ	1152	(70	11	TISYPQCLTQMYFLISFANVDTFLLPIMALDH
543	1893	A	4153	678	' '	YVAICSALO*CSITTP/ELCQGLPVLA*AGSSLIS
	1					PVHTVIMSRLAFCSSAQISHFYRDAYLLMKIA
			İ			CSHT*\NQHVFLGAVVLFLAPCALILVSYIRIA
		1	i	1		AAILRIPSPTRRRKACSICSSHLSLVTLFYGTV
			1			LGICI*PPDSFSAQDAIATIMYTVVTSMLNPFIY
		1				SLMNKEVQEAVRRLFSRGSHSSWCW
	1894	A	4158	3	538	LLYAQAGVQ*LNLSSLQPQPAGLKQSSHPSLP
544	1894	^	4130			SSWDYRYSTPHPANFFVEMEFHHVAQAGLEL
		1		ļ		LGSGDLPTSTSHSAGITGV\SHHAPPRLISSEGS
		-				LLGHLLCLPMVFPLLCVFVLISSSLAGEEAAG
				İ	1	LRVQKLWPAVVLSHLPVCWFHCSGIWSEVIE
			l	1		LKVGREGHVLPWQAHVVEF
545	1895	A	4160	1	412	HPLGLGLVPSEIFSPQDKKAADGSILAPARGE
3,3	1075					DLEAGLKGSFMDGRLQASVSVFRIQRVGSAM
ŀ			1			QDTASAMPCLPYYPTSHCFMAGGKSRSQGW
1			}			ELELSGEPAPGWQVLAGYTYTQARYLRDASE
-	1	1		1		ANVGQPLRPVDPR FFQVFIFLFLIFFKTEFHSCCPGAVQWHDLDSL
546	1896	A	4174	1252	1190	OPPPRFKGFSCLSLPSSWDYRHAPAHPANFV
		ł				FLVETGFLHV\GQ\ASLELPTSGDTPAS\ASQSA
ļ					1	GITGVSHHA*PRASGRRCW
			<del></del>	12020	1	AGPDGLAAPASCQGARGQTRVPGAFSWLAP
547	1897	A	4176	3029	1	GSHHASEGLAPGVPPAGGVSAQELTAPPQEG
<b>{</b>						WGLGAPPAAPRPESDEKRAGSDAVRSFSRGA
					!	RDSLGQRRLGGTRGAGPAGKGAQRTMGPAS
		1	ł	İ	Ì	GEHSEPPRPHOEPSPRSSCWOHLLWHCPWPQ
				1		PSRLPRLTPAOLLOGPGVLAAPPGP*HVPGFL
		1				AOSPWPLPSGPRSP*DPLHQGALVPLPQGGSP
					1	HTAPHCLPSVLSPAIQQPLLPTAST/SSRSPPAS
	1			<u>}</u>		TMAPIPSALAVWEPAGSSPOLSSAPADSSVPLP
	ŀ		ĺ			ALPKVLPPWTOKPLLGCLCOSPLPLLSPPDQI/
1				1		RCPPACSPAAASSFSFESQPCPSAPSKASPAPA
	ļ					AL\IVGPHHPP*SOQPQSQSVHPHGPGGPQPPL
					1	AASSLFWMFCQPPPPHPQFLWHRPLPVTGKA
[ .	1					LASYPLCFRPAPGSLRQTPLPPQFHIPRPGLSAP
1	1	-		-	ļ	PPPASGTSDSSDSRSPSASAARVWPPA\SPPPP
				1	Ī	AARHRPHPPEYFLSPCPFSCGFPRLLGRPRRPQ
	1				1	ALQTPRAWDLPPGSSPAPLCSGPELP*APPPLP
1	1		1	1	Í	PFPRVA*LGSGHPPSAQVPGLW*RCV*GHPIP
		- [				RPVGHS*SGPPHSPPL*APPQAWPLELPPSRQC
						LQPLHLRAAQPLDPCCSLSPPGPPLPVPALPS
		1				WPGRP*SPSPASSQPPYHAGLPGPQSSPLPPGL
r						PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ
1		1	1	l	1	PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL
		- 1	į	1	1	The second secon
						TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP
						TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP
						TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP

PCT/US01/03800 WO 01/57188

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-Aspertic Acid F=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
-pas	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	donoc		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uence	ļ		}	amino acid	of peptide	T=Threonine, v=valine, w=Ttypiophian,
			ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ì	peptide	<u> </u>	/-possible nucleotide deletion, \-possible
	1	l	1	sequence		nucleotide insertion
	<u> </u>	ļ	<del> </del>	3cquonec	<del> </del>	GTPASPGLGRSCLGKPQTLPWISFWPPSGRLA
	ļ	ł		}		PCTWOPW/PVSPAPLSCLSAWDPWELPSPQPQ
		1	ì			VCCTATI DTCCI I SSPGP\PAFOPPREGCL*GFF
	1	1	ì	1	ì	GPPGLPPLQSSLSFPPPPPPVPQPPAPPALQWG
		1	Ì		ľ	LUI DGGRTK
	Ţ	1	1		<u> </u>	RIHREEDFQFILKGIARLLSNPLLQTYLPNSTK
548	1898	A	4180	2369	844	KIQFHQELLVLFWKLCDFNKVGQPRGALQGD
346	1030	'`	1			KIQFHQELLVLF WALCDFIR V GQF KOLEQUE
		1	ì	1		GEQLPQ*PGGRDSVRLRGVGQSCPSLELSPLG
		1	1	]	ì	PSPHP*KFLFFVLKSSDVLDILVPILFFLNDAR
		ļ	ì	}	1	ADQSRVGLMHIGVFILLLLSGECNFGVRLNKP
	į	1				VerbypMDIPVFTGTHADLLIV\VFHKII13UHQ
i		Į	1	1	1	PLOPI FOCI LTIVVNVSPYLKSLSMV TANKLL
		1		1	1	UTITE A FOTTWFI FSAAONHHLVFFLLEVFNNI
		-	1		1	TOVOEDGNSNI, VYAIIRKRSIFHQLANLPIDPP
	i	1	- }	ļ		TILLY AT ORRESTPEPLSRTGSQGGAPPWRAFA
	1		Į.	ļ		DI DI OSOAPSRPVWWLLOALTS*PRSPRCQR
	1	ĺ		ļ		MAPCGPWNLSPSRAWRMAARLRGSPARHGG
		1	1	ļ		SSGDRP/HSSASGQWSPTPEWVLSWKSKLPLQ
		1		1	ľ	TIMRLLQVLVPQVEKICIDKGLTDESEILRFLQ
]	1		ł	1	ł	HGTLVGLLPVPHPILIRKYQANSGTAMWFRT
1	1.		1			HGTLVGLLPVPHPILIKK I QANSOTAMINI
	1,		ł	1		YMWGVIYLRNVDPPVWYDTDVKLFEIQRV
	<del></del>	A	4191	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKT
549	1899	A	4151	650		ALLQDGRRKVHYLFPDGKEMAEEYDEKTSE
1			1	1	1	TI VOK WRVK SALGAMGOWOLEVGUPAPLG
1	į.	1	į			A CNI GPELIKESNANPIFMRKDTKMSFQWRIK
			i		ļ	MIPVPKDVYSVSVDQKERCIIVKTINKKIIK
1		İ		1	ļ	L KECIPDI DRHOLPI DDALLSFA IPIAP
1			1		1000	TRHTGSDIAGVCGWLLLSGPCGVGLDLDSKLL
550	1900	A	4192	1	1980	CASAMPRIEVI AFESIVCLOKALNHLKEIWE
""	-				i	LIGIPEDQRLQRTEVVKKHIKELLDMMIAEEE
			1			SLKERLIKSISVCQKELNTLCSELHVEPFQEEG
1	l l	1	1			ETTILQLEKDLRTQVELMRKQKKERKQELKL
	1		ı			LQEQDQELC\EILCMPHYDIDSASVPSLEELNQ
i	1	- 1	l l			LQEQUQELCIEILCIVITITIDIDAN VI SELEZI
	1	- 1		1		FRQHVTTLRETKASRREEF/VSSIKRQIILCME
	l		1	}		ELDHTPDTSFERDVVCEDEDAFCLSLENIATL
1	1		•	1		QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW
	]					DDI OIPEEREAVATIMSGSKAKVRKVALQUE
		ļ		ļ		TODE FEI EVENTMERVIEARVELVUI WEVU
1	1					FVSOFOROAFAPFCAEDYTESLLQLHDAEIVK
1						I V V V V V V V V V V V V V V V V V V V
			Ì			LASIDENDETNEGGNILLKEEKORAKLOKMLP
1						VICEGI VARIFI WEOEHSKAFMVNGQKFME
			- [			YVAEQWEMHRLEKERAKQERQLKNKKQTET
1						EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT
1	Ì	1			1	EMLYUSAPKIPSKKULAFNII UKAIGENT
		1		1		TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK
1	-	l		- 1		PVAASTCSGKKTPRTGRHGANKENLELNGSI
				Į		LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS
1		i		1		DeetyGLORFLSKASKSDATSGILNSTNIQS
					1008	AUTURGI VSSPAIGAYLSASYGDSLVVLVATV
551	1901	A	4194	3	1000	UALI DICEIT VAVPESLPEKMRPVSWGAQISW
	Ì	1				LOADPEASI KKVGKDSTVLLVCII VCLSYLPE
						AG\QYSSFF\LYLR\QVIGFG\TVKIAAFIAMVGI
		1				LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML
1		- 1				LSIVAQIAFLSILMRSLUINGI TELEGEGI QINE
1			1	J		QLAWYGFGSQAWMMWAAGTVAAMSSITFP
1	1	- 1			i	AISALVSRNAESDQQGVAQGIITGIRGLCNGL
		1				GPALYGFIFYMFHVELTELGPKLNSNNVPLQ
						GAVIPGPPFLEGACIVLMSFLVALFIPEYSKAS
		1				GVQKHSNSSSGSLTNTPERGSDEDIEPLLQDS
l.	<b>3</b>					
			ļ		ì	SIWELSSFEEPGNQCTEL

SEQ ID No. of nucleotide peptide coiled sequence peptide coiled sequence coile					<del></del>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Solid countries   Section   Sectio	SEQ ID	SEQ ID	Met	SEQ	Predicted		D-Aspertio Acid F=Glutamic Acid
uence unce unce unce unce unce unce unce	NO: of	NO: of	hod	1		( '	E-Phenylalanine G=Glycine H=Histidine.
enice unice of 19496 of 19496 sequence of 19496 seq	nucl-	peptide	Ì	1			I-Isoleusine K=I vsine I =Leusine
uence    Second   Sec	cotide	seq-	1	USSN			Nandathionine Nanaragine Pappline
amino acid residue of sequence periodic sequence periodic sequence periodic sequence periodic sequence periodic sequence	seq-	uence	ł			1	O-Chutamine P=Arginine S=Serine
Sequence   Sequence	, .		ĺ	914	_	1	T. Therepine V-Valine W=Tryptophan
#possible nucleotide deletion, "possible nucleotide insertion sequence sequ		)	1				V-Turceine V-Unknown *=Ston coden
nucleotide ilsertion SQUINCE S		Ì	1			sequence	/ = resible evalentide deletion \=nossible
1902 A 4197 2 14302 RAPPPARGSRQÓKÇKAPGAAAAELROAR EPAPARRGTMADGGGEDEIGENTDDEVV LQCTATHKEQQKLCLAAEGFORNLCLEST SKNNYPEDISICTYLOGSISVBAUQEMLANT VEKSEGQVDVEKWEFMKTAQGGGHEDLIVANT VEKSEGQVDVEKWEFMKTAQGGGHEANT VEKSEGQVDVEKWEFMKTAQGGGHEANT VEKSEGQVDVEKWEFMKTAQGGGHEANT VEKSEGQVDVEKWEFMKTAQGGGHEANT VEKSEGQVDVEKWEFMKTAQGGGHEANT VEKSEGQVDVEKWEFMKTAQGGGHEANT VEKSEGQVDVEKWEFMKTAQGGGHEANT QGTLWSVAPISSGSEAAQGVLIGGDVLRLIH GHMDECLTYPSGEMGECRENTYPEGGAVS VHARSLWILETLRVAWSGHRWQOPFEL HVTTCKYLSLMEGHGEQRRTVYBEGAVS VHARSLWILETLRVAWSGHRWQOPFEL HVTTCKYLSLMEGHEADDGISLSRSQHEESEKTARVING VEKSELDVGVEKEVDGMGTSERKYGOS VEYIQHDVTGLULTYQSVDVXSVBMGSIQR KAIMHHEGHMDDGISLSRSQHEESEKTARVING VEYIQHDVTGLULTYQSVDVXSVBMGSIQR KAIMHHEGHMDDGISLSRSQHEESEKTARVING VEYIQHDVTGLULTYQSVDVXSVBMGSIQR VAIMHHEGHMDDGISLSRSQHEESEKTARVING VEYIQHDVTGLULTYQSVDVXSVBMGSIQR VAIMHHEGHMUNTQSVBUXSAMFAD VAGREAGESWKSILNSLYSLLAKHGRINGKUL VAING VAGREAGESWKSILNSLYSLLAKHGRINGKUL VAING VAGREAGESWKSILNSLYSLLAKHGRINGKUL VAING VAGREAGESWKSILNSLYSLLAKHGRINGKUL VAING VARFAGESUM VAING VARFAGESWKSILNSLYSLLAKHGRINGKUL VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VARFAGESUM VAING VA		1		1			=possible nucleoude deterion, \ possible
EPAPARRRGTMADGGEGEDE(OFLRTIDDEV)  LOCTATHKEQOKICLAAEGFORNICTLESI'S NSKNYPPDISICTITVLEQSISVRAUQEMLANI VEKSEGQVDVEKWKFMMKTAQGGGHRTILL YGHALLRHSYSGMYLCCLSTSRSSTDKLEGH OQLUSVSSERYHLISYGNGSLHVDAAF OQTLWSVSSERYHLISYGNGSLHVDAAF OQTLWSVSSERSEAAQGYLIGGDVLRLH GHMDECLTVPSGEHGEGRRTVHYEGGAVS VIARSILWRLETILAVAWSGHRIW WGOPFRLR HYTTGKYLSLMEDKNLLLMDKEKADVKSTA FIFRSSKEKLDWGVRKEVDGMGTSEIR YODS VCYIGHVDTGLWILTYQSVDVKSVBMGSIQ KAMMHEGHMDGISLSSRQHEESHTARVIRS THYELFINEFIRGLDALSKKAKASTVDLPIESYS SLODLIGYHHPPEHLEHDKONGRIKALKNR ONLFGEGMINLVLECIDRLHYYSSAAHFAD VAGREAGESWKSLINSLYELLAALIRGNRKN CAGPSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIKEGHIKSIISLLDKHGNIKKYLL VLCSLCVCHGVAVRSNQHLICDNLLPGRDLL LOTRLYNHVSSMRPNIFLGVSSGAQYKKWY YELMVDHTEFFVTAFATHLRVGWASTEGYYP YGGGEWGGNOCODLFSYGFGGHLWSG CLARTVSSPOQHLLRTDDVISCCLDLSAPSISS RINGGOPVQGMPSNFNIDLIFPEVSSAAGIKV RFLLGGRIGEFKELPPGVAPCYEAVLPKSK KELLGGRIGEFKELPPGVAPCYEAVLPKSK KELLGGRIGEFKELPPGVAPCYEAVLPKSK KELLGGWYGVPVDDNKRQHFCLVFSKLPGE ERNYNLQMSLETILKTLLALGCHVGISDEHA VELLGGWYGVFVDDNKRQHFCLVFFSKLPG ERNYNLQMSLETILKTLLALGCHVGISDEHA DKVKKMELPKNYQLTSYKFARDLSFRILT FSQEAMVDKLAENAHNWARDRRGGWTY GIQQDVKNRRPRPRLVPTTLDDBTKKSNKDS GRERFRFFARKTYAVKAGRWYGEFETVTA GDMRVGWSRFGCQPDQELGSDERAFAPTGPG KAQRWHGGNEHVGRSWAGADVYGCMVDM NEHMMFTLNGEILLDDSGSELAFKDFPTOL GFCSLGVAGVGRNNFGKDSVLLAPTFTOL GLGGGYEFFANNTNRDITMWLSKRLDGPLOY PSHEHEINTRIGDTDSSPCLLVTQKSFGSQN SNITDMFYRLSMFECAEVPSKTVAGGLFGSRQA LGFGFNDLEDFUNGTDSSPCLLVTQKSFGSQN SNITDMFYRLSMFECAEVPSKTVAGGLFGSRQA LGFGFNDLEDFUNGTDSSPCLLVTQKSFGSQN SNITDMFYRLSMFECAEVPSKTVAGGLFGSRQA LGFGFNDLEDFUNGTDSSPCLLVTQKSFGSQN SNITDMFYRLSMFECAEVPSKTVAGGLFGSRQA LGFGFNDLEDFUNGTDSSPCLLVTQKSFGSQN SNITDMFYRLSMFECAEVPSKTVAGGLFGSRQA LGFGRNDLGDFUNGTRAFFTOLDERGENTYMFLSGELAF DFIQOTGFBLDAFAFAPTOL BCHARGESTYTYGFSFGRNNNGLEIL BCHARGTARAGESTYTYGFESTLAP DFIQOTGFBLDAFAFAPTOL BCHARGESTYTYGFTSHALTE BCHARGTARAGESTYTYGFTSHALT BCHARGARAGESMFROGE NVDAASGLLTFLAGGESAGATAGFTOY BCHARGESTYTYGFTSHALTE BCHARGTARAGESTYTYGFTSHALT BCHARGESTATARAGALAGAR LGFRYDLEGFLARAFTOY BCHARGESTATARAMMRNFYLYMF BCHARGTARAGESTYCTAAGGLFAGGE NVDALBERLER SKSSNCYMCAG		1	]	_	sequence		ADDRADGEDOOKOK AARGAAAAFI RGAR
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VCYIQHYDTGLWLTYQSVDVSXYMGSIQR KAMHHEGHMDGISLSRSQHEESRTARVIRS TVFLFNRIRGLDALSKKAKASTVDLPIESVSL SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR QNLFQEEGMINLVLECIDRLHVYSSAAHFAD VAGREAGESWKSLINSLYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIIKEGHKSIISLLDKHGRNIRVLUD ULSSLCVCHGVAVRSHULCDNLLPORDLL LQTRLVNHYSSMRPNIFLGVSEGSAQYKKWY YELMYDHTEFFVTAFATHLRVGWASTEGYSP YFGGGEEWGGNGVGDDLFSVGFDGLHLWSG CLARTVSSNOPHLRTDDVISCCLDLSAPSISF RINGQPVQGMEENNHDGLFFPVVSFSAGIKV RFLLGGRIGEFKFLPPPGYAPCVFAVLPKEL KVEHSREYKQERTYTTDLLGFTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENHELWVMN KIELGWQYGPVRDINGFIPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DEVKKMKLPKNYQLTSGVKPAPMDLSFIRLT PSQEAMVDKLAENAHNWARDRIRQGWTY GIQQDVKNIRNPRLYPYTLDDTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSPGCQFDGLGSDERAFADGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILDDSGSLAKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQGGYEPFAVNTNRDITMUSKRLPCPLQV SNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVSEXTVAGGLPGAG LFGPKNDLEDYDADSSELAKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQGGYEPFAVNTNRDITMUSKRLPCPLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVSEXTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDVAQEKPSRLKQ RFLLRTKYPDYSTSHSARLTEDVLADDRDDV DPLMQTSTYYYSVRIPFQQEPANWWGWTS DFHQYDTGFDLDRVRTTVTTLDEKGKVHE SKRSNCTWACGSESMSPQGGRNNNGLEIGG VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNYFOFGERINNYMPLSAGLFKS EHKNPVPQCPRILHVQFLSHVLWSRMPNOFL KVDVSRISERQGWLVQCLDPLOFMSLHIPEN RSVDLLETGEBLLKRYHTLRLSAVCALG NIRVAHALCSHVPEPQLLVARAMMNNSLYPMT EETKSITLFPDENKKHGLPGLISTSLRPMOFF SSPSFVSINSFCYQSFEPPLDLKSKTIOMLTE	İ		ļ	1			HVIIGKILSEMEDANELEMBREIGIBYRGIS
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QNLFQEEGMINLVLECIDRLHYYSSAAHFAD VAGREAGESWKSLIN YELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIKEGHIKSIISLIDKHGRNHKVLD VLCSLCVCHGVAVRNOHLICDNLLFORDLL LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY YELMVDHTEPFVLAETHIR VGWASTEGYSP YPGGGEWGGNGVGDDLFSGFDGLHLWSG CLARTVSSPNQHLLRTDDVISCCLDLSAPSISF RINGQPVQGMFENNIDGLFFPVVSFSAGIKV RFILGGRHGEFKLPPGVAPCYEAVLFKEKL KVEHSREYKQBETYTRDLLGFTVSLTQAAFT PIPVJTSQIVLPHLERREKLAENIFELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETILKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAFMDLSFIKLT PSQEAMYDKLAEHAHNVWARDRIRQGWTY GIQQDWKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAORWHOGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYSPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSECLKVTQKSFGSQN SNTDIMFYRLSWPECAEVFSKTVAGGLPGAG LFGPKDLEDYDADSDFEVLMKTAHGHLP DRVDKMCKENSTHENDYAGERSRSKGGRAN STIDIMFYRLSWPECAEVFSKTVAGGLPGAG LFGPKDLEDYDADSDFEVLMKTAHGHLP DFHQTGFFLDRVRTVTVTLIGDEKGKVHE SIKRSNCYMVCAGESMSPGGRNNNGLEIGG VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVTQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSTNLWSRMPNQFL KVDWSRISERQGWLVQCLDPLGFMSLHPEEN RVDLLIDHLISSVATARLMMNNEYLVPMT EFIKSITLFPDENKKHGLFSIGLSTSLRYMGPELR RVPULLIDHLISSVATARLMMNNEYLVPMGLR AGYYDLLIDHLISSVATARLMMNNEYLVPMGLR			į	Ĭ		į.	OF ONLICYEUPPDEHI EHEDKONRI RALKNR
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RINGGPVQGMFENFNIDGLFFPVSFSAGIKV RFLLGGRHGEKFLPPPGYAPCYEAVLPKEKL KVHSREYKQERTYTRDLLGPTVSLTQAAFT PJPYDTSQIVLPPHLERIREKLAENIHELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRGGWTY GIQQDVKNRRIPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRNNFGKDVSTLKYFTIC GLQEGYEPFAVNTINRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRIKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWYGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SKKSNCYYWCAGESMSPGQRNNGLEIGC VVDAASGLLTFIANGKELSTYQVEPSTKLFP AVFAQATSPNVTQFELGRIKNVMPLSAGLFKS EHKNPVPGCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTILRLYSAVCALG NHRVAHALGSHVDEPGULYAIENKYMPGLEI RGYYDLLIDHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEPFLDILKSKTIQMLTE	1		i	j	ļ		CIARTYSSPNOHLLRTDDVISCCLDLSAPSISF
RFLLGGRHGEFKFLPPPGYAPCYFAVLPKEKL KVEHSREYKQERTYTRDLLGPTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENIHELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNIRINPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFFFETVTA GDMRYGWSRPGCQPDQELGSDERAFADGF KAQRWHQGNEHYGRSWQAGDVVGGMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDLELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMFGLLR AGYYDLLIDHLSSYATARLMMNNE YLVPMT EETKSTL-IPDENKKHGLPGIGLSTSLRPRMQF		Ì					RINGOPVOGMFENFNIDGLFFPVVSFSAGIKV
KVEHSREYKQERTYTRDLLGPTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENIHELWVMN KELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTELDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCOPDQELGSDERAFAFDOF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEFFAVNTNRDITMWLSKRLPQFLQV PSHEHEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNHKDYAGEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFGQEPANVWVGWITS DFHQYDTGFDLDRVATTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPQQRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDLLETEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLL AGYYDLLIDHLSSYATARLMMNNE YIVPMT EETKSTLYFDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQVSPEPPLDILKSKTIQMLTE							RFLLGGRHGEFKFLPPPGYAPCYEAVLPKEKL
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KELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRRQGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGFEFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAPDGF KAQRWQGRNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMCAGESMSPCQGRNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLR AGYYDLLIDHILSSYATARLMMNNEYIVPMT EETKSITLFPENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE				1		\.	PIPVDTSOIVLPPHLERIREKLAENIHELWVMN
ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTILGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNOFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NIFRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLIFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSINFCYQYSPEPFLDILKSKTIQMLTE	}	i	-	1			KIELGWOYGPVRDDNKRQHPCLVEFSKLPEQ
DKVKKMLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFADGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEFSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NIRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDHLSSVATARLMMNNEYIVPMT EETKSTILFPDENKKHGLPGIGLSTSLRPRMQF		ı					ERNYNLOMSLETLKTLLALGCHVGISDEHAE
PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSYDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE	į	l l	}	1		ļ	DKVKKMKLPKNYOLTSGYKPAPMDLSFIKLT
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GTGERFRIFAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLY AIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE					ì		GIOODVKNRRNPRLVPYTPLDDRTKKSNKDS
GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFLANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE							LREAVRTLLGYGYNLEAPDQDHAARAEVCS
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GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE				1			KAQRWHQGNEHYGRSWQAGDVVGCMVDM
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SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVVGFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSTSNECYOYSPEFPLDILKSKTIQMLTE			i	}	1		GLQEGYEPFAVNTNRDITMWLSKKLPQFLQV
LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSTSNECYOYSPEFPLDILKSKTIQMLTE							PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN
DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSTSNECYOYSPEFPLDILKSKTIQMLTE		1			1		SNIDIMFYRLSMPIECAEVISKIVAUGLPUAG
RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSTSNECYOYSPEFPLDILKSKTIQMLTE		}		}	İ		LFGPKNDLEDYDADSDFEVLMK TAHUHLYP
DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE		}		1	1		DRVDKDKEA I KPEFNNHKD I AQEKPSKLKQ
DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE			1			1	RFLLRRTKPDYSISHSAKLIEDVLADDRUDI
SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE	}	l	1	1			DFLMQTSTY YYSVKIFFGQEFANV W VGWITS
VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE	1				1		DFHQYDTGFDLDKVKIVIVILUDEKUKVKE
AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE	1		1		1		SIKKSNCYMVCAGESMSPUQGKINNIGLEIGC
EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDHLSSYATARLMMNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE							VVDAASGLLIFIANGKELSI I I QVEFSI KLFF
KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE							AVFAQATSPNVFQFELUKIKNVMFLOAULFKO
RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE	1		1		1		EHKNPVPQCPPKLHVQFLSHVLWSKWFNQFL
NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE							KADAZKIZEKOGATA KERANET BI ASVACATO
AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE		1					RSVDILELI EQEELLKIH IHILKLI SAVCALU
EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE							NHRVAHALCSHVDEPQLLYAIENKY MPOLLK
SSPSFVSISNECYOYSPEFPLDILKSKTIQMLTE							AGYYDLLIDIHLSSYATARLMMNNE YIVPMI
SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE AVKEGSLHARDPVGGTTEFLFVPLIKLFYTLLI						1	EETKSITLFPDENKKHGLPGIGLSTSLKPKMQF
AVKEGSLHARDPVGGTTEFLFVPLIKLFYTLLI					1		SSPSFVSISNECYQYSPEFYLDILKSKIIQMLIE
					1		AVKEGSLHARDPVGGTTEPLFVPLIKLFTTLLI

						(1 Al : C-Cuttains
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	-		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1 2000	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	Y=1yrosine, X=Unknown, V=Sup codon,
				peptide	{	/=possible nucleotide deterion, (-possible
				sequence		nucleotide insertion  MGIFHNEDLKHILQLIEPSVFKEAATPEEESDT
	<del>                                     </del>					LEKELSVDDAKLQGAGEEEAKGGKRPKEGLL
		1		!		QMKLPEPVKLQMCLLLQYLCDCQVRHRIEAI
		1	İ			VAFSDDFVAKLQDNQRFRYNEVMQALNMSA
}	1	1		1		ALTARKTKEFRSPPQEQINMLLNFKDDKSECP
1		,				CPEEIRDQLLDFHEDLMTHCGIELDEDGSLDG
				İ		NSDLTIRGRLLSLVEKVTYLKKKQAEKPVES
		ļ				DSKKSSTLQQLISETMVRWAQESVIEDPELVR
1			1			AMFVLLHRQYDGIGGLVRALPKTYTINGVSV
	1	-	+	1	(	EDTINI LASI GOIRSLLSVRMGKEEEKLMIKG
		1	1			LGDIMNNKVFYQHPNLMRALGMHETVMEV
						MVNVLGGGESKEITFPKMVANCCRFLCYFCR
1		1				ISRONOKAMFDHLSYLLENSSVGLASPAMRG
						STPLDVAAASVMDNNELALALREPDLEKVVR
1				1	Į	VLAGCGLOSCOMLVSKGYPDIGWNPVEGER
				İ		VI DELREAVECNGESVEENANVVVRLLIKKPE
1			ļ	1	ļ	CEGPALRGEGGNGLLAAMEEAIKIAEDPSRD
	İ	ļ	1			GPSPNSGSSKTLDTEEEEDDTIHMGNAIMTFY
	}	ŀ				SALIDLLGRCAPEMHLIHAGKGEAIRIRSILRS
,						LIPLGDLVGVISIAFQMPTIAKDGNVVEPDMS
		ł		ĺ		AGFCPDHKAAMVLFLDRVYGIEVQDFLLHLL EVGFLPDLRAAASLDTAALSATDMALALNRY
				Į		LCTAVLPLLTRCAPLFAGTEHHASLIDSLLHT
ł						VYRLSKGCSLTKAQRDSIEVCLLSICGQLRPS
l l		1		}		MMQHLLRRLVFDVPLLNEHAKMPLKLLTNH
	1	}				VERCWKYYCLPGGWGNFGAASEEELHLSRK
				1		I FWGIFDALSOKKYEQELFKLALPCLSAVAG
1	1		1			ALPPDYMESNYVSMMEKQSSMDSEGNFNPQ
1			1		1	PVDTSNITIPEKLEYFINKYAEHSHDKWSMDK
						LANGWIYGEIYSDSSKVQPLMKPYKLLSEKE
		-	1			KEIYRWPIKESLKTMLARTMRTERTREGDSM
						ALYNRTRRISQTSQVSVDAAHGYSPRAIDMS
						NVTLSRDLHAMAEMMAENYHNIWAKKKM
				1		ELESKGGGNHPLLVPYDTLTAKEKAKDREKA QDILKFLQINGYAVSRGFKDLELDTPSIEKRFA
]				1		YSFLQQLIRYVDEAHQYILEFDGGSRGKGEHF
1	-			1		PYEQEIKFFAKVVLPLIDQYFKNHRLYFLSAA
		1		- [		SRPLCSGGHASNKEKEMVTSLFCKLGVLVKH
		1			i	DIST FGNDATSIVNCLHILGOTLDARTVMKTG
						I ESVKSALRAFLDNAAEDLEKTMENLKQGQF
						THTRNOPKGVTOINYTTVALLPMLSSLFEHI
1		1	[			GOHOFGEDLILEDVOVSCYRILTSLYALGISK
1			ľ			STYVERORSALGECLAAFAGAFPVAFLETHLD
			ĺ	1		KHNIYSIYNTKSSRERAALSLPTNVEDVCPNIP
			}			SLEKT MEETVELAESGIRYTOMPHVMEVILPM
			-			I CSYMSR WWEHGPENNPERAEMCCTALNSE
						HMNTLLGNILKIIYNNLGIDEGAWMKRLAVF
		l				SQPIINKVKPQLLKTHFLPLMEKLKKKAATVV
		1				SEEDHLKAEARGDMSEAELLILDEFTTLARDL
						YAFYPLLIRFVDYNRAK WLKEPNPEAEELFR YAFYPLLIRFVDYNRAK WLKEPNPEAEELFR
						MVAEVFIYWSKSHNFKREEQNFVVQNEINN
						MSFLITDTKSKMSKAAVSDQERKKMKRKGD RYSMQTSLIVAALKRLLPIGLNICAPGDQELIA
						LAKNRFSLKDTEDEVRDIRSNIHLQGKLEDP
						AIRWQMALYKDLPNRTDDTSDPEKTVERVL
	1					DIANVLFHLEQKSKRVGRRHYCLVEHPQRSK
	1	-				KAVWHKLLSKQRKRAVVACFRMAPLYNLPR
						HRAVNIFLOGYEKSWIETEEHYFEDKLIEDLA
						KPGAEPPEEDEGTKRVDPLHOLILLFSRTALT
		1				EKCKLEEDFLYMAYADIMAKSCHDEEDDDG

SEQ ID Net DI Monto of Not of							(A-Alonino C-Curtaine
NO: of much entire entre entire ntire entire entire entire entire entire entire entre e	SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
entide sequence   USSN   corresponding corresponding to first samino acid residue of peptide sequence   version of peptide sequence   version of peptide sequence   version of peptide sequence   version of peptide sequence   version of peptide   version of pe		NO: of	hod	ID NO:			D=Aspartic Acid, E=Olutainic Acid,
denice werker werker was a state amino acid residue of peptide residue of peptide sequence when the pertial sequence werker was a state of peptide sequence when the pertial sequence werker was a state of peptide sequence when the pertial sequence werker was a state of peptide sequence when the pertial s	-	peptide					I Jest alevaine K-I veine I = Leucine
1949   194		,		USSN			1=1soleticine, K=Lyshie, D=Dettonie,
914 ng to first amino acid residue of peptide sequence pe			ĺ	09/496			M=Methionine, N=Asparagine, 1-1 forme,
residue of peptide sequence sequence y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide insertion nucleotide nucleotide insertion nucleotide inserti	-		1	914	ng to first		Q=Glutamine, K=Arginine, 5-5ct nc,
## Approach   ##	denos	Ì		ļ		of peptide	T=1 hreonine, V=Valine, W=1 typuphian,
nucleotide insertion  Sequence  EEEVKSEKEMERKOKLLYQQARLHDRGAA EMVLQITISASKGFTGPMYAATLALGIALINGG NSTYQQKMLDYLERKUVGFPGSLGALGMOS CSVLDLNAFERQNKASGIGMYTEGGSGEKV LQDDEFTCDLERFLQLLCEGHNSDFOYNLET GTGNNTTVNIIISTVDYLLRVQESISDFYWYY SGKDVIDEGOGRNFSKARIOVAKQYFNTLTSYI QGPCTGNQQSLAHSRLWDLAVOFHVFAHM QMKLSQDSSQIELLEEMDIQKDMYWMLLS MLEGNVYNGTIGKOMYDMLVESSNNYEMIL KFPMRLKLKDLTSSDTREYDPDGKGVISK RDFHKAMESHKHYTQSETEFLLSCASTDENE TLDYEFVKRFHEPASKDIGFNVAVLTINISEH MPNDTRLQTFLELASSVLNYTQFFLGRIEMG SAKRIERYVFEISSSTRÖMERQVESSKRQFI FDVVNRGGEKEMELFVNPCEDTTFEMQLAA QISESDLMRSANKEESKERPEGOFRMAFF SILTVRSALFARLYNILTLMRMLSLKSLKKQM KKVKKMYTKDMYTAFSSYNSIFMTLHFV ASVPRGFRICSLLLGGSLVEGAKKKVAELL AMMPDPTODEVROGEGEGRKPLEAALPSED LTDLKELTESSDLSDIFGJDLKREGGQYKLIP HNPNAGLSDLMSNPVPPEVCEKFQCKAK EEEKEETKSFFKAGGDGEKEEKAKED CKGKQLRQHTHRYGFEPYESSAFWKIJAY QGKLINTFARNFYNMRMLALFVAFAINFILL FYKVSTSSVYGEKELFTRSSSENAKSVILDSS SHRIILAVHYVLEESSGYMEPTVRILPHLHTVISF FCHGYYCLKYPLVFKREKEVARRLEFFGLYI TEQPSEDDIKGOWDRLVINTOSFPNNYDKF VRRKWMDKYGEFFGRRISELLGMKAALD FSDAREKKPKKDSSLSAVLNSDVXYQMW KLGVYTDNSFLYLAWMT LFSSGGRAFTLYNNIPOMSTDTER FCHGYTCLKYPLVFREKEVARRLEFFGLYI TEQPSEDDIKGOWDRLVINTOSFPNNYDKY GREDISHRSTRANGERGGRAFTQVA A 4199 31 767 LPELNGRGAGLBRAEFFSEGGGAERTQVA FSDAREKKPKDSSLSAVLNSDVXYQMW KLGVYTDNSFLYLAWMT LFSSGGRAFTLYNNIPOMSTDTER FRODTISHNRLTGELEYATKISRSFNXYHLSI HISKNGADTIKVFYIGLRGEWTELRRIEVTI CYYEASANPADHRWQVTYOTHFIET STAREKKPKORNITVOFTIGETLKYTYLLPH RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGKRKTGVQVTYVTLPP RSSGGRAFTGGGAGGSEETLFQDH NHEMERER WQOFRLHREEATYTGNENELD LPDQGKLRKSPVLRAKAQAFQWKAHSFN LPDGPSTLOSFRWHPLRAKADKYEDSVPOS TRAQLQSVSVHILGTLARRVFLGGTOPSL HGGLCLVVLGAKNLPVRGAGFGTNSELLGDAG TRAQLGVSSVELLGTLARRYFTGGTOPSL HGGLCLVVLGAKNLPVRGAGFGTNSELLGDAG RGETSFLEHTVAHENGGFERIGEDTYDPLI NDTMLLUH KENKAGRINAKNOGSRSSDGGSEETLFQDH NHEMERER WQOFRLHREEATYTGINELDGE RUTDMTLLUH KENKAGRINAKNOGSRSDGGSEETLFQDH NHEMERER WQOFRLHREEATYTGINSELNOR RDDYBLARGHNLLGTFRYSTSVFNN		1	1	[	residue of	sequence	Y=1 yrosine, X=Unknown, *-stop codon,
EEVKSFEKEMBKOKLLYQQARI-IBRGAA PMVLQTISASKGETOPMVAATILAIQALINGG NSTVQKMLDYLKEKKDVGFFQSLAGLMQS CSVLDLINAFRRONKAGIGMYTEEGSGEKV LQDDEFTCDLFREIQLLCEGHNSDFQNYLKT GTONNTTVMIISTVDYLINVQESISDFYWYY SGKDVIDEQGGRNFSKAIQVAKQVFNYLTEY OOPKTCDNQSLAHSKLIDAVGGFLIVFABM OOKKLSQDSSQIELIKELMDLQKDMVVMLLS MLEGOVYOMILVESSNYVMIL KFDMFLKLKULTSSDTFKEYDPDGKGVISK RDFHKAMESHKIYTOSSTEFLLSCAETDENE TLDYEFFVRRHIPPAKDIGFNVAVLITINISEH MIPDTELQTFLLASSVINVGPFLGRISMG SARRIERVYFEISESSRTQWERPQVKSSKRQFI FDVVNRGGGREKEMBLEVNTCPDTIFEMQLAA QISESDLNERSANKEESEKERPEQGRNAAFF SILTYRSALFARYNITLTMMMLSISLAKOM KKVKKAMFKOSHLOGSLVEAKKVABLL ANMPDFTQLESDLLSDFGLDLKREGGOKYKLE HYPMAGLSDLMSPRYPAPEVQEKTQGKAK EEKEREKETKAFTARSTALTARMSLAKKVABLL ANMPDFTQLESDLLSDFGLDLKREGGOKYKLE HYPMAGLSDLMSPRYPAPEVQEKTQGKYKLE HYPMAGLSDLMSPRYPAPEVQEKTQGKYKLE FYKVSTSSVVEEKSKYMSPTVALPLHTVISS FYKVSTSSVVEEKSLAKVABLLANDELDTVISSF FYKVSTSSVVEEKSKYMSPTVALPLHTVISS FYKVSTSSVVEEKSKYMSPTVALPLHTVISSF FUIGYYCLKVPLVFFRRKEVAKLEFDGLYV TEQPSDDIKGQVDRLVTHTOSPTPNYVDKF VRKWMKYGFFYGRORISELLGMDKAALD FSDAREKKPKRDSSLSAVLNSDWKYQMW KLGVVFTDNSFFLLAKMY GRINGGROCKCAAERVGAARGSAAC AYGLYLRIDKGRLQCLMSERRGGGRCKEPW FRADDISKRYGGADELIFNIPTGTHYLK GIIMGEDDSHPSIMRLYSNIPQMSFDDTER FPDQTTSSNRVITGLEVATILTSRNYTHLS HISKNRGADTTKVFYIGLRGEWTELRRIEDTT CYYCLKVPLVFTOKRTLAKVTYLLIP RSSQCKRKTTGVQNTVDTTGFSTPNYTHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS NGEFTSNLEITHVARKUTYNTTHTS HIGGEDDSHPSIMRLYNTYDGTLTRSRNYTHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVFYIGLARFFERSTENTYHLS HISKNRGADTTKVRYLIGLARFFERSTENTYHLS HISKNRGADTTKVRYLIGLARFFERSTENTYHLS HISKNRGADTTKVRYLIGLARFFERSTENTYHLS HISKNRGADTTKVRYLIGLARFFERSTENTYHLS HISKNRGADTTKVRYLIGLARFFERSTENTYHLS HISKNRGADTTKVRYLIGLARFFERSTENTYHLS HISKNRGADTKVRAKTYNTYDFTOTTLNSTVKGCLT HYTDMTLVLH KENKKARNIKNNOSRSRDGGSEETLPODH MHENERREWQOELHREERYYGPHSLIDGUSKE QUANTEPTSLEHTVNHENGGFERIGGDVYTD		1		ŀ	peptide		/=possible nucleotide delenon, \=possible
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WDFEDSTTQSFRWHPLRAKADKYEDSVPQS NGELTVRAKLVLPSRTRKLQEAQEGTDQPSL HGQLCLVVLGAKNLPVRPDGTLNSFVKGCLT LPDQQKLRLKSPVLRKQACPQWKHSFVFSGV TPAQLRQSSLELTVWDQALFGMNDRLLGGTN RLGSKGDTAVGGDACSQSKLQWQKVLSSPN LWTDMTLVLH  KENKKARNLRMNQSRSRSDGGSETLPQDH NHHENERR WQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORSTNSPVARRTRSQTSVNFN					Į.		OLVTROLOVSVWHLGTLARRVFLGEVIIPLAT
NGELTVRAKLVLPSRTRKLQEAQEGTDQPSL HGQLCLVVLGAKNLPVRPDGTLNSFVKGCLT LPDQQKLRLKSPVLRKQACPQWKHSFVFSGV TPAQLRQSSLELTVWDQALFGMNDRLLGGTN RLGSKGDTAVGGDACSQSKLQWQKVLSSPN LWTDMTLVLH  KENKKARNLRMNQSRSRSDGGSEETLPQDH NHHENERR WQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORSTNSPVARRTRSQTSVNFN			1		1		WDFEDSTTOSFRWHPLRAKADKYEDSVPQS
HGQLCLVVLGAKNLPVRPDGTLNSFVKGCLT LPDQQKLRLKSPVLRKQACPQWKHSFVFSGV TPAQLRQSSLELTVWDQALFGMNDRLLGGTN RLGSKGDTAVGGDACSQSKLQWQKVLSSPN LWTDMTLVLH  KENKKARNLRMNQSRSRSDGGSEETLPQDH NHHENERR WQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORSTNSPVARRTRSQTSVNFN							NGELTVRAKLVLPSRTRKLOEAQEGTDQPSL
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RLGSKGDTAVGGDACSQSKLQWQKVLSSPN LWTDMTLVLH  555 1905 A 4211 331 2419 KENKKARNLRMNQSRSRSDGGSEETLPQDH NHHENERR WQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORSTSPVARRTRSQTSVNFN					1		TPAOI ROSSI ELTVWDOALFGMNDRLLGGT
LWTDMTLVLH  555 1905 A 4211 331 2419 KENKKARNLRMNQSRSRSDGGSEETLPQDH NHHENERRWQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORSTSPVARRTRSQTSVNFN			1	}	1	1	RLGSKGDTAVGGDACSOSKLOWOKVLSSPN
555 1905 A 4211 331 2419 KENKKARNLRMNQSRSRSDGGSEETLPQDH NHHENERR WQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORST\SPVARRTRSQTSVNFN			1		1		I WTDMTI VI H
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QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORST\SPVARRTRSQTSVNFN							DVDI MRIDHNI I GTPGEITSFELOORLDGVKE
WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANROORST\SPVARRTRSQTSVNFN					1		OLASOPDI ROGTNYROSEVPRESSHEDSLLE
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GSSSNIPKTRLASKOQNI ALOSI BTESIGLIA (G			- [				CECENIED TRI A SEGONDA FOSFSTI GELENGI
		1	l				G999NILK LYTWOYOOTH ATON BIT POTOTOR

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Boquesi	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<u> </u>	ļ	<del> </del>	sequence		GGAAGIPRANASRTNFSSHTNQSGGSELRQRE
	}	)	}	1		GQRFGAAHVWENGARSNVTVRNTNQRLEPI
	1	1		}		RLRSTSNSRSRSPIQRQSGTVYHNSQRESRPV
			1	}		QQTTRRSVRRRGRTRVFLEQDRERERRGTAY
			i			TPFSNSRLVSRITVEEGEESSRSSTAVRRHPTIT
					1	LDLQVR\RIRPGENRDRDSIANRTRSRVGLAE
				ļ		NTVTIESNSGGFRRTISRLERSGIRTYVSTITVP
		1				LRRISENELVEPSSVALRSILRQIMTGFGELSSL
			1	Į		MEADSESELQRNGQHLPDMHSELSNLGTDN MEADSESELQRNGQHLPDMHSELSNLGTDN
		1				NRSQHREGSSQDRQAQGDSTEMHGENETTQP HTRNSDSRGGRQLRNPNNLVETGTLPILRLAH
						FFLLNESDDDDRIRGLTKEQIDNLSTRHYEHN
		i		1		SIDSELGKICSVCISDYVTGNKLRQLPCMHEF
	1		1	1	1	HIHCIDRWLSENCTCPICRQPVLGSNIANNG
		ļ				LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKR
556	1906	Α	4212	3	462	KSPENTEGKDGSKVTKQEPTRRSARLSAKPA
	1	İ				PPKPEPKPRKTSAKKEPGAKISRGAKGKKEEK
		ì				QEAGKEGTAPSENGETKAEEIHISRSTVNVST
				į.		SRGTPPSTLSVKGQIETVRVKGTEN
		<u> </u>			507	ARRESCLTLQTSWGHRH\GPPRP\ANFVFLVET
557	1907	Α	4213	774	507	GFLHIGQAGHKLPTSGDPPASASQSARITGMS
		1	Ì			HRTWFLASFLIDSCKNFIVYKIMYTL
			1005	3	1253	TVRHAEREHPETSSATKVSYDYRHKRPKLLD
558	1908	A	4225	3	1255	GDODESDGRTOKYCKEEDRKYSFQKGPLNRE
				1		I DOENTGRGRETODGOVKEPFKPSKKDSIAC
			ì		ĺ	TYSNKNDVDLRSSNDKWKEKKKKEGDCKKE
		1	İ			SNSSSNQLDKSQKLPDVKPSPINLRKKSLTVK
		1	İ			VDVKKTVDTFRVASSYSTERQMSHDLVAVG
	1					RKSENFHPVFEHLDSTQNTENKPTGEFAQEIIT
			1			IIHQVKANYFPSPGITLHERFS\KMADIHKADV
						NEIPLNSDPEIHRRIDMSLAELQSKQAVIYESE
ļ		1		Ì		QTLIKIIDPNDLRHDIERRRKERLQNEDEHIFHI ASAAERDDQNSSFSKNYTTQRKDIITHKPFEV
		1		1		EGNHRNTRVRPFKSNFRGGRCQPNYKSGLVQ
ł		İ		ļ		KSLYIQAKYQRLRFTGPRGFITHKFRERLMRK
ļ			1	1	ŀ	
						KKVP KFSIPFFLRWSFTLV\PRLEGNDMISVHCNLGL
559	1909	A	4235	1	323	LGLSHSPASASQVGGITGTQHHTGLIFGFLIET
	-		}		İ	EFHHVGQAGLELLTSGDPPALAFQSAGITGVS
]		- 1	-	)		HHAWLQVLNS
ļ			<del></del>		1569	TI SLI ER VLMKDIVTPVPQEEVKTVIRKCLEQ
560	1910	Ā	4246	_ 2	1509	A AL VNIVSRI SEY AKIEGKKREMYELPVFCLA
1		Į		1		SOVMDLTIONOKDAENVGRLITPAKKLEDTIR
}		1				1 AFL VIEVLOONEEHHAEAFAWWSDLMVEH
1		1				A ETEL SI FAVDMDAALEVOPPDTWDSFPLFQ
						LI NOFERTGLLICGNGK\FHKHLQDLFAPLVV
1				- 1		RAYMWDLDGSSPIAOSIHRGLLSRESWEPYNN
1		- 1				GSGTSEDLFWKLDALQTFIRDLHWPEEEFGK
		-		}		HI FORLKLMASDMIESCVKRTR\IAFEVKLQK
			1			TSSIOOIFRVPOFNMAPCFNVMGLMAKGSIQP
			- }			KI \CSMEMGOEFAKMWHQYHSKIDELIEET V
1			1			KEMITLLVAKFVTILEGVLAKLSRYDEGTLFS
		1				SEI SETVKAASKYVDVPKPGMDVADAYVTF
1		1		1		VRHSODVLRDKVNEEMYIERLFDQWYNSSM
1	1					NVICTWLTDRMDLOLHIYQLKTLIRMVKKTY
						RDFRLOGVLDSTLNSKTYETIRNRLTVEEATA
	1		1			SVSEGGGLQGISMKDSDEEDEEDD
1	1		1			
561	1911	A	4257	1300	654	SELVQFLLIKDQKKIPIKRADILKHVIGDYKDI FPDLFKRAAERLQYVFGYKLVELEPKSNTYIL

		N (	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ì		ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	!				sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	ì	residue of	sequence	/=possible nucleotide deletion, \-possible
		<b>\</b>	ì	peptide	1	nucleotide insertion
		<u> </u>	1	sequence	ļ	INTLEPVEEDAEMRGDQGTPTTGLLMIVLGLI
			1		}	FMKGNTIKETEAWDFLLAL\GVYPTKKHLIFG
	ţ	1			1	DPKKLITEDFVRQRYLEYRRIPHTDPVDYEFQ
	1					WGPRTNLETSKMKVLKFVAKVHNQDPKDW
		1	1	1	1	PAQYCEALADEENRARPQPSGPAPSS
		1				MVTWLYRFLPTSNMAAKLRSLLPPDLRLQF
562	1912	A	4260	1	1498	WLHARLQKCFLSRGCGSYCAGAKASPLPGK
	1 3 3		l			WLHARLQKCFLSKOCOSTCAOAICASI DI OL
	ì			,	}	MAMGLMCGRRELLRLLQSGRRVHSVAGPSQ MAMGLMCGRRELLRLLQSGRRVHSVAGPSQ
	1	1				WLGKPLTTRLLFPAAPCCCRPHYLFLAASGPR
	Ì	1				SLSTSAISFAEVQVQAPPVVAATPSPTAVPEV
	1					ASGETADVVQTAAEQSFAELGLGSYTPVGLI
		}				QNLLEFMHVDLGLPWWGAIAACTVFARCLIF
		1			1	PLIVTGQREAARIHNHLPEIQKFSSRIREAKLA
	1	1			1	GDHIEYYKASSEMALYQKKHGIKLYKPLILPV
	ì	1	l			TQAPIFISFFIALREMANLPVPSLQTGGLWWF
	1		1	1	}	QDLTVSDPIYILPLAVTATMWAVLELGAETG
						VQSSDLQWMRNVIRMMPLITLPITMHFPTAV
						FMYWLSSNLFSLVQVSCLRIPAVRTVLKIPQR
•		1				VVHDLDKLPPREGFLESFKKGWKNAEMTRQ
	j	1			1	LREREQRMRNQLELAARGPLRQTFTHNPLLQ
	1	ļ	]			PCKDNPPNTPSS\SSSSSKPKSKYPWHDILG
			1065	623	116	MGGLAPTOTLEPT\REYONTQLSVSYLLPEQN
563	1913	Α	4265	623	110	THGTRRTLSSGPSNNLPLPLSSSATMPSMQCK
		i				HR SPNGGLEROSPVK/TPPIPMSFQPVPGGV\L
	1	ì				PRGSGNPPHGTSILTAPPALLPHPPTHPTQQSF
	. ]	1	i		1	LIQENNNTNHTHSHTHTYTETLSFFLYICVNN
	1	1				DRMEWGKSVF
			1000	<del> </del>	368	II KRKI SSI NSEVSTIONTRMLAFKATAQLFIL
564	1914	A	4270	3	300	GCTWCLGLLOVGPAAOVMAYLFTIINSLQGF
1	j					FIFLVYCLLS\QQVQKQYQKWFREIVKSKSES
}	ł	Ì	1			FTYTI SSKMGPDSKPSEGDVFPRTSE
					406	RNSRPI WCSPPASOPROAPVSQSCCCPLPSSSS
565	1915	A	4288	83	400	PPSALLAPTKPRALGTLRLYECSPELCTTMLP
l	Į.	- 1			İ	PAWLLMLCQAPRPQDPDPRLTQPEKSLQEAP
		- [				GOTGASRTPRT
		١				LNSSQKLACLIGVEGGHSLDSSLSVLRSFYVL
566	1916	A	4298	1041	229	GVRYLTLTFTCSTPWAESSTKFRHHMYTNVS
					}	GLTSFGEKVVEELNRLGMMIDLSYASDTLIRR
l		1				VLEVSQAPVIFSHSAARAVCDNLLNVPDDILQ
1		İ			ľ	LLKKNGGIVMVTLSMGVLQCNLLANVSTVA
1		1				DHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLE
	1	l		1	1	DVSTYPVLIEELLSRSWSEEELQGVLRGNLLR
i				J	1	DASLALATINEED VOODAE VEEDAGOI CACOT
1			Ì			VFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
1	1					FHLGASEWTPRLLIWR
600	1917	+	4299	1	1106	GATPLGSVGGRTGKMDAATLTYDTLRFAEFE
567	1917	^	7277	1		DFPETSEPVWILGRKYSIFTEKDEILSDVASRL
		}				WETTYRKNEPAIGGTGPTSDTGWGCMLRCGQ
		1				MIFAQALVCRHLGRDWRWTQRKRQPDSYFS
				1		VINAFIDRKDSYYSIHOIAOMGVGEGKSIGQ
		1		1		WYGPNTVAOVLKKLAVFDTWSSLAVHIAMD
1		1		1		NTVVMEEIRRLCRTSVPCAGATAFPADSDRH
1						CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLID
1		- 1				INFAYVETLKHCFMMPQSLGVIGGKPNSAHY
		1	[			FIGVVGEELIYLDPHTTOPAVEPTDGCFIPDES
				•		FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF
	!			İ		GAECCLGMTRKTFGFLRFFFSMLG
			j	_L		SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS
568	1918	A	4300	2012	1843	LMSVLIPKLPQLHGVRIFGINKY
, 500	,	1 1 1	1	i	1	L EMANULIENTEOLEGY AUGUNALI
		1		<b>!</b>	531	WTFCLFL/WWVPESARWLLTQGHVKEAHRY

					· · · · · · · · · · · · · · · · · · ·	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-Aspartic Acid F=Glutamic Acid,
10: of	NO: of	bod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		in	nucleotide	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uenœ	ļ	09/496	correspondi	acid residue	O=Glutamine R=Arginine, S=Serine,
ence	1		914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1		sequence	/=possible nucleotide deletion, \=possible
		1		peptide sequence		nucleotide insertion
		<del>  </del>	<del></del>	Sequence		LI HCARI NGRPVCEDSFSOEVRVNVCVSMHI
	ļ	1		ļ		CVWWGVGCVKCLPPRAHHIWQEKPLGPHRI
		1			1	VTESKLEAEGKTKEKAREKERKKKS
	1.000		4308	3	869	RSGQGKVYGLIGRRRFQQMDVLEGLNLLITIS
570	1920	Α	4300			CKRNKI RVYVI SWLKNKILHNDPEVEKKUG
	ļ	1	j			WTTVGDMEGCGHYRVVKYERIKFLVIALKSS
						VEVYAWAPKPYHKFMAFKSFADLPHRPLLV
	1			1		DLTVEEGQRLKVIYGSSAGFHAVDVDSGNSY
	1	1	1		•	DIYIPVHIQSQITPHAIIFLPNTDGMEMLLCYE
		1			1	DEGVYVNTYGRIIKDVVLQWGEMPTSVAYIC
		1		ļ		SNQIMGWGEKAIEIRSVETGHLDGVFMHKRA
						QRLKFLCERNDKVFFASVRSGGSSQVYFMTL
						NRNCIMNW
	1921	A	4309	9	524	ASREMDVTKVCGEMRYQLNKTNMEKDEAE
571	1921	1	1,505	1		KEHREFRAKTNRDLEIKDQEIEKLRIELDESK
	1	1		1		QHLEQEQQKAALAREECLRLTELLGESEHQL
	į	ł				HLTRQEKDSIQQSFSKEAKAQALQAQQREQE HLTRQEKDSIQQSFSKEAKAQALQAQQREQE
	İ	1	į	1	1	LTQKIQQMEAQHDKTENEQYLLLTSQNTFLT
		ĺ				KLKEECCTLAKKLEQISQ GATPLGSVGGRTGKMDAATLTYDTLRFAEFE
572	1922	A	4318	1	1119	DFPETSEPVWILGRKYSIFTEKDEILSDVASRL
312	1922	1.				WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ
	ì	l	}			MIFAQALVCRHLGRDWRWTQRKRQPDSYFS
			}			VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ
						WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD
	ļ	1			}	NTVVMEEIRRLCRTSVPCAGATAFPADSDRH
	1					CNGFPAGAEVTNRPSPWRPLVLLIPLRLGL\T
ł	١.	- 1		1	i	DINEAYVETL\KHCFHGWPQFPG/VVHREGK
l		ţ				PNSAHYFIGYVGEELIYLDPHTTQPAVEPTDG
}	ļ		ĺ			CFIPDESFHCQHPPCRMSIAELDPSIAVVRGGH
ļ ·	.	1	]			I STOAFGAECCLGMTRKTFGFLRFFFSMLG
					1066	GGVPVGLASKPFOILYGHTNEVLSVGISTELD
573	1923	A	4333	363	1066	MAVSGSRDGTVIIHTIOKGOYMRTLRPPCESS
l	ı	1				I EL TIPNI AISWEGHIVVYSSTEEKTILKUKMI
						UVICESINGKYLGSOILKEOVSDICHGEHIVIG
	ı	- }				SIGGELSIRDLHSLNLSINPLAMRLPIHCVCVI
		1		Ì	1	PEVCHII VGLEDGKLIVVGVGKPAEVKPSISN
ľ						FISHAVGDYFGSPSFQLIEKSPLGINKLKAKFD
1				ĺ		DONCON
	_				1234	MOTI FEVTWANGSTALPPPLAPNISVPHRCL
574	1924	Α	4346	359	1234	I I VEDIGTSRVRYWDLLLLIPNVLFLIFLLWK
1		1			l.	IDSARAKIRITSSPIFITFYILVFVVALVGIAKA
	1	- 1				VVSMTVSTSNAATVADKILWEITRFFLLAIEL
1	1	l l	1	1	j	SVIII GI AFGHLESKSSIKRVLAITTVLSLAYS
1	1				1	TOGIL FIL YPDAHLSAEDFNIYGHGGRQFWL
1		}			,	Vescerei vyslvvii PKTPLKERISLPSKRSF
-		)			1	VVACILALINI LOGLGSVLLCFDIEGLCCVD
1	i		ļ		ļ	ATTFLYFSFFAPLIYVAFLRGFFGSEPKILF
1_				2070	1512	GCWWRHPWLASORDCLDCRIQLAEKFVKA
575	1925	A	4360	2038	1212	CKPSRPDMNPIRVKEVYRLEEMEKIFVKLEM
1		İ		ļ		VIIKGSSGTPKLSYTGRDDRHFVPMGLYIVRI
1						VNIEPWTMGFSKSFKKKFFYNKKTKDS1FDL
		Ì				ADSIAPFHICYYGRLFWEWGDGIRVHDSQK
	1			1		ODODKI SKEDVI SFIOMHRA
1		_ 1			- 1	OVEGROGREVKRTAWRISPVWRPARCKRKS
576	1926	A	4365	69	500	POP/PE/PGAOOOERHROGEAPMQALDPRAE
				1		GPQAQSHAACQPEPEPPRVLLDPTAARGGV
1						GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCA
			]	1		EPLPLGGIRPTPGLEPKGRDLM
		1	1	1	1	LPLDIPOOH II OPPLIES DIST

	OFO ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
VO: of	peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	uence	į	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	derrec		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience	Ì	ļ	/1-	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \=possible
		[		sequence	<b>\</b>	nucleotide insertion
577	1927	A	4366	785	502	SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW
)	1921	^	1000			ASSNSRASTPKVAGITGARPHARIIFVFLIEMG
				Ì		FHNVGQAGL/DTLTLVICPPQPPKLLGLQM
578	1928	A	4367	1	221	FFFFLKKSRCVTQAGVQG\PISLHPPPPGFKRF
376	1720	1 .,	,,,,,,			SRLSLLSSWDYRHP/HAANFCIFSRDG\VSPYW
						SGWSRTPDLR
579	1929	1 <sub>A</sub>	4383	1	224	FETESHSVTQAGMQWHNLGSLQPMP/PGLKR
317	1727	1	10.00	Į.	1	FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP
		1	1			CWPGWSSTPDLK
580	1930	A	4397	410	94	SRLKPYSTNVTAKKLPATNIPNLDCFTAKLYC
J60	1750	1				VFKKGNHILHELFQNKEEGAFPNS/FYEASFI
						LRPKSDRDIAKEESYSTISLLSTDTKILMSKYK
				İ		QLKSSDL PLANCE AVEVED SADIEVED
581	1931	A	4414	670	3	VLVHRQCGGILRLRRKEAVSVLDSADIEVTDS RLPHATIVDHRPQHRWLETCNAPPQLIQGKA
301	1,751					REPHATIVDHRPOHRWLETCHATIQEIGGER
		l			}	RDVAGDTPLAVRGLLKDGP\AQRCGRLEVGL
	1		1		}	LVLHINGESTQGLT\HAQAVERIRAGGPQLHL
		1				VIRRPLETHPGKPRGVGEPRKGVVPSWPDRSI
		1			Ì	DPGGPEVTGSRSSSTSLVQHPPSRTTLKKTRG
			***			SPE SPE
						VLYIRKKKRLEKLRHQLMPMYNFDPTEEQDI
582	1932	A	4424	194	449	LEQELLEHGRDAASVQAATSVQAMQGKTTL
						PS\QGPLQRPSRLVFT\DVANAIHV
					166	APGPPVPPPGSPPEQMPGPCPASMPP/DPPPGS
583	1933	Α	4435	1	100	PPEQMPGPCPVSAPP/GPPPGSPPEQMPGPCPV
				1		SAPPALLODTSV
			1400	1	628	SATPOOPSAPOHOGTLNOPPVPGMDESMSYC
584	1934	A	4439	1	020	APPOOLPSAOPPOPSNPPHGAHTLNSGPQPGT
		1			Ì	APATOHSOAGPATGOAYGPHTYTEPAKPKK
		İ		1		GOOLWNRMKPAPGT\EVSSSTSRSDPLLLPPF
						ALAPTORASTVVLAPSPT/SEKVQNHSGSSAR
					1	GNLSGKPDDWP/LGHERVCGALLHRL*VGGC
		1			}	QGPHGKAAQGGAAGAAAGRLGLYH
	1935	A	4463	10	144	HKPVTNSRDTQEVPLEKAKQVLKIIATFKHT
585	1935	^	4403	1.0		SIFDDFAHYEKRQ
	1026	<del>                                     </del>	4464	1309	103	LNAESYVSFTTKLDIPTAAKYEYGVPLQTSD
586	1936	A	4404	1303		FLRFPSSLTSSLCTDNNPAAFLVNQAVKCTRI
						INLEQCEEIEALSMAFYSSPEILRVPDSRKKVI
		1				TVQSIVIQSLNKTLTRREDTDVLQPTLVNAG
		1			i	FSLCVNVVLEVKYSLTYTDAGEVTKADLSF
		- 1				LGTVSSVVVPLQQKFEIHFLQENTQPVPLSGI
		]				PGYVVGLPLAAGFQPHKGSGUQTTNRYGQL
ĺ	Ì	1		l l		ILHSTTEQDCLALEGVRTPVLFGYTMQSGCK
	1	ļ				LRLTGALPCQLVAQKVKSLLWGQGFPDYVA
			Į		1	PFGNSQGP/ADMLDWVPIHFITQSFNRKDSCO
						LPGALVIEVKWTKYGSLLNPQAKIVNVTAN
		ļ				SSSFPEANSGNERTILISTAVTFVDVSAPAEA
		İ				FRAPPAINARLPFNFFFFV
587	1937	$-\frac{1}{A}$	4471	614	387	LLGRASAC/LQLQSSW/D/HRPMLPYLANFVI
201	1937	1	''''	_		CKDR/SFTWLPRLVLNSWLQVILLPWPPTGC
1	}		1		!	NKHEPPCPATKRRHSGSI
400	1938	A	4480	1720	1458	HDLGSLQPPPPGFKRFSCLSLPSSWDYRLMP
588	1936	^	17700	1	ĺ	CPANFCIIIVDFLVETGFHHVGQASHELLTSG
	1		1			PPTSASQSAGITGMSYHTWFGES
589	1939	A	4487	922	332	APVTTSPRVGQPW/RTALALRSLYRARPSLR
	1737	^	7701	- ==		PPVELPWAPRRGHRLSPADDELYQRTRISLL
289	1					
389		1				REAAQAMYIDSYNSRGFMINGNRVLGPCAL PHSVVQWNVGSHQDITEDSFSLFWLLEPRIE

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	1	D=A spartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
denies			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ĺ	(	residue of	sequence	/=possible nucleotide deletion, \=possible
		Į		peptide		/=possible nucleotide deterion, /-possible
		ļ	ļ.	sequence		nucleotide insertion
			<del> </del>	<del>                                     </del>		VVVGTGDRTERLQSQVLQAMRQRGIAVEVQ
		1	i			DTPNACATFNFLCHEGRVTGAALIPPPGGTSL
		ł			}	TSLGQAAQ
	1940	A	4492	1	472	FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT
590	1940	^	1772	1 1		PFSCLSLPSSWDYRRPPLRPANFFVFLVETGFP
	1	1	]			RFSRDGLDLLT/S/GDPPTSASQSAGITGVSHR
	1	1	i			ARPKRIGEPRRKCGNAVVWPSTSLGDHRVTS
			1			VPHOGGLPGPIRVAPSSAGQREASQGPPGR
		<del> </del>	1405	1444	1116	IAARFTLAKTWNOLKRP\TMIDSIKKTR\YIYT
591	1941	Α	4495	1444	1110	MEVY ADTERNEIMSF\AGTWVELEAIILSKLM
			1			LKDNWVEDTIPQGAVPCTATAEGMKRLLFAL
ļ	ŀ		1		i	EPWDSSCEPHPSSGV
		<u> </u>		<del></del>	919	RTRPLESGRPTRPVCTMSDERRLPGSAVGWL
592	1942	Α	4496	2	713	VCGGLSLLANAWGILSVGAKQKKWKPLEFL
1	1	1				I CTL A ATHMI NVA VPIATYSVVQLRRQRPDF
}		İ	1	1		EWNEGLCKVFVSTFYTLTLATCFSVTSLSYHR
		1		]		MWMVCWPVNYRLSNAKKQAGHTVMGIWM
						GSFILSALPAVGWHDTSERFYTHGCRFIVAEI
Ĭ						GLGFGVCFLLLVGGSVAMGVICTAIALFQTL
	1	1	1	1		AVQVGRQADHRAFTVPTIVVEDAQGKRRSSI
1		1	1	j	İ	DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL
	1	Ţ	- 1	l l		GPFSLADTHLSDLPYTWGDRDSGGACVM
						FFFEAESCSVPQAGVQRPDLGWLHAPPP\GSC
593	1943	A	4506	2	193	HFPASASQVAGTTHARHHTQLIF\AFLVENGL
1				1		
			_			C KMAGGVRPLRGLRALCRVLLFLSQFCILSGG
594	1944	Α	4507	1327	647	ESTEIPPYVMKCPSNGLCSRLPADCIDCTTNFS
"			ļ			CTYGKPVTFDCAVKPSVTCVDQDFKSQKNFII
İ	1	1	l			NMTCRFCWQLPETDYECTNSTSCMTVSCPRQ
	1	1	ł	-		RYPANCTVR\DHVHCLGNRTFPKMLYCNWT
	1	1	-			GGYKWVYGLWLLRHHPRWGLGADRF\YLGP
		ĺ	l	Ì	İ	VAGTASGKLFSFGGLGIWTLIDVLLIGVGYVG
	Į		1			
i		Ì				PADGSLYI FFFKMESYSVARLECSGAISAPCNLHLLGSNN
595	1945	A	4512	533	264	FFFKMESYSVARLECSUAISAFCNLHLLOSMIN
393	1,743	1		1		SPASASRV/AGNIGARHHTQQIFVLLVQMRVH
1						YVGQDGLDLL/NLMIHPPRSPKVLGLQA
506	1946	A	4513	3	1674	HASDHLYPNFLVNELILKQKQRFEEKRFKLD
596	1740	^	7313			HSVSSTNGHRWQIFQDWLGTDQDNLDLANV
		- 1			1	AT MEET VOKKKOLEAESHAAOLQILMEPLK
1			ļ			VARRIKREOLEOIOKELSVLEEDIKRVEEMS
		- 1				GLYSPYSEDSTYPOFEAPSPSHSSIDSTEYSQP
		1	1			PGFSGSSOTKKOPWYNSTLASRRKRLTAHFE
1						DIEOCYFSTRMSRISDDSRTASQLDEFQECUS
						KENTRYNSVRPLIATLSYASDLYNGSQYKSLV
			1	-		FFFORDCDYFAIAGVTKKIKVYEYDTVIQDA
			1	1		VDIHYPENEMTCNSKISCISWSSYHKNLLASS
			ĺ			DYEGTVILWDGFTGQRSKVYQEHEKRCWSV
						DFNLMDPKLLASGSDDAKVKLWSTNLDNSV
	1			ì		ASIEAKANVCCVKFSPSSRYHLAFGCADHCV
1	1		1	1	İ	HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG
1			1	- 1		EEIVSASTDSQLKLWNVGKP\YCLRSFKGHIN
ļ		ļ			ļ	EKNFV:GLASNGDYIACGSENNSLYLYYKGLS
1						EKNFY/GLASNGD LIACOSENNOL LET TROBE
l l	1					KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV
	l l			Ī		CWRALPDGESNVLIAANS\QGTI\KVLELV
	1	l	ı	Į.		CHIE ID DODGE
	1042	<u></u>	1519	536	824	PSI ALSPGI ECSGMISAHCNLHLLGSSDPPTS
597	1947	A	4518	536	824	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS ASOVAFITSVRHHTWLIFCILGQMGFHHVGE
597	1947	A	4518	536	824	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE OAGLELLTSWDPAILPSOSAGIIGMSPHAWPP
597	1947	A	4518	536	384	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS ASOVAFITSVRHHTWLIFCILGQMGFHHVGE

					<del></del>	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spertic Acid. E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	1	in	nucleotide location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	}	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence		İ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Ì	1		peptide	Sequent	/=possible nucleotide deletion, \=possible
	1	1		sequence		nucleotide insertion
	<del> </del>	<b>├</b> ──	<del> </del>	Sequence		RRREMQSQSVMLALRRGDAVWLLSHDHDG
	Į.	1			ļ	YGAYSNHGKYITFSGFLVYPDLAPAAPPGLG
		1	1		ļ	ASELL
	1949	A	4526	366	776	MGQPAPYAEGPIQGGDAGELCKCDFLVFTSP
599	1949	ΙΛ.	7520	300		NPEAVCEAGTPAMFQTAWRQMESCSI/AQAG
	1					VQWRDPGSLHPPPLGFKRFSCLSLPSSWDYK
		ł				HAPPHPANFCIFSRDQVSPCWPGWSRSLDLVI
	1	1				PPPWLPKVLGLQA
	1950	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPG\SS
600	1950	Α .	4327	'''		DPPASASRVAGTTGARHHTQLIFVFLVETGFH
	1	1				WILARDGLKLLTSSDPPASASQSSWDYRREPF
	1					RLANFFVFLVETGSRYVAQAGVQWLFTGAIP
	}	1		1	1	LLISTGVLTCSVSDLGRFTPP
	1051	A	4533	1460	403	HEVQESIHFLESEFSRGISDNYTLALITYALSS
601	1951	^	2000	1	1	VGSPKAKEALNMLTWRAEQEGGMQFWVSS
	1	1				SKLSDSWQPRSLDIEVAAYALLSHFLQFQTSH
	1	1			Ì	GIPIMRWLSRQRNSLGGFASTQDTTVALKAL
		1				EFAALMNTERTNIQVTVTGPSSPSPVKFLIDT
		1	İ	İ		HNRLLLQTAELADGTANGSV/SISANGFGFAI
		.,,		Ì	1	CQLNVVYNVKASGSSRRRRSIQNQEAFDLDV
					ł	AVKENKDDLNHVDLNVCTSFSGPGRSGMAL
	İ	ļ		1		MEVNLLSGFMVPSEAISLSETVKKVEYDHGK
	1	ļ			ļ	LNLYLDSVNETQFCVNIPAVRNFKVSNTQDA
	1					SVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSI
		1				VQRLPSL
602	1952	A	4540	1963	295	MRAPGRPALRPLPLPPLLLLLLSSPWGRAVPO
602	1932	1 1	,,,,,,			VSGGLPKPANITFLSINMKNVLQWTPPEGLQ
	ļ	1				VKVTYTVQYFIYGQKKWLNKSECRNINRTY
			1			DLSAETSDYEHQYYAKVKAIWGTKCSKWAI
		1		1		SGRFYPFLETQIGPPEVALTTDEKSISVVLTAI
		ļ			ł	EKWKRNPEDLPVSMQQIYSNLKYNVSVLNT
	1	į.				KSNRTWSQCVTNHTLVLTWLEPNTLYCVH
	ļ		l l			ESFVPGPPRRAQPSEKQCARTLKDQSSEFKA
	ŀ	- 1				IIFWYVLPISITVFLFSVMGYSIYRYIHVG\KE
	ļ	j			Į.	HP\ANLILIYG\NEFDKRFFVPA\EKIV\NFI\TL
		İ	1	ļ		NIS\DDSKISHQDMSLLGKSSDVSSLNDPQPS
	1	.	j			NLRPPQEEEEVKHLGYASHLMEIFCDSEENT
	i		ļ	j	}	EGTSFTQQESLSRTIPPDKTVIEYEYDVRTTD
		1	ļ	l		CAGPEQELSLQEEVSTQGTLLESQAALAVI
				1	1	GPQTLQYSYTPQLQDLDPLAQEHTDSEEGPI
		ļ				EPSTTLVDWDPQTGRLCIPSLSSFDQDSEGC
ļ		İ				PSEGDGLGEEGLLSRLYEEPAPDRPPGENET
		1		ļ		LMQFMEEWGLYVQMEN
602	1953	A	4543	3	600	YSAVEFVEQASGISDWWNPALRKRMLSDSG
603	1900	1	1,5.5	1		GMIAPYYEDSDLKDLSHSRVLQSPVSSEDH
İ	-					LQAVIAGDLMKLIESYKNGGSLLIQGPDHCS
1			\			LHYAAETGNGEIVKYILDHGPSELLDMADS
		1	- [			TGETALHKAACQRNRAVCQLLVDAGASLR
					1	TDSKGKTPQERAQQA\GDPDLAA/YTIESRQ
]	1	}		1		YKVIGHEDLETAV
	1051		4548	3	938	QDNKVQNGSLHQKDTVHDNDFEPYLTGQA
604	1954	A	4348	١	1	OSNSYPSMSDPYLSSYYPPSIGFPYSLNEAP
					1	STAGDPPIPYLTTYGOLSNGDHHFMHDAVE
	1					OPGGLGNNTYOHRFNFFPENPAFSAWG1SG
1		1				OGOOTOSSAYGSSYTYPPSSLGGTVVDGQF
		ļ				FHSDTLSKAPGMNSLEQGMVGLKIGDVSSS
		]	)		1	VKTVGSVVSSVALTGVLSGNGGTNVNMPV
1	1	ĺ				KPTSWAAIASKPAKPOPKMKTKSGPVMGG
ı	1	- 1				LPPPPIKHNMDIGTWDNKGPVPKAPVPQQA
1	1	1				LPPPPIRMINIDIGI (I DI III CI I I I I I I I I I I I I I I

NO: of NO: of nucleotide eotide sequence uence uence   NO: of nucleotide   ID NO: beginning nucl	Predicted end nucleotide location corresponding to last amino	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
nucl- eotide seq- uence uence    NO: 01   NO: 01   IIIOU   IIIIII   IIIIIIIIIIIIIIIIIIII	location corresponding to last amino	F=Phenylalanine, G=Glycine, H=Histidine,
eotide seq- eotide seq- uence USSN location correspondi ng to first amino acid residue of peptide	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine,
eotide seq- uence	to last amino	1=1SOleucine, R-Lysnie, B Beating
seq- uence   09/496   correspondi   1 914   ng to first   amino acid   residue of   peptide		
uence 914 ng to first amino acid residue of peptide		M=Methionine, N=Msparagille, r=r toline,
amino acid residue of peptide	acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of peptide	of peptide	T=Threonine, V=Valine, W=Tryptophan,
peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	504201101	/=possible nucleotide deletion, \=possible
		nucleotide insertion
sequence		SPQAAPQPQQVAQPLPAQPPALAQPQYQSPQ
		QPPQ   ILLQEKRNCLLMQLEEATRLTSYLQSQLKSLC
605 1955 A 4553 2	2304	ILLQEKRNCLLMQLEEATRL151LQSQLRSLC
003 1755 12		ASTLTVSSGSSRGSLASSRGSLASSRGSLSSVS
		FTDIYGLPQYEKPDAEGSQLLRFDLIPFDSLGR
		DAPFSEPPGPSGFHKQRRSLDTPQSLASLSSRS
		SUSSUSPESSPLDTPFLPASRDSPLAQLADSCE
		GPGLGALDRLRAHASAMGDEDLPGMAALQP
		HGVPGDGEGPHERGPPPASAPVGGTVTLRED
		SAKRLERRARRISACLSDYSLASDSGVFEPLT
		KRNEDAEEPAYGDTASNGDPQIHVGLLRDSG
		SECLLVHVLQLKNPAGLAVKEDCKVHIRVYL
		SECTIVE AND THE COLOR AT EEO VELVENE VENE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AND THE COLOR AT EEO VELVE AN
		PPLDSGTPNTYCSKALEFQVPLVFNEVFRIPV
		HSSALTLKSLQLYVCSVTPQLQEELLGIAQIN
		LADYDSLSEMQLRWHSVQVFTS\LNHQGRGR
		I GVOER APPOTLHTPSPSPA/STDAVIVLLAR
		TTAOLOAVERELAEERAKLEYTEEEVLEMER
		KEEOAEAISERSWOADSVDSGCSNCTQTSPPY
		PEDCCMGIDSILGHPFAAOAGPYSPEKFQPSPL
		KVDKETNTEDLFLEEAASLVKERPSRRAKGSP
		FVRSGTIVRSQTFSPGARSQYVCRLYRSDSDS
		STLPRKSPFVRNTLERRTLRYKQSCRSSLAEL
		MARTSLDLELDLQASRTRQRQLNEELCALRE
		MARTSEDLELDEQASKTRORQENEDEGIALR
		LRQRLEDAQLRGQTDLPPWVLRDERLRGLLR
		EAERQTRQTKLDYRHEQAAEKMLKKASKEI
		YQLRGQSHKEPIQVQTFREKIAFFTRPRINIPPL
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	)	GFYGMYDKILLFRHDPTSENILQLVKAASDIQ
		EGDLIEVVLSASATFEDFQIRPHALFVHSYRA
		PAECDHCGEMLWGLV\ROGLKCEGCGLNYH
	1	KRCAFKIPNNCSGVRRRRLSNVSLTGVSTIRT
	İ	SSAELSTSAPDEPLLQKSPSESFIGREKRSNSQ
	1	SYIGRPIHLDKILMSKVKVPHTFVIHSYTRPTV
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		CQYCKKLLKGLFRQGLQCKDCRFNCHKRCA
		PKVPNNCLGEVTINGDLLSPGAESDVVMEEG
		SDDNDSERNSGLMDDMEEAMVQDAEMAMA
		ECQNDSGEMQDPDPDHEDANRTISPSTSNNIP
	1	I MRVVOSVKHTKRKSSTVMKEGWMVHY1S
		KOTI RKRHYWRLDSKCITLFONDTGSRYYKE
		TPL SETL SLEPVKTSALIPNGANPHCFEITTANV
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	1	FKLHGDMLEMILSSEKGRLPEHITKFLITQILV
		AT RHI HEKNIVHCDLKPENVLLASADPFPQV
		KICDEGEARIIGEKSFRRSVVGTPAYLAPEVL
		PNKGYNRSLDMWSVGVIIYVSLSGTFPFNED
		EDIHDQIQNAAFMYPPNPWKEISHEAIDLINN
		LLQVKMRKRYSVDKTLSHPWLQDYQTWLDL
		LLUAKWKK 12ANY ITSUL AFOR 161 AFOR
		RELECKIGERYITHESDDLRWEKYAGEQGLQ
		VPTHI INPSASHSDTPETEETEMKALGERVSIL
607 1957 A 4563 1	4499	SRPWWLRASERPSAPSAMAKRSRGPGRRCLL
607 1957 A 4563 1	1	ALVI FCAWGTLAVVAOKPGAGCPSRCLCFRT
		TVRCMHLLLEAVPAVAPQTSILDLRFNRIREI
		QPGAFRILRNLNTLLLNNNQIKRIPSGAFEDL
	1	ENLKYLYLYKNEIQSIDRQAFKGLASLEQLYL

NO: of nucleotide sequence white the period of the period		0EQ ID	N/at	CEO.	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucle could could contend the contended contended to the contended country of the contended country of the contended country of the contended country of the	SEQ ID	SEQ ID	Met	SEQ			D=Aspartic Acid. E=Glutamic Acid,
uence USSN jester 1914	-		noa	1 :		1	F=Phenylalanine, G=Glycine, H=Histidine,
uence of the control		• •	1				I=Isoleucine, K=Lysine, L=Leucine,
uence  914  914  914  914  915  914  915  915	eotide			I .			M=Methionine, N=Asparagine, P=Proline,
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nucleotide insertion HPNQETLOPDSFORM_PKLERLFLHNNRTHL VPGTFNHLESMKRLRLDSNTLHCDCEILWLA DLLKTYAESGNAQAAGCYPRRQGRSVATI TPEELNCERRRTISEPQDADVISGNTVYTTCR AGGNYKPEILWLRNNRLSMKTDSRINLLDD GTLMQNTQETDQGTYQCMAKNVAGEVKTQ EVTLRYFGSPARPTFUPQPQNTEVLYGESVTL ECSATGHPPRISWTRGDRTPLPVDPRVNIDTY GGLYQNVQQDSGEVACSATNINDSWHATA FILVQALPQFTVTPQDRVVEGGTVDFQCEAK GNPPPVJAWTKGGGSJQSVDRRHLVLSSGTLR SGVALHDQGQYECQAVNIIGSQKVVAHLTVV PRVTPVTASIPSDTTVEVGANVQLPCSSQGEP EPAITWNKDGQVTCTSGKFHISPEGFLTINDV GPADAGRYECVARNTIGSASVSMULSVNPP VSRNGDPFVATSIVEALATVDRAINSTRTHLF DSPRSSPDLLALFRYPRPTYTEQCRAGEIE ERTLQLQEHVQHGLMVDLNOTSYHYNDLV VSRNGDPFVATSIVEALATVDRAINSTRTHLF DSPRSSPDLLALFRYPRPTYTEQCRAGEIE ERTLQLQEHVQHGLMVDLNOTSYHYNDLV VSRNGDFFVATSIVEALATVDRAINSTRTHLF DSPRSSPDLLALFRYPRPTYTEQCRAGEIE ERTLQLQEHVQHGLMVDLNOTSYHYNDLV VSRNGDFFVATSIVEALATVDRAINSTRTHLF DSPRSSPDLLALFRYPRDYTYTEQRAGEIE ERTLQLQEHVQHGLMVDLNOTSYHYNDLV VALSQARSDQQHCARVSNVENDPFCSWMFPP DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREGINQLSTURJONATVGSTEHERLLSSVY VALSQARSDQQHCANVCSNDPFCSWMFPP DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREGINQLSTURJONATVGSTEHERASIKU LASHRGLLRQGIVQRSGKPLLFFATGFPTEC RDRNSSPPCFLAGDHANDQLGLTSHAFILW FREHNRIATELLKLNPHWDGDTTYYETRKIV AEQMITTYQHLVPRLLGGVMRTLGGYHGYT PGINAGIFNAFATNAFRGGTDFLL RGLFGVAGKMRVPSQLLNTELTELERSMAH AEQMITTYQHLVPRLLGGVMRTLGGYHGYT PGINAGIFNAFATNAFRGGRPLL ERQPQDELLPHATGFFTHAMSGGDPLL RGLFGVAGKMRVPSQLLNTELTELERSMAH AFSTRSDASGTNDFGRYCSWEMQKTITDLS LFPALVYDLIVPGSRLGFHATSTRYNNCSGDEPRV LRVWQDCCEDCRTRGQFNAFSYHRGGRSL LFPALVYDLIVPGSRLGFHATSTRYNNCSGDEPRV LRVWQDCCEDCRTRGQFNAFSYHRGGRSL FSYQEGKFTKKTRFKRKINSGRGGEBPL TOKKLESRUSTITECVDAGGESHANNTEW KQACTCECKDGQVTCFVEACPPATCAPVY LRVWQCCCGGTTLTLTGSKKLACGLNEFN FSFLCGVSGRLGGLDSEDVYTPQKVVVPFA FSCLSRPSSWDYRRPLRFANNTEW KQACTCECKDGQVTCFVEACPPATCAPVY LRVWQCCCGGTTLTLTGSKKLACGLNEFN FSFLCGVSGRLGGLDSEEDVYTPQKVVVPFA FSCLSLFSSWDVRRPLRFANNTEW KQACTCECKDGQVTGFVEACPPATCAPVY FFFETESSRSVAQAGVQWRDLGSLQAPPGG FFSCLSLFSSWDVRRPLRFANNTEW HANDQCCGGTTLTLTGSKKLACGLNEFN FFFETESSRSVAQAGVQWRDLGSLQAPPGG FFSCLSLFSSWDVRRPLRFANFFVLVETGG LGVGNYKKLGGNPASSASGAGTGVSI RARRINLRNVTSFAVTYCLNYSLA		ł	1	ŀ		sequence	/
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AEGNPKPEIIWLRNNNELSMKTDSRUNLGDU GTLMIONTOETIDGOTGYCMANGEVKTIQ EVTLRYTGSPARPTFVIOPGNTEVL/GESVIT ECSATCHPPPISISWTGDRIPLYDPRVNITP GGLYIONVVQGDSGEYACSATNNIDSVHAT FIIVQALPQFTVTPODRVVEGGTVDFCQCEAK GNPPPVAMTKGGSQLSVDRRHLVLSSGTLR SGVALHDQGYECQANNIGSGVAVAHLTV PRVTPYFASIPSTTYEVGANVQLPCSSGCPEP EPAITWNRDGVQVTESKERHISPEGFLTINDV GPADAGRYECVARNTIGSASVSMVLSVNDPI VSRNGDPFVATSIVEAIATVDRAINSTRTHLF DSPRSPNDLLALFRYRPRPYTYTVQARAGOLI ERTLQLIGEHVQHGLMYDLNGTSYRYNDL PRVTPTASIPSTALAFRYRPRYTYTVQARAGOLI ERTLQLIGEHVQHGLMYDLNGTSYRYNDL PRVTNLIANLSGCTAHRRVNNOSDMCFRIQK RTHDGTCNNLQHPMWGASLTAFERLLSXY PROTTPRINPRILNYGHALPMPRLVSTTL GTETVTPDEQFTHMLMQWGQFLDHELDST VALSQARFSDQOHCSNVCSNDPPCFSVMIPP DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREQNNQLTSYIDASNVYGSTLARSKINL LASHRGLLRQGIVQRSGKPLLFFATGPTER DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREQNNQLTSYIDASNVYGSTLARSKINL LASHRGLLRQGIVQRSGKPLLFFATGPTER CREENINATELLKLNPHWDGDTTYYETRKLARSKIL LASHRGLRQGIVQRSGKPLLFFATGPTER REGNRAFATAAFRGGTLVNPLLLGTER REGNRAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGY PGINAGGTNAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGY PGINAGGTNAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGY PGINAGGTNAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGY PGINAGGTNAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGYY PGINAGGTNAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGYY PGINAGGTNAFATAAFRGGTLVNPLLLGTUR AEIGHTVQHWLPKLIGEVGMRTLGEYHGYY PGINAGGTNAFATAAFRGGTLVNPLLGTUR AEIGHTVQHWCACHAUR AEIGHTVQHWLPKLIGEVGMRTLGERSLLTTQCTRACH VAUCAGCMGTNAFATAAFRGGTLVNPLLLGTOR LATATTONTHAWACCGCGERPAV NACHTECKOGQVTGVVACAGCHERNST AUTSTRADASGTNAFATHERSLLRAG LNCACCHAUR LTVAVCCGCGTFLLTQSGKVLACCLLEFTER LSTPLCGVSGRLGGTSEEDYTPFQKVDVPKA INVAVCCGCGTFLLTQSGKVLACCLLEFTER LSTPLCGVSGRLGGTSEEDYTPFQKVDVPKA INVAVCCGCGTFLLTQSGKVLACCLLEFTER LSTPLCGVSGRLGGTSEEDYTPFQKVDVPKA INVAVCCGCGTFLLTQSGKVLACCLLEFTER LSTPLCGVSGRLGGTSEEDYTPFQKLVPYCGG LGVGWYKRLGGTGSEEDYTPFQKVDVPKA INVAVCCGCGTFLLTQSGKVTACCGGMTT VEKVLNSKTIRSNSSGLSIGTVFGSSSGGGG GGPDAW  BFFLCGSTSWRPPFGGLHVPTTSFTLAKQU LCVGWYKRLGGTGSEEDYTPFGGLHVPTTSFTLAKQU LCVGWYKRLGGTGSEEDYTPFGGLHVPT		1	1				DLLKTYAESGNAQAAAICEYPRRIQGRSVAII
GTLMIONTOETDOGNYCAMENVAGENTLU GESVIL EVERNYGSBARFFFVIQPORNYLLYGESVIL ECSATCHPPRISWTRGDRTPLPVDRVNYHTH GLYONVVQGDSGEYACSATNIDSVHATH FILVQALPQFTVTPODRVVEGQTVDFCCEAK GNPPPVLAWTRGGGSLSVDRRHUSSGTLR SGVALHDQGQYECQAVNILGSQKVAHLTVV PRVTPVFAGRSGLSVDRRHUSSGTLR GNPPVLAWTRGGGSLSVDRRHUSSGTLR GNPPVLAWTRGGGSLSVDRHUSSGTLR GNPPVLAWTRGGGSLSVDRHUSSGTLR GNPPVLAWTRGGGSLSVDRHUSSGTLR GNPTPTRGISPHTVEVGANCY VERNGDPFVATSIVEAGLSVDRAMSTRTHLF DSRPRSPRDLLALFRYPRDPYTVEQAACGIF ERTLQLIQEHVQHGLMYDLAGTSTHYNDLV PQVLNLLANLSGCTAHERVNNCSDMCFHQL ERTLPTPDEQFTHMLMQWGGPLDHDLDSTV VALSQARFSDGOHCSNVCSNDPPCFSVMIPP DSRARSGARCMFVSSSPVCSGMTSLLMN VYPPEQINOLISYDASNVCSTEHEARSIND LASHRGLLRQGIVQRSGKVELPTGPFTCA RDENESPTCFLAGDHRANEQLGLTSMHTLW FREINRAHTELLKLNPHVDGOHDYFTRKIV AEQHITYQHWPRCLIGEVGMRTLGFYHGYT PGINAGIFNAFATVAFRFGHTLVNPLLIPGL ENCPHAQDHLPHLKAFFSPRTVNEGGIPPL RGLEGVAGKMRVPSQLJNTELTBRLFSNAH VALDLAANINGRBHGDPPTDVRVYCNLS AAHTFEDLKNEKKPEIRFKLKKLRYGSTIND LFPALVVEDLVPGSRLOPTLMGTSLABL LFPALVEDLVPGSRLOPTLMGTSLABLANTLWK KDACTICECKDGQVTCFVFACOPATCAVPVP PGACCPVCLQKRAEEKP  FFIC.GGVGSRLGILDSEDVTPQKVTDPAA HIVAVCGCDGTFILTIQSGKVLACGLABL TYKRITAPGKTHTAADDRGRRLTPGCRCCC LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGGKQVIRVSCG LGVGYYKRLGINLGGELGG			ł	ı			TPEELNCERPRITSEPQDADVTSGNTVYFICR
EVILRYFGSPARTFYJOPONTEVLYGESVJORGEN LECSATCHPPPRISWTGDRIPLPJOPDRVNTEP GGLYJONVVQGDSGEYACSATNNIDSVHAT FINQALPQFTYTPDDRVVEGGTYDFOCEAK GNPPPVLAWTIGGSOLSVDRRHLVLSSGTLR. SGVALHDQGYECQAVNIIGSGVAVAHLTV ROMEN FRETTYPFASIPSDTTVEVGANVQLPCSSOGEP EPAITWNKDGVQYTESGKFHISPEGFLTINDV GPADAGRYECVARNTIGSASVSWLSVNVPI VSRNGDPFVATSIVEALATUDRAINSTATHLE DSPRPSPDLLALAFRYPRDFYTYSQARAGEI ERTLQLIGEHVGHGLMYDLNGTSYHYNDL VSRNGDPFVATSIVEALATUDRAINSTATHLE DSPRPSPDLLALAFRYPRDFYTYSQARAGEI ERTLQLIGEHVGHGLMYDLNGTSYHYNDL POYLNLIANLSGCTAHREVNINCSDMCFHIQK RTHDGTCNNLQHEMWGASLTAFERLLXN ENGTHRENGLAFELLAFRYBRDFYTYSQARAGEI ERTLQLIGEHVGHGLMYDLNGTSYHYNDL FORDTPRGGNPHRLYNGHLAPPRLVSTTL GTETYTPDEQFTHMLMQWGQFLDHDLDSTY VALSQARFSDQOHCSNVCSNDFSTWMIPP SORRAGGARCMFYRSSPVGSGGMTSLLMN VYPREQINQLTSYHDASNYVGSTEHEARSIKD LASHRGLLRQGTVQRSGKPLIPFATGPTECA RDENESPIPCHLAGDHRANEQLGITSMHTHL FREHNRLATELLKLNNHWDGDTTYFETRIN AEIGHTYGHWLPRLIGEVGMRTLGEYTHG FREHNRLATELLKLNNHWDGDTTYFETRIN AEIGHTYGHWLPRLIGEVGMRTLGEYTHG FREHNRLATELLKLNNHWDGDTTYFETRIN AEIGHTYGHWPRUGGRDHGDTYTFTRIN AEIGHTGHAMPRUSGLITHALLSTORM ALDLAANIQRGRDHGDPYHDYRVTCHL BRICGVGRKKKEYPSTLNIBGLITHALL BRICGVGRKKKEYPSTLNIBGLITHALLSTORM ALDLAANIQRGRDHGDPYHDYRVTCHL BRICGVGRKKKEYPSTLNIBGLITHALL BRICGVGRKKKEYPSTLNIBGLITHALLSTORM ALDLAANIQRGRDHGDPYHDYRVTCHL BRICGVGRKKKEYPSTLNIBGLITHALLSTORM ALDLAANIQRGRDHGDPYHDYRVTCHL BRICGVGRKKKEYPSTLNIBGLITHALLSTORM ALDLAANIQRGRDHGDPYHDYRVTCHL BRICGVGRKKKEYPSTLNIBGLITHALLSTORM ALDLAANIQRGRDHGDPYHDYRVTCHL BRICGVGRKKKEYPSTLNIBGLITHALLSTORM AUSTRSDASGTNDFQRVCSWEMQKITILDT TOKKKLSRULSTREVPAGGESHANNTKWK KDACTICECKDGQVTCTVEACPPATCAVPV PGACCPVCLOKRÆFKP PGACCPVCLOKRÆFKP FSCGVKJKKTRRNSSGLIGTVFQSSSDGGG GGFDAW BRITGTWRTPIGSLHHVPLDLCRGWHTH VEKVLNSKTIRSNSGLIGTVFQSSSSGGGG GFTAAATDDNHIFAWGNGNGRLAMTTFT HERDTATDDNHIFAWGNGNGRLAMTFTE HERDTCTSWPRPIGSLHHVPLSCGGWHTH VEKVLNSKTIRSNSGLIGTVFQSSSSGGGG GFTAATDDNHIFAWGNGNGRLAMTFTY FFETESRSVAQAGVOWRDLGSLOAPPFA GOOD 1959 A 4567 1 412 FFFETESRSVAQAGVOWRDLGSLOAPPFA FFFETESRSVAQAGVOWRDLGSLOAPPFA FFFTETERSSVAGAGVOWRDLGSLOAPPFA FFFTETERSSVAGAGVOWRDLGSLOAPPFA FFTETERSSVAGAGVORVBLGSLOAPP			ļ	ł			AEGNPKPEIIWLRNNNELSMKTDSRLNLLDD
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CSATGHPPRISWTRGDRTPLFVDPRVNTFF   GGLYiONVOGDSGEVASATNNIDSVHATA     GGLYiONVOGDSGEVASATNNIDSVHATA     FIIVQALPQFTVTPQDRVTEGQTVDPCCEAK     GNPPVLAWTKGSQLSVDRRHLVLSGGTLK     SGVALHDGGVYECQAVNIIGSQKVVAHLTVC     PRVTTVFASISDTTVEVGANDLPCSSQGEP     FPAITWNKDGVQTTESGKHISPBGETLINDV     GPADAGRYECVARNTIGSASVSMVLSVNVPJ     VSRNQDPFVATSIVEALATVDRAINSTRTHLF     DSRRSSPNDLLALRRYPRDPYTVEQARAGEI     ERTLQLIQEHVOHGMWVDLNGTSYHYNDLV     PQYLNLIANLSGCTAHRRVNNCSDMCFHQK     RTHDGTCNNLOHPMWGASLTAFERLLKSVY     ENGRYTPRGINPHRLYNGHALPMRLSTIL     GIETVTPDEGTHMLMQWGPLDHDLDSTY     VALSQARSDOQHCSNVCSNDPPCSSWIPP     SRRASGARGMFVRSSPVCGSGMTSLLMN     VYPREQINQLTSYIDASNVYGSTEHEARSIKD     LASHRGLLRGGVYGRSGFLIPATGPTECK     REFINEATELLKLNPHWOGPLDHDLSTY     VALSQARSDOQHCSNVCSNDPPCSSWIPP     DSRRASGARGMFVRSSPVCGSGMTSLLMN     VYPREQINQLTSYIDASNVYGSTEHEARSIKD     LASHRGLLRGGVYGRSGFLIPATGPTECK     REFINEATELLKLNPHWOGPLDHDLSTY     VALSQARSDOQHCSNVCSNDPPCSSWIPP     DSRRASGARGMFVRSSPVCGSGMTSLLMN     VYPREQINQLTSYIDASNVYGSTEHEARSIKD     LASHRGLLRGGVYGSGLEPATGPTSHTP     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGPTECK     REFINEATELLKNPHWOGPLIPATGPTECK     REFINEATELLKLNPHWOGPLIPATGH     REFINEATELLKNPH     REFINEATELLKNPH     REFINEATELLKNPH     REFIN		}	1	1	}		EVTLRYFGSPARPTFVIQPQNTEVLVGESVIL
GGLYIQNIVQGDSGEYACSATINIDSYHATA FIRVQALPGTYTPQRV VIEGOTYDFQCEAK GNPPYUAWTKGGSQLSVDRRHU.VSGGTLR SGVALHDGGQVECQAVIIGSQKVVAHLTV PRVTTVFASIPSDTTVEVGANVQLPESSGGEP EPAITWNKDGVQVTESKHISPEGELTINDV GPADAGRYECVARNTIGSASVSMVLSVAVPI VSRNGDPFVATSIVESALATVDRAINSTRHLF DSRRSSPDLLALRFYRPBDFYTVEQARAGEI! ERTLQLIQEHVQHGLMVDLNGTSYTYDNLV PQYUNLIANI.SGCTAHRRYNNCSDMCFHQK RTHDGTCNNLQHPMWGASLTAFERLIKSVY ENGFNTPRGINPHRLYNGBALPMPRLSYNTL GTETYTPDEQFTHMLMQWGQFLDHIDLDSTV VALSQARSDQHCSNVCSNDPFCSVMIPP] DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREQINQLTSYHDASVYSTEHAASIRD LASHRGLLRQGIVQRSGKPLLPFATGPTPECK RDENESPIPCFLAGDHRANRQLGLTSMHTLW FREINRIATELIKKINPHUDDTTYYFETRKIV AEIQHITYQHWLPKILGEVGMRTLGEVHGY AEIQHITYQHWLPKILGEVGMRTLGEVHGY FORMAGFNAFATAAFREGIDPLL GRIGGVAGKMVPSQLLNTBLIFERLFSNAH VALDLAANINQRGRDHGIPPYHDVRVVCNLS AAHTFEDLKKINFUNGEKKIKRI,VGSTLGT ENGPJAQDHLPLHKAFFSPFRIVSEGIDPLL GRIGGVAGKMVPSQLLNTBLITERLFSNAH VALDLAANINQRGRDHGIPPYHDVRVVCNLS AAHTFEDLKKINFUNGEKKIKRI,VGSTLGT LRVWQDCCEDCRITRQGFNAFSYHFGRRSL FSYQEDKFTKTRJRFIKSVGRQGEHLSNSTI AUSTRSDASGTNDFGRVCSWEMQKTITDLF TQIKKLESRUSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPV PGACCPVCLQKRAEEKP  FSFLGVSGRIGLDSEEDYYTPGKVDYPKA IIVAVQGCGDFTBLTQSGKVLACGLNEFNK KDACTICECKDGQVTCFVEACPPATCAVPV PGACCPVCLQKRAEEKP FSFLGVSGRIGLDSEEDYYTPGKVDYPKA IIVAVQGCGDFTBLTQSGKVLACGLNEFNK KDACTICECKDGQVTCFVEACPPATCAVPV PGACCPVCLQKRAEEKP GGPDAW  FFFFTESRSVAQAGYQWRDLGSLQAPPGG FFTIAATDDNHIFAWGNGGGRIAAMFTER HGSDLCTSWRPFFGSLHHVPDLSCRGWHTI VCKVLNSKTTRSNSSGLSICTVFQSSSPGGGG GGPDAW  609 1959 A 4567 1 412 FFFFETSRSVAQAGYQWRDLGSLQAPPGG FFTSCLSLPSSWVRRPPLRAMFFVLVETGG GGPDAW  FFFFTESRSVAQAGYQWRDLGSLQAPPGG FFSCLSLPSSWVRRPPLRAMFFVLVETGG HRSBCDCTLSWRPPGSSHAWFTLAKAMSTI KLSPHVLSGS  610 1960 A 4570 697 467 GCCGVSAAACCTCLUCPSSSDSASAFRVARRT		1		1		1	ECSATGHPPPRISWTRGDRTPLPVDPRVNITPS
FINOALPQFTVTPQDRVVEGQTVDPCCEAR GNPPVIAWTKGSQSUSTORRHLVUSSGTLR SGVALHDQGYECQAVNIIGSQKVVAHLTVU PRVTTPVRASIPSDTTVEVGANDLPCSSQGEP EPAITWNKDGVQVTESGKEHISPEGELTINDV GPADAGRYECVARNTIGSASVSMVLSVNVPI VSRNODPFVATSIVEALATVDRAINSTRTHLF DSRPSSPNDLLALFRYPRDPYTVEQARAGEIF ERTLQLIQEHVQHGEMVDLNGTSYTYNDLV PQYLNLIANLSGCTAHRRVNNCSDMCFHQK RTHDGTCNALOHPMWGASLAFEELLKSVY ENGPHTPRGINFHRLYNGHALPMPRLVSTIL GTETVTPDEOFTHIMLMOWGOPLDHDLDSTY VALSQARFSDQHCSNVCSNDPPCFSWIPP) DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREGINQLTSYIDASNVYOSTEHEARSIRD LASHRGLLRQGIVQRSGKPLLPFATGFPTECN RDENSSPPCTLAGDHRANREQLGLTSMHTLW PREINRIATELLKLNPHWDDDTYYTETRIV AEIGHTYQHMLPKILGEVGRWRTLGFHGV PGINAGIFNAFATAAFRGHTLVNPLLIFGLL ENFOPIAQOHLPLHAFFSPRIVNEGGIDPLL RGLFGVAGKMRVPSQLLNTELTERLFSMAH VALDLAANNQRGRDHGPPPYDRVYVYCNLS AAHTFEDLKNEIKNPEREEKURLYGSTILND LFPALVVEDLVPGSRLGPTLMCLISTJCFKRL DGDRLWYENPGVFSPAQLTQIRQTSLARILC NADNITRVQSDVRVAEFPHGYGSCDEPKV LRVWDCCEGDCTRGGPNASYHFRGRRSL FSYGEDKPTKKTPRRKIPSVGRQGEHLNSTT AUFSTRSDASGTNDFGRVCSWEMQKTITDLE TQUKKLESRLSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPVP GORAGINHEAVHEVPYTTSTLAKQLS YKIRTLAPGKRTHADHERFRUSHORGGEHLNSTT AUFSTRSDASGTNDFGRVCSWEMQKTITDLA TQUKKLESRLSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPVP GORAGINHEAVHEVPYTTSTLAKQLS YKIRTLAPGKRTHADHERFRUSHORGGHEHNSTT AUFSTRSDASGTNDFGRVCSWEMQKTITDLA TQUKKLESRLSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPVP GORACCPVCLOKRAEEKP HGSDLCTSWPFPFGSLHTPVCSNCGMHTH VVXVCCLOKRAEEKP HGSDLCTSWPFFFGSLHTPVCSNCGMHTH VVXCVLOKRAEEKP HGSDLCTSWPFFFFGSLHTPVCSNCGMHTH VVXCVLNSKTIRSNSSGLSIGTVFQSSSFGGG GGPDAW  609 1959 A 4567 1 412 FFFFETESSRVAQAGVQWRDLGSLQAPPGF PFSCLSLPSSWDYRPPLRAPMFFVLVETGG LGVGNYKKRLGINLTGGPPASASQSAGITGVSI RAPRRNLRNVTYSFAVTYCLNYISLAMSSTI LSTFHVLSGS  610 1960 A 4570 697 467 GCGVSNSAFAVCCTLCLPSSSDASAFAVART		ł		1			GGLYIONVVOGDSGEYACSATNNIDSVHATA
GNPPYVAWTKGGSQLSVDRRHUVLSGILR SGVALHDGGVECQAVNIGSQKVVAHLTVC PRVTPVFASIPSDITTVEVGANVQLPCSSQGEP EPAITWNKDGVVTESGKFHSPEGELTINDV GPADAGRVECVARNTIGSASVSMVLSVNVPI VSRNGDPFVATSIVEALATVARNSTRHLE, DRRRSSPDLLALFRYPRDPYTVEQARAGEI ERTLQLIQEHVQHGLMVDLNGTSYTYDLV PQYLNLANLSGCTAHRRVNNCSDMCFHQK RTHDGTCNNLQHPMWGASLTAFEELILKSVY ENGRYPREDITHALNQWGQFLDHDLDSTV VALSQARFSDOHENVYSSTEHEARSIKD ULASHRGLLRQGIVQRSGKPLLPFATGFHECN RDENESPTCFLAGDHRANFGLGTGHPTECN RDENESPTCFLAGDHRANFGLGTGHTAGHLAGTGHTAGHTAGHTAGHTAGHTAGHTAGHTAGHTAGHTAG		<b>\</b>					FILVOAL POFTYTPODRYVIEGOTYDFQCEAK
SGVALHDQGGYECQANTIIGSQKVAHLTW PRYTPVFASPISDTTVEVGANVQLPCSSQGEP EPAITWNKDGVQYTESGKFHISSGETINDV GPADAGRYECVARNTIGSASVSMVLSVNVPI VSRNGDPFVATSIVEAIATVDRAINSTRTHLE, DSRPKSPNDLLALFRYPRDPYTVEQARAGEII ERTICQLQEHYQHGLMVQLNGTSYHYNDLV PQYLNLIANLSGCTAHRRVNNCSDMCFHQK RTHDGTCNIN, QIFBWGASLTAFERLLKSVY ENGFNTPRGINPHRLYNGHALPPRLVSTTLL GTETVTPDEQFTHALM MQWGQFLDHDLDSTY VALSQARFSDGOHCSNVCSNDPPCSVMIPP DSRARSGARCMFFVRSSPVCGSGMTSLLMN VYPREQROLTSYIDASNVYGSTEHEARSIRD LASHRGLLRQGIVQRSGKPLLPFATGPTECA RDENESPEPCHAGDHEANBQLGLTSMHTLW FREHNRIATELLKLNPHWDGDTIYFETRIV AEIQHITYQHVPKILGEVGMRTLGEVHGYT PGINAGIFNAFATAAFRIGHITVHPLLLPGIL ENFQPIAGDHPLHIKAFSPFRIVNEGGIDPLI RGLFGVAGKMRVPSQLLINTELTERFSNAH VALDLAANNQRGDHGPHYDDVXVCNLS AAHTFEDLKNEKNPEIREKLKRLYGSTLND LIPPALVYEDLVPGSRLOFTIMCLISTOFKRL DGDRLWYSNPOVESPAQLTQIKQTSLARILC NADNITRVQSDVFRVAEFPHGYGSCDEIRV LRWWQDCCDCTRTGGPNAFSYHFRGRRSL FSVQEDKPTKKTRPKKIPSVGRQGEHLSNSTT AFSTRSDASGTNDPGNVCSVEMGKTITDLE TQIKKLESRLSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPYX KRYLAPGSHCTSTLAGUS. YKRTLAPGKHTAAADBGRGRLLAMPTER GLNQCMSGIINIEAYHEVPYTTSTLAGUS. YKRTLAPGKHTAAADBGRGRLLAMPTER GLNQCMSGIINIEAYHEVPYTTSTLAGUS. YKRTLAPGKHTAAMBGRGRLLAMPTER HGSDICTSWPRPIPGSLHHVPDLSCRGWHTI VEKVLNSKTIRSNSGLSIGTVFQSSSPGGGG EFTIAATDDNHIFAWGNGGRILAMPTER HGSDICTSWPRPIPGSLHHVPDLSCRGWHTI VEKVLNSKTIRSNSGLSIGTVFQSSSPGGGG GFDAW  609 1959 A 4567 1 412 FFFETESRSVAQAGVQWRDLGSQAPPGG GGPDAW  609 1959 A 4567 1 412 FFFETESRSVAQAGVQWRDLGSQAPPGG GGPDAW  610 1960 A 4570 697 467 ECKGVISAHCCTLCLPSSSDSASAFRVARTT GTCDYAQLIFAFLVYMGFHHVQQDGCHLLNC SCHOOL STANDAR SANGARRYARATT GTCDYAQLIFAFLVYMGFHHVQQDGCHLLNC GTCDYAQLIFAFLVYMGFHHVQQDGCHLLNC		ì					CNEDENTAWTKGGSOLSVDRRHLVLSSGTLRI
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GLNQCMSGIINHEAYHEVPYTTSFTLAKQLS YKIRTIAPGKTHTAAIDERGRILITFGCNKCGG LGVGNYKKRLGINILGGPLGGKQVIRVSCGI EFTIAATDDNHIFAWGNGGNGRLAMTPTERI HGSDICTSWPRPIFGSLHHVPDLSCRGWHTII VEKVLNSKTIRSNSSGLSIGTVFQSSSPGGG GGPDAW  FFFFETESRSVAQAGVQWRDLGSLQAPPPGF PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAHCCTLCLPSSSDSASAFRVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLLM	608	1958	A	4300	334	1	ITVAVOCGCDGTFLLTOSGKVLACGLNEFNKL
YKIRTIAPGKTHTAAIDERGRLLTFGCNKCGI LGVGNYKKRLGINLLGGPLGGKQVIRVSCGI EFTIAATDDNHIFAWGNGGNGRLAMTPTERI HGSDICTSWPRPIFGSLHHVPDLSCRGWHTII VEKVLNSKTIRSNSSGLSIGTVFQSSSPGGG GGPDAW  FFFFETESRSVAQAGVQWRDLGSLQAPPPGF PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAHCCTLCLPSSSDSASAFRVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL/M	[		1			1	GLNOCMSGIINHEAYHEVPYTTSFTLAKQLSF
LGVGNYKKRLGINLLGGPLGGKQVIRVSCGI EFTIAATDDNHIFAWGNGGNGRLAMIPTERI HGSDICTSWPRPIFGSLHHVPDLSCRGWHTII VEKVLNSKTIRSNSSGLSIGTVFQSSSPGGG GGPDAW  FFFFETESRSVAQAGVQWRDLGSLQAPPPGF PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAHCCTLCLPSSSDSASAFRVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLLM	1					1	YKIRTIAPGKTHTAAIDERGRLLTFGCNKCGQ
609 1959 A 4567 1 412 FFFETESRSVAQAGVQWRDLGSLQAPPPGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RAPPINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS 610 1960 A 4570 697 467 ECRGVISAHVCCTLCLPSSSDSASAFRVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL/A	[	1					LGVGNYKKRLGINLLGGPLGGKQVIRVSCGD
HGSDICTSWPRPIFGSLHHVPDLSCRGWHTII VEKVLNSKTIRSNSSGLSIGTVFQSSSPGGG GGPDAW  FFFFETESRSVAQAGVQWRDLGSLQAPPPGF PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAHVCCTLCLPSSSDSASAFRVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLLM	1	1		[			FETIAATDDNHIFAWGNGGNGRLAMTPTERP
VEKVLNSKTIRSNSSGLSIGTVFQSSSPGGGGGPDAW  609 1959 A 4567 1 412 FFFFETESRSVAQAGVQWRDLGSLQAPPPGFPSCLSLPSSWDYRRPPLRPANFFVFLVETGFHRFSRDGLDLLT/S/GDPPASASQSAGITGVSFRARPRINLRNVIYSFAVTYCLNYISLAMSSTLKLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTIGTCDYAQLIFAFLVEMGFHHVGQDGLHLL\(\text{T}\)	1		-		1	1	HCSDICTSWPRPIFGSI HHVPDLSCRGWHTILI
GGPDAW  GGPDAW  FFFFETESRSVAQAGVQWRDLGSLQAPPPGF PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS  G10  1960  A 4570  697  467  GTCDYAQLIFAFLVEMGFHHVGQDGLHLLM		1	-				VENT NEXT PENSON SIGTVEOSSEPGGGGE
609 1959 A 4567 1 412 FFFFETESRSVAQAGVQWRDLGSLQAPPPGF PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSF RARPRINLRNVIYSFAVTYCLNYISLAMSSTIKLSFHVLSGS 610 1960 A 4570 697 467 ECRGVISAH/CCTLCLPSSSDSASAF/RVARTIGTCDYAQLIFAFLVEMGFHHVGQDGLHLL/M	1		1	}	}		
PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\(\text{T}\)			1		1		GGPDAW CACACOUNTS COLOARDOCET
PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSI RARPRINLRNVIYSFAVTYCLNYISLAMSSTL KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\(\text{T}\)	600	1959	A	4567	1	412	FFFFETESRSVAQAGVQWKDLGSLQAPPPGFT
RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS 610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\tau	1003	1739	1		- [		PFSCLSLPSSWDYRRPPLRPANFFVFLVETUF
RARPRINLRNVIYSFAVTYCLNYISLAMSSTI KLSFHVLSGS 610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\tau			1				HRFSRDGLDLLT/S/GDPPASASQSAGITGVSH
KLSFHVLSGS  610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\(\text{T}\)			- 1	Ì	1		RARPRINLRNVIYSFAVTYCLNYISLAMSSTL
610 1960 A 4570 697 467 ECRGVISAH\CCTLCLPSSSDSASAF\RVARTI GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\tau				Ì			KLSFHVLSGS
610 1960 A 4370 GTCDYAQLIFAFLVEMGFHHVGQDGLHLLM				1570	607	467	ECRGVISAH\CCTLCLPSSSDSASAF\RVARTT
	610	1960	A	4570	09/	407	GTCDYAOLIFAFLVEMGFHHVGQDGLHLL/N
	1						LVIRPPRPPKVLGLQA

	1 450 15	L	1.000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met   hod	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	nod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	i	İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1			sequence	/=possible nucleotide deletion, \=possible
	1		]	peptide		nucleotide insertion
		<u> </u>	<del> </del> -	sequence	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT
611	1961	A	4571	25	1390	WNPNVPESPRIPAPRLPKRMSGAPTAGAALM
		1				LCAATAVLLSAQGGPVQSKSPRFASWDEMN
	1		1			VLAHGLLQLGQG\CANT\GAHPQSAERAGA\R
			1			LSACGSACQGTEGSTDLPLAPESRVDPEVLHS
	1		1	ì		LQTQLKAQNSRIQQLFHKVAQQQRHLEKQHL
		1	ļ			RIQHLQSQFGLLDHKHLDHEVAKPARRKRLP
	1			1		EMAQPVDPAHNVSRLHRLPRDCQELFQVGER
		1	İ		1	QSGLFEIQPQGSPPFLVNCKMTSDGGWTVIQR
l		ł	1	ì		RHDGSVDFNRPWEAYKAGFGDPHGEFWLGL
1		1	1			EKVHSITGDRNSRLAVQLRDWDGNAELLQFS
	1	j	1		Į	VHLGGEDTAYSLQLTAPVAGQLGATTVPPSG
		1	1			LSVPFSTWDQDHDLRRDKNCAKSLSGGWWF
			Į.			GTCSHSNLNGQYFRSIPQQRQKLKKGIFWKT
	1		İ			WRGRYYPLQATTMLIQPMAAEAAS
1	1	<u>.</u>				FFFETESRSVAQAGVQWRDLSSLQPPPPG\SR
612	1962	Α	4575	162	3	GSPASASPVAGITGTRHHRTRG
			1	<u></u>	<u> </u>	PLAQRRPFLWYTVKTNGHIWGSSTYPHFWGS
613	1963	·A	4584	687	321	SNS/PASASQVAGIPNARHQARIIFVFLVEPRF
						HHVGRAGLGFL/NLAICLPQHPKVLGLQACN
1	1					LNIKPHPAHKYISMIQFNVHFMCMSVHIYI
			<u> </u>	<u></u>		PGSAQSAQRGRGRRARAGSATQITMYSFMG
614	1964	A	4589	727	299	GGLFCAWVGTILLVVAMATDHWMQYRLSGS
		1	}		İ	FAHQGLWRYCLGNKCYLQTDSIAYWNATRA
			1			FMILSALCAISGIIMGIMAF/GWVAVLMTFFA
l			I	i	1	GIFYMCAYRVHECRRLSTPR
						TILPEKIQAWAQKQCPQSGEEAVALVVHLEK
615	1965	A	4590	2	414	ETGRLRQQVSSPVHREKHSPLGAAWEVADFQ
}	1	1				PEQVETQPRAVSREEPGSLHSGHQEQLNRKR
		Ì	1			ERRPLPKNARPSPWVPALADEWNTLHQEVTT
		l l				TRLPAGSOEPVKD
1 _					400	DFALVAQAGVQWHNLGSPQPLPPGFKRFSCL
616	1966	A	4592	773	488	SLPSSWEYRCVPP/RLANFVFLVEMGFLHVGQ
						AGLELPTSGDPPALASQSAGITGVTTVPSGPG
1						XRHGLREPLLERRCAAASSFQHSSSLGRELPY
617	1967	В	4595	84	478	DPVDTEGFGEGGDMQERFLFPEYILDPEPQPT
1				1		REKQLQELQQQEEEERQRQQRREERRQQNL
			İ	j		RARSREHPVVGHPDPALPPSGVNCSGCGAEL
				1		· ·
1				1	1100	HCQDAR* ARSRNSARGVYGMCVDTLFLCFLEDLERNDG
618	1968	A	4596	2945	1188	SAERPYFMCSTLKKPLARRCFPAIHAYKGVL
			1	ŀ		MVGNETTYEDGHGSRKNITDLVEGAKKANG
				1	1	VLEARQLAMRIFEDYTVSWYWIIGLVIAMA
			1			VLEAKQLAWINITED I I VOW I WILIOE VIAMA
1				1		MSLLSIILLHLLAGIMGWVMIMEISELGYRIF
1		-				HCYMEYSRLRGEAGSDVSLVDLGFQTDFRV
	1			İ	1	YLHLROTWLAFMILSILEVIIILLIFLRKRILI
1		-				AIALIKEASRAVGYVMCSLLYPLVTFFLLCLCI
1		1				AYWASTAVFLSTSNEAVYKIFDDSPCPFTAKT
		1				CNPETFPSSNESRQCPNARCQFAFYGGESGYH
		1			1	RALLGLQIFNAFMFFWLANFVLALGQVTLAG
1		1		1		AFASYYWALRKPDDLPAFPLFSAFGRALRYH
						TGSLAFGALILAIVQIIRVILEYLDQRLKAAEN
					1	KFAKCLMTCLKCCFWCLEKFIKFLNRNAYIM
					1	IAIYGTNFCTSARNAFFLLMRNIIRVAVLDKV
						TDFLFLLGKLLIVGSVGILAFFFFTHRIRIVQDT
1					1	APPLNYYWVPILTVIVGSYLIAHGFFSVYGMC
						VDTLFLCFLEDLERNDGSAERPYFMSSTLKKL
				Į.		LNKTNKKAAES
710	1000	<del>-  </del>	4601	12	357	RTSVEPYILGEF/RKLSNNTKVVKTEYKATEY
619	1969	A	1 4001	<u></u>		<u> </u>

252 ED	CCO ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	поа	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l		ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	}	1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	ļ	Ì	residue of	sequence	/=possible nucleotide deletion, \=possible
	Į.	1	ì	peptide		nucleotide insertion
	1	ĺ	1	sequence	ļ	GLAYGHFSYEFSNHRDVVVDLQGWVTGNGK
				<u> </u>		GLAYGHFSYEFSNHRDVVVDLQGWVYGHGK
	1	1	1	i		GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFN
	İ	ļ	i			NOHVECNEICHRLSLTRPSMEKPCKS
620	1970	A	4606	1	2415	MERLWGLFQRAQQLSPRSSQTVYQRVEGPR
020	1370	1 ' `			1	KGHLEEEEEDGEEGAETLAHFCPMELRGPEP
					}	LGSRPRQPNLIPWAAAGRRAAPYLVLTALLIF
	1		İ			TGAFLLGYVAFRGSCQACGDSVLVVSEDVN
	1		ì	Ì		YEPDLDFHOGRLYWSDLQAMFLQFLGEGRL
	ļ	1	ł	ļ	Ì	EDTIRQTSLRERVAGSAGMAALTQDIRAALS
	ł			l .		RQKLDHVWTDTHYVGLQFPDPAHPNTLHWV
			1		1	DEAGKVGEQLPLEDPDVYCPYSAIGNVTGEL
	1			Į.	1	VYAHYGRPEDLQDLRARGVDPVGRLLLVRV
i				Į.	1	GVISFAQKVTNAQDFGAQGVLIYPEPADFSQ
	1	1		{		DPPKPSLSSQQAVYGHVHLGTGDPYTPGFPSF
		1		1		NOTOFPPVASSGLPSIPAQPISADIASRLLRKL
		}		1		KGPVAPQEWQGSLLGSPYHLGPGPRLRLVVN
		1		1	1	NHRTSTPINNIFGCIEGRSEPDHYVVIGAQRDA
		}	1		1	NHKISIPINNIPUCIEUKSEPURI VVIDAQIDA
	ì	1				WGPGAAKSAVGTAILLELVRTFSSMVSNGFR
		1	}			PRRSLLFISWDGGDFGSVGSTEWLEGYLSVL
ì		[	-	į	1	HLKAVVYVSLDNAVLGDDKFHAKTSPLLTSL
1		[				IESVLKQVDSPNHSGQTLYEQVVFTN\PSWD\
	1		1	1	1	AEVIRPLPM\DSSAY\SFTAFVGVPAVEFSFME\
	ļ	ļ			ļ	DDQ\AYPFLHTKEDTYENLHKVLQGRLPAVA
	j	]	1	1		QAVAQLAGQLLIRLSHDRLLPLDFGRYGDVV
[	ļ	1		1		LRHIGNLNEFSGDLKARGLTLQWVYSARGDY
ł			1			IRAAEKLRQEIYSSEERDERLTRMYNVRIMRV
Ì	l	1	1		Ì	EFYFLSQYVSPADSPFRHIFMGRGDHTLGALL
			ì			DHLRLLRSNSSGTPGATSSTGFQ\ESRFRRQL\
		}	Ì	1	1	ALL\TWDACKGAANALSGDVWNIDNNF
					334	ISRVDDFVGSGIANVIIAVAIFSIPAFARLVRG\
621	1971	Α	4610	793	334	NTLVLKQQTFIESARSIGASDMTVLLRHILPGT
	ı	1	1			GSSIVVFFTMRIGTSIISAASLSFLGLGAQPPTP
					ļ	EWGAMLNEARADMVIAPHVAVFPALAIFLTV
		i	1	į		LAFNLLGDGLRDALDPKIKG
	}	Ì	1	1		LAFNLLUDULKDALDFRIKU
622	1972	A	4614	2	820	LVYVMIAIFCIASAMSLYNCLAALIHKIPYGQ
						CTIACRGKNMEVRLIFLSGLCIAVAVVWAVF
1		}		1	1	RNEDRWAWILQDILGIAFCLNLIKTLKLPNFK
1			1	1		SCVILLGLLLYDVFFVFITPFITKNGESIMVEL
1	1	1		1		AAGPFGNNEKNDGNLVEATGQPSAPHEKLPV
1			1			VIRVPKLIYFSVMSVCLMPVSILGFGDIIVPGL
	i			}		LIAYCRRFDVQTGSSYIYYVSV\TVAYAIGMIL
				1		TFVVLG\LMKKGQPALLYLVPCTLITA/CQFV
						AWETVREMKKFWERVTS
	-		12:0	17	691	TLVSVVEFVRRADLTREDLAPSSVDSGQAGF
623	1973	Α	4619	17	071	GGCCESGLPNTMPSAFSVSSFPVSIPAVLTQT
						DWTEPWLMGLATFHALCVLLTCLSSRSYRLQ
1		}				IGHFLCLVILVYCAEYINEAAAMNWRLFSKY
1	1	}	}	1	1	OYFDSRGMFISIVFSAPLLVNAMIIVVMWVW
			1		1	ALL DIVIDIDI ANY DEDDAEANDDDAED‡CY V
		1	}	}	1	KTLNVMTDLKNAQERRKEKKRRKED*GAA
1		- [				AAWSLRPSRPPSAAPSAAVCVAWASFQLTHG
	1	1	ì			LKNRCFI
624	1974	A	4622	164	668	VSCYTALQSIMNQPESANDPEPLCAVCGQAH
024	17/4	^	7022	1.5.	1 -	SLEENHFYSYPEEVDDDLICHICLQALLDPLD
				}	1	TPCGHTYCTLCLTNFLVEKDFCPMDRKPLVL
1					1	OHCKKSSILVNKLLNKLLVTCPFREHCTQVL
	1					QRCDLEHHFQTSQAWGTHL*SQLLGRLRQED
1			İ			CLSPGVHHCSEV
	ı	i	1			CLOI OTHICOLT
1	1					
625	1975	A	4625	474	473	CFLSPSPLLPPLLLSSSSSPSFPLPPPPTLLPSTLP PPLLIPSS*LSP

<u> </u>	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	nou.	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	[	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	uence	Į	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uaicc		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
rence	Į.	ł	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	į.	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	ļ		peptide	3-4	/=possible nucleotide deletion, \=possible
	1			sequence		nucleotide insertion
		<b>↓</b>	4600	249	3	KLKGNECFCYHCNVCIFLMIKK*GLFLC*IYFI
626	1976	Α	4629	243		LFFET*SHSFTRLECSGTISAHCSLQLQGSSNSP
		1				ASASOVAGIAGTHH
			1605		301	FEFFETKPFFAPOAGGOGPSRGSLNPLPTGLK
627 1977	1977	Α	4635	1	301	OFSGLTLSRSGNNGPRPPPRVNFGILRGNGVP
	1	1				PGGAG*PRPPDLRGPPGLAPPQGGNNGGDPP
	1	1				ARAYL
	1				1 200	KLFSSQRLFGPHIQAINPSFLLLSFFPS*LLAMR
628	1978	Α	4648	1357	782	TVGNNAFILVFLVYRIVLLLF*HV*PAYFQPSK
		1				NKTAKINCN*RPFLFLVCYLL*AELHIGIFIANF
	j	Ì				YDCIPNKLNEHLWPKLLQSLIFHVDFCGFLHK
		1			1	VFYICFTEFLLFLYFL*LFIIKVSCSII*CSTICVF
	į					SYKSFAVIIFFVDNTRFFSFGF
	ļ	1	1			HHELHTLELLQNPKEVLTRSEIQDVNYSLEAV
629	1979	A	4660	18	999	KVKTVCQIPLMKEMLKRFQVAVNLAEDTAH
0	1	1				PKLVFSQEGRYVKNTASASSWPVFSSAWNYF
	1	1				AGWRNPQKTAFVERFQHLSCVLGKNVFTSG
		1			1	KHYWEVESRDSLEVAVGVCREDVMGITDRS
	1	1		1		KHYWEVESKUSLEVAVOVCKED VINGTER
				1		KMSPDVGIWAIYWSAAGYWPLIGFPGTPTQQ
						EPALHRVGVYLDRGTGNVSFYSAVDGVHLH
						TFSCSSVSRLRPFFWLSPLASLVIPPVTDRK*G
		ļ			1	FSSPDQNSFPVVQLRDTHPWALFCPSCLYPG
	{	1			1	WSIFWVSLTVPFGICPLCASQEAVPWEVGLA
		1				NGDGTGNFPRRFWEIFL
630	1980	A	4669	2	358	FFFFETESHSVAQAGMQWRNLGSLPAPPPGF
630	1960	1 ^	1005	_		TPFFCLSLLNGWDYRRPPPHLANFFVLLVETG
		1				FHDVGQDGLDLLTS*STPSASQSAEITGVSHC
	1	1			1	TRLKKIRFAKGHVEFFFESHVE
(21	1981	+	4674	953	614	TPIRGTDDEHEECTVQEYSAGKNTCLRPGAV
631	1901	^	10/1	700		AHTCNPCTLGGRGRWIT*GSGVQDQPGPTWC
	ł	i				NPVFLERRPRALHSSPGLTTQRILWAQGLWV
		1				GAGSTGCSRGPRGEGVFREG
	1000		4678	34	314	RSTHASGMISPSFGFMGHLLRLEFEILPSTPNP
632	1982	2   A	A 4678	1 24	34 34	*LPSYQGEAAGSSLISHLQTFSPDLKGVYCTFI
		1	ŀ			ASGLAPVPTHWTVSELSRSPVATATFC
		$\dashv$ $\leftarrow$ $-$	4606	1	1365	RTI GMEGERRASOAPSSGLPAGGANGESPGG
633	1983	A	4696	1 1	1505	GAPEPGSSGSSALLOAEVLDLDEDEDDLEVES
	1					KDASLMDMNSFSPMMPTSPLSMINQIKFEDE
-	1	1	Ì			DIKDLEITVDEPESHVTTIETFITYRIITKTSRG
				}		FEDSSEFEVERRYODFLWLKGKLEEAHPTLII
1						PPLPEKFIVKGMVERFNDDFIETRRKALHKFL
	}					NRIADHPTLTFNEDFKIFLTAQAWELSSHKKQ
1		1				GPGLLSRMGQTVRAVASSMRGVKNRPEEFM
	)		}		i	EMNNFIELFSQKINLIDKISQRIYKEEREYFDE
	ŀ	1	ļ	,	ł	MKEYGPIHILWSASEEDLVDTLKDVASCIDRO
		1				CKATEKRMSGLSEALLPVVHEYVLYSEMLM
			Ì			GVMKRRDQIQAELDSKVEVLTYKKADTDLL
				1		PEEIGKLEDKVECANNALKADWERWKQNM
	- [		İ	1		QNDIKLAFTDMAEENIHYYEQCLATWESFLT
		1	1			QNUIKLAR IDMAGENINI ILQCEAT WESTER
	İ	- 1	1			SQTNLHLEEASEDKP
				421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDTC WISKAVYKHREMCGLTSTGRKSHGLEKDRM
634	1984	A	4708	1 421		THE TRANSPORT OF THE PROPERTY
634	1984	A	4708	421		WISKAV I KIRCINCOLISI GIGGOTOLOGI
634	1984	A	4708	421		FPHAIGGSCRAA*RRRKTLQFPCYH
					341	FPHAIGGSCRAA*RRKTLQFPCYH VIKOPDAKERRRTVHWKKETESEASEITIPPS'
634	1984	A	4708 4709	421	341	FPHAIGGSCRAA*RRKTLQFPCYH YTKQPDAKERRRTVHWKKETESEASEITIPPS' PGVPOAPGHWEDYGRGDNFYLPH*DPGGIVI
					341	FPHAIGGSCRAA*RRKTLQFPCYH YTKQPDAKERRRTVHWKKETESEASEITIPPS' PGVPOAPGHWEDYGRGDNFYLPH*DPGGIVI
					341	FPHAIGGSCRAA*RRKTLQFPCYH  YTKQPDAKERRRTVHWKKETESEASEITIPPS' PGVPQAPGHWEDYGRGDNFYLPH*DPGGIVI WNIFNRMPIARKNITDGEHHEYLIEVPRLFHT
					341	FPHAIGGSCRAA*RRKTLQFPCYH YTKQPDAKERRRTVHWKKETESEASEITIPPS PGVPQAPGHWEDYGRGDNFYLPH*DPGGIVI WNIFNRMPIARKNITDGEHHEYLIEVPRLFHT

			666	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
10: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience			717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	,			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	1 .	/=possible nucleotide deletion, \=possible
	1	ļ	ļ	sequence		nucleotide insertion
			<del> </del>	0.4		ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK
		ĺ			1	MYFTTPSNHNAYQVDSVQST
	1987	A	4726	664	253	NTGLTCSIQRKCGETQLYRREENRLILLLQDH
637	1987	Δ.	1720	1	1	LKSESFQVLTLSPRLEFSGLISAHCNLRLPGSS
	1					DSSASSSRAAGITGVHHHAWLIFFFLVETGFL
		1	}	İ	1	HAG*AGLELLTSGDPPASASRSAGITGVSHHA
	i		Ĩ			RPRETRFL
(20	1988	A	4734	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG
638	1900	1 1	1,75			TLERGHWNNKMEFVLSVAGEIIGLGNVWRFP
	1	-	}			YLCYKNGGGAFFIPYLVFLFTCGIPVFLLETAL
						GQYTSQGGVTAWRKICPIFEGIGYASQMIVIL
	1			1		LNVYYIIVLAWALFYLFSSFTIDLPWGGCYHE
		1	ļ		)	WNTEHCMEFQKTNGSLNGTSENATSPVIEFW
639	1989	A	4743	1040	699	QGLTLLPRMECSATITAHCSLELPGSIDLPTSA
639	1707	1 '				S*VARTTGTHHHPWLILVLLL*TWGSYYVAQ
	l l	1		]	1	AGLELLGSSNLPAAMVSQSAQIIGHDHCAWA
	j					TSNHVLYTQEGLRRGKEG
640	1990	A	4771	527	2	GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN
640 133	1990	1 ' `	1,,,,			WIRRRPCLPSGCLKMNREIGPLQHSLCCPGWS QTPGLKAILLRQPPK*LGLQMESHSCPPAWSA
		1				QTPGLKAILLRQPPK*LOLQMESHSCHAWSK MARSRLTATSASQVQAILLPQPPGTTDSCSPS
	1	1	-	ł	į –	MARSRLTATSASQVQAILLFQFFGTTDSCSTO
		1			Ì	PDHEQQPLSWVLPPPQKDMNPREQQVALGP
	}	i				QAAALPWAVWRNDCFPR RPSSQCGGIPTGWKKGLAPELSSELSSPPLPAR
641	1991	A	4780	16	473	LQLAASPYFSPSWAECPQPVPAGTHATWCLA
041	1	Ì	ļ	}		RVWARMTPPGPAGIPSHPLPPPPPERSVPIPSP
		İ		1		FPARDSGSRQGHSTDRYKHTDAPRDAHRRVF
		ì				QRDTDTGVHTGSGTHTHAHTPPEK
	1					GYSFRCDIVDYSRSPTALRMARTCWLYYFSK
642	1992	A	4798	1	487	FIELLDTIFFVLRKKNSQVTFLHVFHHTIMPW
		-		1		TWWFGVKFAAGGLGTFHALLNTAVHVVMY
		İ			1	SYYGLSALGPAYQKYLWWKKYLTSLQLVQF
		Ì				VIVAIHISQFFFMEDCKYQFPVFACIIMSYSFM
	}	1		}		FILE
	<u> </u>				391	I MAFIEMHISGSLVYLKIKTKIYSYFSMLNFLI
643	1993	A	4799	2	391	OF IPI SEIL RISSPRDFTNISOGSNPHCFEITTDT
	1					MVYFVGENNGDSSHNPVLAATGVGLDVAQS
		1	1	•	1	WEKAIRQALMPVTPQASVCTSPGQGKDHSK
	1			[		O*ASVCTSPGOGKDHSKQ
L			- 1222	400	101	A VPI FA VHPVHTECVAGVVGRAYLLCALFFI
644	1994	A	4800	488	101	L SFLGYCKAFRESNKEGAHSSTFWVLLSIFLG
			- 1			AVAMLCKEQGITVLVRAATWLGPAFSVCPFI
	1		1	i		SYKDIWGWPCLCGVLHAYIPLLV
				450	126	LI WITVI COTPARPOSTMIHLGHILFLLLLPV
645	1995	Α	4805	458	120	AAAOTTPGERSSLPAFYPGTSGSCSGCGSLSL
1				1	1	PLLAGLVAADAVASLLIVGAVFLCARPRRSP
1						▲ OEDGK VYINMPGRG
L			- 1015	42	1033	LOGDTWHLSFLSHFSRLHGGVPGRGLLEGNI
646	1996	A	4817	47	1033	I OPO A PGHDMTSIPFPGDRLLOVDGVILCGL
		1			1 1 F	HKOA VOCI KGPGOVARI VLERR VPRSTQQC
		-	ł		į	PSANDSMGDERTAVSLVTALPGRPSSCVSVI
1		İ	-			DGPKF*SSN*KRIANGLGFSFVQMEKESCSHI
			1			KSDI VRIKRLEPGHPAEENGALAAGDIILGRE
		1	1		ļ	WEGPRKASSSRCRGSWAMQLSVQAGPSFAS
1				J		VVPAAVEVLHLLRGAPOEVTLLLCRPPPGAL
1					ì	PEL FORWOTPELSADKEFTRATCTDSCTSPIL
1					1	GSRGQLGGTVPPQMQGKAWGLRPESSQKAI
1		1			i	FGTMGAKTERDLGPVP
				1	1	
L_	1997	- <del> </del> A	4854	1044	335	PRVRGDWPLEKKKSNSNIHPIFSWCGSTDSK

				Deadiated	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	Glutamine, R=Arginine, S=Serine,
ence	1		914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	]		ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
		İ	1	peptide	Į.	nucleotide insertion
	ļ	Ì	1	sequence	<u> </u>	IVMPTYDLTDSVLETMGRVSLDMMSVQANT
			1			GPPWESKNSTAVWRGRDSRKERLELVKLSRK
		]	ļ	ł	}	GPPWESKNSTAV W KOKDSKREKELE V KESTAL
	1		ł		ļ	HPELIDAAFTNFFFFKHDENLYGPIVKHISFFD
	1	l	1			FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK
	1	1	ì	Ì	1	QDSIYYEHFYNELQPWKHYIPVKSNLSDLLEK
	1		ì	ì		LKWAKDHDEEAKKIAKAGQEFARNNLMGD
	ŀ			ĺ	1	DIFCYYFQTFPRNMPIYK
		<u> </u>	4867	2030	837	AGMLPAVGSADEEEDPAEEDCPELVPMETTQ
48	1998	Α	4867	2030	057	SEEEKSGLGAKIPVTIITGYLGAGKTTLLNYI
		ì	ì		1	1 TEOHSKRVAVILNEFGEGSALEKSLAVSQG
		1	1		Ì	GELYEEWLELRNGCLCCSVKDNGLRAIENLM
		1			1	QKKGKFDYILLETTGLADPGAVASMFWVDA
		1				FI GSDIYLDGIITIVDSKYGLKHLAEEKPDGLI
		1			ļ	NEATRQVALADAILINKTDLVPEEDVKKLRT
	1		ļ			TIRSINGLGQILETQRSRVDLSNVLDLHAFDSL
		1	1	ļ		SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG
	1	ł	1	1		NAKEEHLNMFIQNLLWEKNVRNKDNHCMEV
	1		ì			IRLKGLVSIKDKSQQVIVQGVHELYDLEETPV
	ì		1	1		SWKDDTERTNRLVLLGRNLDKDILKQLFIAT
ì	1	ļ	1			SWKDDIERINKLYLLOKNEDADIERQUI BII
		}	)	}		VTETEKQWITHFKEDQVCT
(10)	1999	A	4873	226	189	DGVSLLLPKLGVQWAQYWAHWQPPLPGFKR
649	1999	^	1015		İ	FSCLSLRSSWD*KCAPPHPAFVFLVEMGFHRV
	1		- 1			GQAGLELRTSGDPPASASQSAGITGVSHLA*P
	1		1			TSMPLLPFQRLCVYI
1-4		-	4874	1 2	437	FFFLRRSFAFVAQAGVQWCDLGSPQPLPPGF
650	2000	A	4874	1 -	1	K*FSCLSLPSSWDYRHAPPPCPS*FLYF**RQG
	1	1	l	1	İ	ETMLARI VI NS*PHDLPTSPSQSAEIKGVSHR
	l	i	l		i i	CPASFYLFLKYYLEAKFCA*GECAPSAGVGA
		Ì			i	GVKRGHKSCLLINCVVOI
				1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATI
651	2001	A	4898	1 /01	1 ′ ′ ¹	PHMERKASCPAAAPLMERKFHVLVGVTGSV
	1	-	1	1	1	AALKLPLLVSKLLDIPGLEVAVVTTERAKHI
	.	Į	}	İ	Ì	SPODIPVTLYSDADEWEMWKSRSDPVLHIDL
-	· -			1	1	RRWADLLLVAPLDANTLGKVASGICDNLLTC
				1		VMRAWDRSKPLLFCPAMNTAMWEHPITAQO
			- 1	}		VDQLKAFGYVEIPCVAKKLVCGDEGLGAMA
		1	1	ļ	1	EVGTIVDKVKEVLFQHSGFQQS*PGISVMGV
	İ	1				LYSEWVQAKSVKMDVGKIGGYPHLLNGGPA
	1	ì				LSLPRGQACSRLNWTEGPGLSFFQPGEAAA
					_l	FRGRQTSRPARGFSPWRPPGTMQEPSSGECP.
652	2002	A	4927	1	611	FRURQISKPAKUFSPWKPPUIMQEFSSUECI
032	2002	1 11	[ ., -,			SP*LPCASNRLAFGGLIFPCAPLVPYPAPFSPL
	1		1			PAFSCAPRPRAHTHSRTHPSAPLVPKPSSRAF
			1	1		GOSPIPSRASSPSCSWAQVPGVALARCAGVC
	}	1		ì		KPGDSWRVAACISGRCCSRGRRRGSGPKNPI
		1	ļ	1		OSFRGAWGPSFWGSWKSQRELSAGGAQAW
				l l		LL GSAGSGLRGEA
			1000	<del></del>	283	FFFFI*DGVSLCHPGWNAVARSWLTATSASR
653	2003	Α	4965	2	203	VOAVSCERLPSSWDYRHATMPG*FF*YF**R
			1			WGETH ATI VINS*POVICPPWPPKVLTLQA
	}	)				RPGIPGRRFRRSWFCQLP*EPEPGLESLATPG
654	2004	A	4968	3 .	437	IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW
		1			İ	DPERDPGCRVQVSRGPRFGEQKTPGLQGCLI
		1	i		1	DEFENDENCE AND STOLE OF SECUL
[					1	PPCLTHLAAASCVVVWCGRWKRDSAECQC
ľ		1	[			HSCSAVSQQEDRCRSSSCS
<b></b>	- 1 5005	_+-	4983	201	397	MNNTTCIQPSMISSMALPIIYILLCIVGVFG
655	2005	A	4703	[ 201	1	TI SOWIFI TKIGKKTSTHIYLSHLVTANLLVC
			1000	222	159	LVHKDMYREFFEEEAQASNKHVTRCLTSLV
656	2006	A	4988	332	137	REVHIKTMR*HFLPIRLEKNKNNIKD
	,	1		1	1	11.000000000000000000000000000000000000
	1	B	5008	129	465	MAGMKTASGDYIDSSWELRVFVGEEDPEAL

200 10	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	delice	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì		1.	peptide		/=possible nucleotide deletion, \=possible
		ł		sequence		nucleotide insertion
		<del> </del>				VTLRVTGESHIGGVLLKIVEQINRKQDWSDH
	i	Į		1		AIWWEQKRQWLLQTHWTLDKYGILADARLF
		1				FGPQHRPVILRLPNRRALRLX*
658	2008	A	5017	1	292	FFFFKETESHSVTQAGVQWHDLGSLQPPPPGF KRFSCLSLLSSWDYRCAPPHPANFVFLVETGF
						HHVAQAGLKLLTL*SANLGLSTSLPIPLFILLS
		]				HHVAQAGLKLLIL-SANCOLSISLII LI LELS
659	2009	A	5018	17	338	RGHGGKSLTGGTPGNWGDGLLVSEDWSHLIF T*NSLVSPVLGKWSPCLQGPGLSAVHTWPWL
		ì			1	MAACWAVHVKTHMRPGLAVLPRLVLNSWS
		1				MAACWAVHVKIHNIKFOLAVLI KLVLING
	ł	1				*AIILLWPPKALGLQA SRVDDFVGERRGGCDECLCGHRGLRAVPLG
660	2010	A	5028	2	310	SRVDDFVGERRGGCDECLCGHROLRAVIES HPGHLCLQPPGGPA*FLDYCRGCCPHPVPGST
		1		1		AGSCPRQKKTTPGPTVLCVCSFWIYQRGEPH
				1	-	
	1	1	1			HRTGARWNH RQSCSSTQAKVQWFHYGPLQSQPPGLKQSSQ
661	2011	A	5050	752	431	RQSCSSTQAKVQWFHTGFLQSQFTGERQSSQ LSLPNSRDHRHVPPRLAIFSFAETGSPYFAQAS
001						LELLGSSHPPTSASQSARITGVSHRAWPLK*F
		-				
	į.	1				NLNQYQTLTMN ELNNGPFQMPLCNGGNLAVTGSWADRSPLH
662	2012	A	5054	48	103	EAASQGRLLALRTLLSQGYNVNAVTLDHVTP
002			1			LHEACLGDHVACARTLLEAGANVNAITIDGV
	1					TPLFNACSQGSPSCAELLLEYGAQAQLESCLP
	1	j		i	1	SPTHEGASKGHHECLDILISWGIDVDQEIPHSG
		1		1		TPLYVACMAQQFHCIWNLIYAGAGVRKGKY
		1			1	WDTPLPGAGHQSTQKLE*LFAMVEIWQ
		}	i			VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK
663	2013	A	5066	951	580	ADLPEGVAVSGPSPAEFCRKHRLPAPVPFSCA
		ļ				GPAEPSTTIFTQLATMAAFPHLVHAELHPSSF
	1				ļ	WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ
	1	Ì		<u> </u>		LSFIEVLSMEQVNKTVVREFVVLGFSSLARLQ
664	2014	A	5071	550	1	QLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTP
		1		ļ		MYFFLAILSCSEICYTFVIVPKMLVDLLSQKK
		j			İ	TISFLGCAIQMFSFLFFGSSHSFLLAAMGYDR
	- [				ļ	YMAICNPLRYSVLMGHGVCMGLMAAAWAC
	ŀ			ļ		GFTVSLVTTSLVFHLPFHSSNQHE
	1					QQYHNTGSAGHHAHCQVGHSPHVHYPSGCG
665	2015	A	5074	496	692	PL*IQRGLPSFNSLEGHSLKDSGHEESVQLDSE
						HDVQRSLYCDTAVNDVLNTSVTSMGSQMPD
ĺ		· ·				HDQNEGFHCREECRILGHSDRCWMPRNPMPI
Ì	1	}				RSKSPEHVRNIIALSIEATAADVEAYDDCGPT
			1			KRTFATFGKDVSDHPAEERPTLKGKRTVDVT
l	ì	1	1			ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL
						PTKPSVSYEIVDPGITARRC
ļ					249	IMLLSTSS*VYFQSSTKDSHFFLFDFQKTGPPL
666	2016	A	5080	408	248	LVGPKAOLSGLOLOPCLYKRR
					<del></del>	DLTNSHFFLFDFQKTGPPLGGPKAQFSSLQLQ
667	2017	A	5081	129	247	PCVY*RR
					<del></del>	NIKSNDRWVQIKTAYKYFF*KNGDNYNWVF
668	2018	A	5086	852	233	RALPTIFADIENLKYLLFTRDASQPFYLGHTV
						IFGDLEYVTVEGGIVLSRELMKRLNRLLDNSE
ì			İ			TCADQSVIWKLSEDKQLAICLKYAGVHAENA
			}	i		EDYEGRDVFNTKPIAQLIEEALSNNPQQVVEG
		(				CCSDMAITFNGLTPQKMEVMMYGLYRLRAF
	1	1	1			GHYFNDTLVFLPPVGSEND
	1			1	i	CHIPNDILVELF A COPIND
			ĺ			DODDED DDL LTLL ALD/CDEDACDCCDCL ACIPC
669	2019	A	5101	1	329	PGRPTRPPLLTLLAHVSPEPAGPSCDSLAQPG
669	2019	A	5101	1	329	ASGV*VOHDSHPPLLCGSQCLSEPVPGSHGPP
669	2019	A	5101	1	329	ASGV*VQHDSHPPLLCGSQCLSEPVPGSHGPP RGCQHEAAPCPRGPGSDGLHHASAACASLPP
669	2019	A	5101	1	329	ASGV*VOHDSHPPLLCGSQCLSEPVPGSHGPP

			CCO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	İ	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	Ì		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		Ì		residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide	)	nucleotide insertion
		1	<u> </u>	sequence		DEL*NMNGRVDYLVTEEEINLTRGPSGLGFNI
				1		VGGTDQQYVSNDSGIYVSRIKENGAAALDGR
			I		1	LQEGDKILSVNGQDLKNLLHQDAVDLFRNA
			1	t		GYAVSLRVQHRLQVQNGPIGHRGEGDPSGIPI
		į				FMVLVPVFALTMVAAWAFMRYRQQL
		_				RDGREELCLQGEPTLPSRICSSAPLLYFLFICPF
671	2021	Α	5105	672	400	VLLLLLISLLCLYWKARKLSTLRSNTRKEKA
		1			i	LWVDLKEAGGVTTNRMED*EEDECN
		1	l	l		IIYFSYNIFLKITELLNDVERLKQALNGLSQLT
672	2022	Α	5148	72	314	YTSGNPTKRQSQLIDTLQHQVKSLEQQLAVS
	1	]	1		1	YISGNPIARQSQLIDILQIQVASSEEQQEITIS
	{	1	Ì			NQAHGALQEYVLAPCS REILCSRIGRLNIV*MSLFPNLTCRLNAIPIKIPA
673	2023	A	5152	210	335	
0.5						NHFVEVT
674	2024	A	5153	3	2953	LTEDQPFDILQKSLQEANITEQTLAEEAYLDA
074	202.	1	1	]		SIGSSQQFAQAQLHPSSSASFTQASNVSNYSG
ļ		1			Į	QTLQPIGVTHVPVGASFASNTVGVQHGFMQH
	1	1		1		VGISVPSQHLSNSSQISGSGQIQLIGSFGNHPS
ł				ł		MMTINNLDGSQIILKGSGQQAPSNVSGGLLV
						HRQTPNGNSLFGNSSSSPVAQPVTVPFNSTNF
		İ	,			QTSLPVHNIIIQRGLAPNSNKVPINIQPKPIQM
						GQQNTYNVNNLGIQQHHVQQGISFASASSPQ
	ĺ				1	GSVVGPHMSVNIVNQQNTRKPVTSQAVSSTG
1	i	1			ļ	GSIVIHSPMGQPHAPQSQFLIPTSLSVSSNSVH
			1			HVQTINGQLLQTQPSQLISGQVASEHVMLNR
						NSSNMLRTNQPYTGPMLNNQNTAVHLVSGQ
	1	1				TFAASGSPVIANHASPQLVGGQMPLQQASPT
	1	1	1	1		VLHLSPGQSSVSQGRPGFATMPSVTSMSGPSR
1			1		-	FPAVSSASTAHPSLGSAVQSGSSGSNFTGDQL
1		1		1		TQPNRTPVPVSVSHRLPVSSSKSTSTFSNTPGT
		1		İ	}	GTQQQFFCQAQKKCLNQTSPISAPKTTDGLR
1			-	· I		QAQIPGLLSTTLPGQDSGSKVISASLGTAQPQ
	1	1	Į	İ		QEKVVGSSPGHPAVQVESHSGGQKRPAAKQ
			1	1		LTKGAFILQQLQRDQAHTVTPDKSHFRSLSD
1	- [	-				AVQRLLSYHVCQGSMPTEEDLRKVDNEFETV
	i					ATQLLKRTQAMLNKYRCLLLEDAMRINPPAE
	İ	-				MVMIDRMFNQEERASLSRDKRLALVDPEGFQ
				1	1	ADFCCSFKLDKAAHETQFGRSDQHGSKASSS
				1		LQPPAKAQGRDRAKTGVTEPMNHDQFHLVP
1						NHIVVSAEGNISKKTECLGRALKFDKVGLVQ
1	İ	1			1	YQSTSEEKASRREPLKASQCSPGPEGHRKTSS
-						RSDHGTESKLSSILADSHLEMTCNNSFQDKSL
1		1	ļ			RNSPKNEVLHTDIMKGSGEPQPDLQLTKSLET
			į			TFKNILELKKAGRQPQSDPTVSGSVELDFPNF
ļ.				1		SPMASQENCLEKFIPDHSEGVVETDSILEAAV
	i	1				NSILEC
(75	2025	-   A	5154	599	1880	LKKMEPFSCDTFVALPPATVDNRIIFGKNSDR
675	2025	^	3134	1 3//		LYDEVQEVVYFPAVVHDNLGERLKCTYIEID
		1				OVPETYAVVLSRPAWLWGAEMGANEHGVCI
						GNEAVWGREEVCDEEALLGMDLVRLGLERA
				1 '		DTAEKALNVIVDLLEKYGOGGNCTEGRMVF
						SYHNSFLIADRNEAWILETAGKYWAAEKVQE
j	1			1		GVRNISNOLSITTKLAREHPDMRNYAKRKGW
-					1	WDGKKEFDFAAAYSYLDTAKMMTSSGRYCE
1		- 1				GYKLLNKHKGNITFETMMEILRDKPSGINME
						GEFLTTASMVFILPQDSSLPCIHFFTGTPDPER
	-					SVFKPFIFVPHISQLLDTSSPTFELEDLVKKKS
1	1		1	1	Í	HFKPDRRHPLYQKHQQALEVVNNNEEKAKI
		ł	Ì			MLDNMRKLEKELFREMESILQNKHLDVEKIV
	i		1			IAIT DIAINING TOTAL TOTAL TOTAL
	1		1		1	NLFPQCTKDEIQIYQSNLSVKVSS

	- AFO 10	\	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	De Aspartic Acid E=Glutamic Acid,
10: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
otide	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	!	ļ	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			ì	residue of	sequence	/=possible nucleotide deletion, \=possible
		]	ì	peptide	}	/=possible nucleodde deterior, \ possible
	i	ļ	1	sequence		nucleotide insertion
(3)	2026	A	5155	2	306	FFFLRRSLALSPRPDCGLQWRNLGSLQAPPPG
576	2020	^	1 3.33	-	İ	FTPFSCLSLPSSWDYRRPPPRPANFLYF**RRG
	ļ	1		1	ì	FTLLARMVSIS*PHDPPASASQSAGITGVSHRA
		]	ì		ļ	DPT .
		ļ	<del> </del>		740	FFHSVDLLALEQSKTFYKPDWFDIVESEVKCC
677	2027	Α	5167	97	/40	LEAVCVIDMSSFTEFEITSTGDOALEVLQYLF
			1			SNDLDVPVGHIVHTGMLNEGGGYENDCSIAR
	1	1	Į.	ļ	1	LNKRSFFMISPTDQQVHCWAWLKKHMPKDS
		1	1			NLLLEDVTWKYTALNLIGPRAVDVLSELSYA
			ļ.	į.		NLLLEDVIWKYIALNLIGPRAVDVLSELSIA
	l.		ļ	1		PMTPDHFPSLFCKEMSVGYANGIRVMSMTHT
	Į.	1	İ	1		GEPGFMLYIPIEYRWGFTMLSTLVSNS
		<del></del>	5183	1919	2018	PALCRLRDDMTVCVADFGLSKKIYSGDYYRC
678	2028	A	3183	1919	20.0	GRIAKMPVKWIAIESLADRVYTSKSDVWAFG
	1	1	1	1		VTMWEIATRGMTPYPGVQNHEMYDYLLHG
		-	1			UDI KOPEDCI DELCKI**SPOSP
		1			100	RESQVKHFKMRKIDLCLSSEGSEVILATSSDE
679	2029	A	5190	39	499	KHPPENIIDGNPETFWTTTGMFPQEFIICFHKH
•		Į.	Į.	į.		VRIERLVIQSYFVQTLKIEKSTSKEPVDFEQWI
	1	ļ				VKIEKLVIQSTF VQTEKIEKSTSKET VETEV
		1	1	1		EKDLVHTEGQLQNEEIVAHDGSATYLRFIIVS
		-	i i			AFDHFASVHSVSAEGTVVSNLSS
		A	5204	541	92	EILAVLKLACGDISLNALALMVATAVLTLAPI
680	2030	A	3204	341		LLICLSYLFILSAILRVPSAAGRCKAFSTCSAH
			]			PTVVVVFYGTISFMYFKPKAKDPNVDKTVAL
	ļ		1			FYGVVTPSLNPIIYSLRNAEVKAAVLTLLRGC
	1					TISRKASHCYCCPLPLSAGIG
	<u> </u>				247	VPDNCDVTKI PVCSTI VEETSLTVSEAMEQS
681	2031	Α	5207	10	247	KNESPLPGTLAHTCNTSTLGGRGRWIT*GREE
	1		ļ		i	DTSMANMVKPCLYRK
				<u> </u>		FFFETESYSITQAGVQWPNLSSLKTLPPGFK*1
682	2032	$\overline{A}$	5210	2	231	SCLSLPSSWDYRCLPPCPANFCIFSRNGVLPC
Ouz	2002	1	ł	i		SCLSLPSSWD1RCLFFCFAMFCH BIG101210
		1	- 1	Į.		WPGWSRTPDLS
- (00	2033	A	5218	85	402	CPSVSGLIKSDLRRHNINIGITNVDVKAVSNIF
683	2033	1 ^	32.0			MIILLRSMYRINVKPYFFI*LFFSRVNC*SVIIG
	Ì		1	1	1	YARCYTFLIF*LFL*IPADSPTDQEPKTVMLSk
	1			Į		OSESAL
			<del>-  </del>	<del>                                     </del>	194	NLMKEMQNLNSENHKTWEEYKDTK*IMSYE
684	2034	A	5220	1	134	YG*ALNVIKMAVLPKLMYRFSATLVKIPQHI
		j	1	1		TDS
	ļ	!				LHSQDGNSDPRKPQGEMSAHAFPVQTCGEE
685	2035	A	5228	260	440	QKKTPQVPINFTELSKCS*S*KIMSGERE
1005	-055			1	<u> </u>	QKKTPQVPINFTELONCO'S AIMOODIC
(0/	2036	A	5239	79	508	GGEAAARAKLSSPRPHRVGRRERGVGGMS
686	2030	1	1 2237	1	1	AFSEAALEKKLSELSNSQQSVQTLSLWLIHH
·		- 1				KHSRPIVTVWERELRKAKPNRKLTFLYLANI
l				-		VIONSKRKGPEFTKDFAPVIVEAFKHVSSETT
1						FSCKKHLGRVLSIWEERS
					120	MAAVVAATALKGRGARNARVLRGILAGAT
687	2037	A	5244	1	428	NKASHNRTRALQSHSSPEGKEEPEPLSPELE
	1	1	{			PRKRGKNPMKAVGLAWAIGFPCGILLFILTK
1		1				PKKKOKNYWAYOLAWAIOI I COIDDI IDTA
l	Ì	1	Ì			EVDKDRVKQMKARQNMRLSNTGEYESQRF
1	- }		1			ASSQSAPSPDVGSGVQT
	<del></del>		5240	-	1407	LOCTEDESLLNOGSSSEEVAGSSQKMGQPG
688	2038	A	5249	1 *	1.0	CODEDI ATAI HRI SI RRONYL SEKOFFAEEV
		}	1	1		OPKIOVI ADOKEGVSGCVTPTESLASLCTTC
				1		EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY
	1	1	Ì			HWQQLAQPNLGTILDPRPGVITKGFTQLPGI
1						HWQQLAQPNLGTILDPREGATIRGITQLI GI
1	1					AIYHISDLEEDEEEGITFQVQQPLEVEEKLST
1			Ì	İ		KPVTGIFLPPITSAGGPVTVATANPGKCLSCT
1			1			NSTETETTCRILHPSDITOVTPSSGFPSLSCGS
1.						GSSSSNTAVNSPALAYRLSIGESITNRRDSTT
			1	1	1	

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleonde	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, 1 =1 tollic,
uence		ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	)	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
	<del> </del>	<del> </del>	<del> </del>			FSSTMSLAKLLQERGISAKVYHSPISENPLQPL
		1	ļ			PKSLAIPSTPPNSPSHSPCPSPLPFEPRVHLSEN
		1				FLASRPAETFLQEMYGLRPSRNPPDVGQLKM
		1				NLVDRLKRLGIARVVKNPGAQENGRCQEAEI
		1	}	1	}	GPQKPDSAVYLNSGSSLLGGLRRNQSLPVIM
	{		1			GSFAAPVCTSSPKMGVLKED
	1		1	L	<del> </del>	LSLFGSRALGRSGARAMAKAKKVGARRKAS
689	2039	A	5254	2	2621	LSLFGSKALUKSUAKAMAKAKA VOAKKAS
	1	1		Į.		GAPAGARGGPAKANSNPFEVKVNRQKFQILG
	1	1		1	1	RKTRHDVGLPGVSRARALRKRTQTLLKEYKE
	1		1			RDKSNVFRDKRFGEYNSNMSPEEKMMKRFA
ļ	1	ļ	ļ	1	,	LEQQRHHEKKSIYNLNEDEELTHYGQSLADIE
	1	i		I		KHNDIVDSDSDAEDRGTLSGELTAAHFGGGG
	1	ì		1		GLLHKKTOOEGEEREKPKSRKELIEELIAKSK
		1	1	1		QEKRERQAQREDALELTEKLDQDWKEIQTLL
1	1		ļ	{	İ	SHKTPKSENRDKKEKPKPDAYDMMVRELGF
			1			EMKAQPSNRMKTEAELAKEEQEHLRKLEAE
			1			RLRRMLGKDEDENVKKPKHMSADDLNDGFV
	-	1	1		1	LDKDDRRLLSYKDGKMNVEEDVQEEQSKEA
ļ	}	1	1			SDPESNEEEGDSSGGEDTEESDSPDSHLDLES
					]	NVESEEENEKPAKEQRQTPGKGLISGKERAG
ł	1	1	. 1			NVESEEENERPAREQROTTOROLISORLISOR
	)	1	}	1	Ĭ	KATRDELPYTFAAPESYEELRSLLLGRSMEEQ
·	ì		1	1		LLVVERIQKCNHPSLAEGNKAKLEKLFGFLLE
<b>!</b>	-	1				YVGDLATDDPPDLTVIDKLVVHLYHLCQMFP
j			}		1	ESASDAIKFVLRDAMHEMEEMIETKGRAALP
1			j	]	ļ	GLDVLIYLKITGLLFPTSDFWHPVVTPALVCL
1		1		1		SQLLTKCPILSLQDVVKGLFVCCLFLEYVALS
1		1	ŀ		İ	ORFIPELINFLLGILYIATPNKASQGSTLVHPFR
1	i	1		<b>,</b>	1	ALGKNSELLVVSAREDVATWQQSSLSLRWA
1			I		1	SRLRAPTSTEANHIRLSCLAVGLALLKRCVLM
1		-	ì	1	(	YGSLPSFHAIMGPLRALLTDHLADCSHPQELQ
		1	]	)		ELCQSTLTEMESQKQLCRPLTCEKSKPVPLKL
1	1				ì	FTPRLVKVLEFGRKQGSSKEEQERKRLIHKHK
	İ			ŀ	1	REFKGAVREIRKDNQFLARMQLSEIMERDAE
	1	1	1			RKRKVKQLFNSLATQEGEWKALKRKKFKK
	- [	1	l			KKKK V KQLFNSLATQEOD W KALKIGAG KIL
690	2040	A	5261	1	304	FFFFVFLVETGFHHVGQAGLELLTSGDPPTW
		1	1	,		ASQSAGITGVSHCSWPVIYVLSTLLHAVRNVL
						FKRTFPLKSSSFLSYDKEIFPILIVLKFYLVTLT
	1	1	1			SFVK
601	2041	A	5270	3	158	NCHTTHCTANWVHLPGTPPGWKIDGPAAAL
691	2041	1^	1 32 / 0	1-	1	EVLSSFFFFFLKFSYKPONIV
100	2042	+	5282	56	1268	GMEPVGCCGECRGSSVDPRSTFVLSNLAEVV
692	2042	Α	3202	} 50	1200	ERVLTFLPAKALLRVACVCRLWRECVRRVLR
	1	1	1		1	THRSVTWISAGLAEAGHLEGHCLVRVVAEEL
}	Ì		1		1	ENVRILPHTVLYMADSETFISLEECRGHKRAR
1			1	1		KRTSMETALALEKLFPKQCQVLGIVTPGIVVT
1			]	1	1	PMGSGSNRPQEIEIGESGFALLFPQIEGIKIQPF
1			1		1	PMGSGSNRPQEIEIGESGFALLFFQIEGIAQIT HFIKDPKNLTLERHQLTEVGLLDNPELRVVLV
1	}		- {	1	1	HIKUPANLILERHULIEVULLURIELRAVET
1		Ì	ļ		1	FGYNCCKVGASNYLQQVVSTFSDMNIILAGG
1	1	-		l .		QVDNLSSLTSEKNPLDIDASGVVGLSFSGHRI
		ł		1		QSATVLLNEDVSDEKTAEAAMQRLKAANIPE
				]		HNTIGFMFACVGRGFQYYRAKGNVEADAFR
1	1	1		1		KFFPSVPLFGFFGNGEIGCDRIVTGNFILRKCN
1		-		1		EVKDDDLFHSYTTIMALIHLGSSK
L				12/2	1507	EEIKERFGPGLVIYWYGFIQELDCNRERGILLK
693	2043	A	5301	362	507	ACFPTNIVTLCHSIA
]		1			<u> </u>	RVLTAINHTLKENLRKFYKGKKDKPLDLRPK
694	2044	A	5310	1	204	KYLIAINHILKENLAATIAUAANATUURAA
1		1			İ	KTRAMRRRLNMHEENLKTKKQHRKERLYPL
	}	- }	i	į	1	RKYAAKA
695	2045	A	5315	125	1596	ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP
275	1 2073	1"				

				D 11 - 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		រោ	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	M=Memionine, N=Asparagine, 1 Tromie,
•	uchee		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	Ì		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ĺ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì				soquente	/=possible nucleotide deletion, \-possible
	1			peptide		nucleotide insertion
	1	ļ		sequence		TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP
			T			SSLFESLISPIKTETFFKEFWEQKPLLIQRDDPA
	Ĭ		1			SSLFESLISPIK TETTERET WEGIN DER GINDVIV
	ì	1		<b>!</b>		LATYYGSLFKLTDLKSLCSRGMYYGRDVNV
	ļ	ļ	1		1	CRCVNGKKKVLNKDGKAHFLQLRKDFDQKR
		l				ATIQFHQPQRFKDELWRIQEKLECYFGSLVGS
	1	1				NVVITPAGSOGLPPHYDDVEVFILQLEGEKH
l	1	1		ľ		WRI VHPTVPLAREYSVEAEERIGRPVHEFML
]	)			ļ		KPGDLLYFPRGTIHQADTPAGLAHSTHVTIST
1	1	1				YQNNSWGDFLLDTISGLVFDTAKEDVELRTG
}			ł	Í		YONNSWODILLDIISOLVIDII COEL PTI ADRI EG
1		1	ŀ	1		IPROLLLOVESTTVATRRLSGFLRTLADRLEG
	ł	1	1	Į.		TKELLSSDMKKDFIMHRLPPYSAGDGAELSTP
1	1					GGKLPRLDSVVRLQFKDHIVLTVLPDQDQSD
j			1	j	1	ETQEKMVYIYHSLKNSRETHMMGNEEETEFH
	1	1	1	1		GLRFPLSHLDALKQIWNSPAISVKDLKLTTDE
1					<b>\</b>	FKESLVLSLWTECLIOVV
	Į.		L		710	LMKXYLEAAELGEISDIHTKLLRLSSSQGTIET
696	2046	Α	5318	1476	742	SLQDIDSRLSPGGSLADAWAHQEGTHPKDRN
		1	i			VEKLQVLLNCMTEIYYQFKKDKAERRLAYN
	į		1	j	]	EEQIHKFDKQKLYYHATKAMTHFTDECVKK
ł	ĺ	-	ŀ			EEQIHKFDKQKLY THATKAWITH TDBC VICE
	i					YEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDI
1	}		1	1	ļ	EEEVSKYQEYTNELQETLPQKMFTASSGIKHT
			i			MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE
	1	İ				LAENNHILESGGSLTMDGGLRNVDCL
		<del></del>	5330	244	478	I DVNEEL FEMTEGLVSOAGVOWHDLGSLQPP
697	2047	Α	5320	244	1770	PPGFKQFSCLSLPSSWDYRHLPPHLANFSREG
	]	Ì	1		1	VSPSWPGWSRTPDFR
			6304	266	714	I PIRKSLRSVRSGFPTSOSPITRNLDGTASGSC
698	2048	Α	5324	200	/ 17	LAKTVTGSLFRINVGLRGLVAGGIIGALLGTP
						VGGLLMAFOKYSGETVQERKQKDRKALHEL
l	1	1	ì	Ì		KLEEWKGRLQVTEHLPEKIESSLQEDEPENDA
İ	- 1			1		KKIEALLNLPRNPSVIDKQDKD
	İ	1				RPHGHLVCISSSAGLSGVNGLADYCASKFAA
699	2049	A	5334	699	277	FGFAESVFVETFVQKQKGIKTTIVCPFFIKTGM
"			1	1		FEGCTTGCPSLLPILEPKYAVEKIVEAILQEKM
	ł	1			}	FEGUL IGCPSLLFILER LAVER PLATE LADVI GI
1		1	ł	1		YLYMPKLLYFMMFLKSFLPLKTGLLIADYLGI
ł	1	Ĭ			1	LHAMDGFADQKK
-	10000	+	5344	3	614	PTAEEMSSLTPESSPELAKRSWFGNFISLDKEE
700	2050	A	3344	1	1	OTEL VI KOKPI SSIKADIVHAFLSIPSLSHSVLS
1	ļ		1			OTSER A EYK A SGGPSVFOKPVRFQVDISSSEG
Į.	ļ	1	l l	i	Ì	PEPSPRRDGSGGGGIYSVTFTLISGPSRRFKRV
1			- 1			VETIQAQLLSTHDQPSVQALADEKNGAQTRP
l	-	1	1	ì		AGAPPRSLQPPPGRPDPELSSSPRRGPPKDKK
i				ļ	Į.	
			1			LLATNGTPL
	2061	A	5346	3	1383	HASVLFCRVMAASKTQGAVARMQEDRDGSC
701	2051	A	1,540	١		STYGGYGYGDSKDCILEPLSLPESPGGTTTLE
	}		-	1	1	GSPSVPCIFCEEHFPVAEQDKLLKHMIIEHKIV
		1		1		IADVKLVADFORYILYWRKRFTEQPITDFCSV
			1			IRINSTAPFEEQENYFLLCDVLPEDRILREELQ
1	Ì	- [				KQRLREILEQQQQERNDTNFHGVCMFCNEEF
		1	1		}	LGNRSVILNHMAREHAFNIGLPDNIVNCNEFL
	l		1	1		LUNKS VILINGIWAKERAFINGEL DIG TROUBLE
	i			-		CTLQKKLDNLQCLYCEKTFRDKNTLKDHMR
	Į.	}				KKQHRKINPKNREYDRFYVINYLELGKSWEE
						VQLEDDRELLDHQEDDWSDWEEHPASAVCL
						FCEKOAETIEKLYVHMEDAHEFDLLKIKSELG
						INFYOOVKLVNFIRROVHOCRCYGCHVKFKS
		1				KADI RTHMEETKHTSLLPDRKTWDQLEYYFP
						TYENDTLLWTLSDSESDLTAQEQNENVPIISE
1						DTSKLYALKQSSILNQLLL
						MAAATRGCRPWGSLLGLLGLVSAAAAAWD
702	2052	A	5356	2502	1540	WIMAATROCKI WOODLODEGE COLUMNIE
1 102	2002					

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid. E=Glutarnic Acid,
10: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		in	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-		USSN 09/496	сопеspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	C-Glutamine R=Arginine, S=Serine,
ience	1		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	'			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			l	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del></del>		<del> </del>	sequence		LASLRCTLGAFCECDFRPDLPGLECDLAQHL
	}			Į.	}	AGQHLAKALVVKALKAFVRDPAPTKPLVLSL
	1	1		ļ		HGWTGTGKSYVSSLLAHYLFQGGLRSPRVH
	1	l				HFSPVLHFPHPSHIERYKKDLKSWVQGNLTA
					Ĭ	CGRSLFLFDEMDKMPPGLMEVLRPFLGSSWV
	}		}	,	Ì	VYGTNYRKAIFIFISNTGGEQINQVALEAWRS RRDREEILLQELEPVISRAVLDNPHHGFSNSGI
	1	ļ	1	ļ		MEERLLDAVVPFLPLQRHHVRHCVLNELAQL
	1	1	-	,		GLEPRDEVVQAVLDSTIFFPEDEQLFSSNGCK
	1					
		1	ı			TVASRIAFFL LFLQKLRMKTEEEARTHTEIEMFLRKEQQKL
703	2053	A	5380	278	657	EERLEFWMEKYDKDTEMKQNELNALKATKA
, 00		1	1		Ì	SDLAHLQDLAKMIREYEQVIIEDRIEKERSKK
		ł			ļ	KVKQDLLELKSVIKLQAWWRGTMIRREIGGF
		•				KM
				<del> </del>	1003	EDGRAVKMAAVVEVEVGGGAAGERELDEV
704	2054	A	5381	1	1003	DAISDI SPEEOWRVEHARMHAKHRGHEAMH
		1		1		A EMANT TI TATT VVAOLLLVOWKORHPRSYN
	}	ļ		1		LAVTI FOMWVVPLYFTVKLHWWKFLVIWILI
		1	}			SAVTAFVTFRATRKPLVOTTPRLVYKWFLLIT
		1				KISVATGIVGYMAVMFTLFGLNLLFKIKPEDA
						MDFGISLLFYGLYYGVLERDFAEMCADYMA
	Į.	-		[		STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV
				1		SEEGHENTYRLSCNHVFHEFCIRGWCIVGKK
		1				QTCPYCKEKVDLKRMFSNPWERPHVMYGQL
	ł	1	Ì		<u> </u>	LDWLRYLVAWQPVIIGVVQGINYILGLE IYDRDPLQLATRAGQPLDINMAGEPKPYRPKP
705	2055	A	5396	3	675	GNKRPLSALYRLESKEPFLSVGGYVFDYDYY
, 03		1			1 .	RDDFYNRLFDYHGRVPPPPRAVIPLKRPRVA
		1			İ	VITTERGEGVESMKGGSRSTASGSTGSKLKS
		ĺ				DELOTIKKELTOIKTKIDSVLGRLDKIEKQQK
İ		ļ		İ		AFAFAOKKILEESLVLIOEECVSEIADHSTEEP
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		٠		12	98	GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI
706	2056	Α	5410	2	1 70	9
L		<del></del>	5415	6	287	DEKT TESEL SHAFSSGOERKVFIELNHIKKCNT
707	2057	A	5415	1	1 20.	VRGVEVLEEFGNYTILLLGLDSHGSNSNLGAP
		[				FEGI GAGRKRTSVEKSGGAGVTRKKRDP
-	2050	+	5423	3	291	SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS
708	2058	A	5425	ا آ		TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS
	1				1	GCTIFKTVTLTARSTASLLKSVRPRTHQKE
700	2059	+	5424	679	347	RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG
709	2039	^	3727	1	· I	SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ
		ì				VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK
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710	2060	A	5442	1073	559	QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS
1 /10	2000	'`				GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK
	)				1	PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI
						RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV
		- [		1		SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP
711	2061	-	5449	1	319	DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL
' ' '	230.	1			1	NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD
				1		NORTH OCE
						LYRDIPELQGF RPTPGHGDFWMQPLTKDAGMSLSSYTLASAL
712	2062	A	5499	91	749	QVRGEALSEEEIWSLLFLAAEQLLEDLRNDSS
, 12	2002	1	1			QVKUEALSEEL WOLL LAVEQUEDEDIG TOO
1		i	į.	1	1	DYVVCPWSALLSAAGSLSFQGRVSHIEAAPF

				70 11:4-4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
VO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ļ ·	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
	1		ļ	peptide		nucleotide insertion
	]	1		sequence	ļ	KAPELLQGQSEDEQPDASQMHVYSLGMTLY
						WSAGFHVPPHQPLQLCEPLHSILLTMCEDQPH
	1	ì	1		Í	RRCTLQSVLEACRVHEKEVSVYPAPAGLHIR
	1		1	1	l	RLVGLVLGTISEVSREPCFSSSSCWSCVAIKI
	1	Ì				VEELILVSRLDPHLHTPMYFFLAHLSFLDLSFT
713	2063	A	5506	22	478	TSSIPQLLYNLNGCDKTISYMGCAIQLFLFLGL
, 13	2003	}	1	4		GGVECLLLAVMAYDRCVAICKPLHYMVIMN
			1	<b>\</b>	Į	GGVECLLLAVMA I DRCVAICATEIT INT MIN
	1	1		Ļ		PRLCRGLVSVTWGCGVANSLAMSPVTLRLPR
	1	1	ļ			CGHHEVDHFLCEMPALIRMACISTV
714	2064	A	5514	25	220	AIRPYWCENNIIGIGKLSTADGKAFADPEVLR
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	2065	A	5526	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAM
715	2065	Ι Δ	3320			GRTALFHHSGGSSGYESLRRDSEATGSASSAP
	-	1	1	1	1	DSMSESGAASPGARTRSLKSPKKRATGLQRR
	1		1		1	RLIPAPLPDTTALGRKPSLPGQWVDLPPPLAG
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	1	<del></del>	5529	458	790	SPGYGENKFTVTSXNIAVPLCEMNKIYSYYSI
716	2066	Α	3329	438	1,70	SSSSERTMDLVLEMCNTNSIHWCGISGRQLG
	ļ		i	1	ì	KLHPSSSLCLALTLLSSVQGLQSISGLRLTDTF
	1	ì	1		1	IKRTYEYDDIAOVCV
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717	2067	A	5531	)	1 400	PSYHDRKSKVDLDRLNDDAKRYSCTPRNYS
		1	İ			VNIREELKLANVVFFPRCLLVQRCGGNCGCG
		1	l		1	TVNWRSCTCNSGKTVKKYHEVLQFEPGHIKI
	1	1	1			PCDAKTMAI VDIOLDHHERCDCICSSRPPR
				311	88	AVIKNMAPMTALGLLDLHILNLILFLSAGED
718	2068	A	5586	311	00	TSVVSEIMMYILLVFLTLWLLIEMIYCYRKVS
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	1				330	KNCANEAVVOKILDRVLSRYDVRLRPNFGSM
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1		i	1	1		CPKDFGNINNCRMDLYFFLLAGIQAVTALLF
l		}				VWIAGRYERASQGPASHSRFSRDRG
		- [				MSALIVRKLRSAELTLFSELPTVLGANVNAA
721	2071	I A	5632	146	536	MSALIVRKLKSAELTLESELFT VLUANVINAA
121	20/1	1 ''	"""		1	KLHETALHHAAKVKNVDLIEMLIEFGGNIYA
1		1				RDNRGKKPSDYTWSSSAPAKCFEYYEKTPL
		1		Ì		LSQLCRVNLRKATGVRGLEKIAKLNIPPRLII
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L			5638	3	3806	CPSLDIRSEVAELRQLENCSVVEGHLQILLMI
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1						I RDLEPNLAVIRGTRLELGYALVIFEMPHLRI
		1	1		ļ	VALPAL GAVERGAVRVEKNQELCHESTIDW
1		1		- 1		GLIOPAPGANHIVGNKLGEECADVCPGVLG
				1		AGEPCAKTTESGHTDYRCWTSSHCQRVCPC
		1		1		UCMACTARGECCHTECLGGCSOPEDPRACY
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						ACRHI VEOGACI WACPPGTYOYESWRCVT
			•			A CRHI YEOGACLWACPPGTYQYESWRCV I
			•			ACRHLYFQGACLWACPPGTYQYESWRCVT. ERCASLHSVPGRASTFGIHQGSCLAQCPSGF RNSSSIFCHKCEGLCPKECKVGTKTIDSIQAA

SEQ ID No. of hod by the hod beginning and the beginning and beginning and the begin							
Not of nucle exists of population and control of population of the control of the	aro ID	CEO ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucleotide ended ended winder with the contraction of the contraction				ID NO:			D=Aspartic Acid, E=Glutamic Acid,
certide sequence control of the cont			nou	,			F=Phenylalanine, G=Glycine, H=Histidine,
sequence uence    14   14   2   2   2   2   2   2   2   2   2		1			location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
uence    Sequence   Se		, -	}	09/496			M=Methionine, N=Asparagine, 1 -1 forme,
residue of peptide peptide sequence per control peptide sequence per control peptide sequence per control per cont		denes		914			Q=Glutamine, K=Algilline, S=Strine,
peptide sequence    Possible meleotide diction,   "possible meleotide insertion   ide   meleotide   me	uence			]	amino acid	of peptide	T=1 hreonine, v= vainte, w=11 y propriate;
mucleotide insertion  GLVETTIGFLKIKHSFALVSLGFKMIKLIRGD  GLVETTIGFLKIKHSFALVSLGFKMIKLIRGD  AMYDGRYTLYVLDNONLQQLGSWYAGLIT  PVGKIYFAFNFRLCLEHIYRLEEVTGTTGGRQN  KAENFRINGDRAAGOTRILREVNYVFADRI LLRWERYEPLEARDLLSFIVYYKESFFQNATE  HVOPDAGOTGSWNILDVELPLSRTGPGAVOT  ASLKPWTOYAFVRAITLITTEDSPRIGGAVS  PIVYLRTLPAAPTYPODVISTSINSSSILLVRW  KPPTQRINGNLTYYLVLWORLAEDGDLYLND  VCHRGIRLFTSNNDFRDGEGDDPFAMESD  CCPCQHPPFQQVLPPLEAGEASFGKKFENFLH  NATTIPSPWKYTSINSFQNSGRIRRAAGPL  RLGGNSSDFEIGEDKVPRERAVLSGLRHFTEY  RDHAACNHAAHTVGSAATFVARATWHEE  ADGIPGKVAWFASSNSVLLRWLEPPDPNOL  ILXYEIKYRRLGEEATVLCVSRLRYAKFGGV  HLALLPPONYSARVRATSLAGNGSWTDSVAF  YLGEEEDAGGLHVLLTATPVGLITLIVLAA  LGFFYGKKRNRTLYASVNPEYFSASDMYVPD  EWEVPPEGISIIRELGGSFGMYTEGLARGE  AGESTPVALKTVNELASPRECIFFLKEASVM  KAFKCHHVYRLLGVYSAGPTLVMIELMTR  GDLKSSLLSSLRPEAENNFGLPQFALGEMCIA  AGELAGMAYLAAKFVHRDLAARNCNVSX  DFTVKIGDFGMTBDVYETDYYRKGGRGLLP  VRWMAPESLKAGIFTHSDWWSGGYGNVLWEIN  TLAEQPYGGLSNEGVVLFVWDGGVLELGG  PLOLGLMSRCWOPNRURSFTHIDSIGGEB  RPSFRLLSFYYSPECRARGSLPTTDAEPDSS  TPRDCSPONGGFGH  TTPCGHYPSKURPMSVQSDPOTLINELDSIGEB  RPSFRLLSFYYSPECRARGSLPTTDAEPDSS  TPRDCSPONGGFGH  LAWIDNIPEKEKKETDKKRKRKGAHEDCT  LAWIDNIPEKEKKETDKKRKRKGAHEDCT  TAMPENDAMPERSKAGIFTHOST STATEMPT  ALMONICAL STATEMPT  TAMPENDAMPT  ALMONICAL STATEMP	ļ					sequence	Y=1 yrosine, X=0 introvin, Stop sodon,
QDLVGCTHVEGSLIBLIR.QGVMLEPQLQIBS  GLVETTIGELKIHERSELVSLGFFRALKLERGD  AMVDGNYTLYVLDNQNLQQLGSWVAAGLTI PYGKLYFAPNRLCLLSLIFYLYEEVTGTRGRQN KAENPRINGDRAACQTRILRFVSNVTEADRI LLRWERYPLEADLLSFIVYYKESPFONATE HVOPDACGTGSWNLLDVELPLSRTQEPGVTL ASLRWTQYAFVRATITITEDSPFGQAQS PIVVLRTLPAAPTVPQDVISTSNSSSILLVRW KPPTORNONLTYVLJWGNLAEDGDLYLND YCHRGLR.PTSNNDPRFDGEDGDPRAEMESD CCPCQHPPPGQVLPPLAQEASFGKKFENFLH NATTEIPPWKYTSNNSPCRDSGRHRRAAGPL RLGGRSSDFFIOENKVPREAALSGLRHTEY RDIHLACNH-AAHTVGCSAATFVFARTMPHRE ADGIPGKVAWPASSKNSVLLRWLEPPPNGL LKYBIKYRLGEEATVLCVSRLRYAKFGGV HLALLPFONYSARVATSLAGNGSVTDSVAA YLGFEGERAMETLYASVPREYMSASDMYVPP EWEVPREQISIRBLGQGSFGMVYEGLAGLE AGESTFVALKTVNELASPRECIEFLKEASVM KAFKCHHVRLLGOVSGCOPTLVMELMTR GDLKSSLLSRIFLEASPECIEFLKEASVM KAFKCHHVRLLGOVSGCOPTLVMELMTR GDLKSSLLSRIFLASPECIEFLKGSGKLLP VRWAAPESLKDGIPTHSDVWSFGVVJLWEID TLAGQPYGGLSNEQVLSTVMDGGGRJCBELGG PLOLGEMSRCWOPNFLRPSFTHLDSIQEE RPSFRLLSFYYSPECRGARGSLPTDAFPDSS TPMCOSTGNIGVLSTVMDGGGVLEELGG PLOLGEMSRCWOPNFLRPSFTHLDSIQEE RPSFRLLSFYYSPECRGARGSLPTDAFPDSS TPMCOSTGNIGVLSTVMDGGGVLEELGG PLOLGEMSRCWOPNFLRPSFTHLDSIQEE RSSWSYSL ATMGFELDBFDGDVDPILKCALCKKVLEPP LTPECGHVPCAGCVLPWVYQGGSCPARCKG LSAKELNHVLLKALLIKLDIRCAYATRGCGU VKLQQPHELERGDFAARCRHAAGGQVL RRDVEAHMRDACDARPVGCQGCGCLPLT GGQRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGCGCCLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGCGCCLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGCGCLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGCGCLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGCGCLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGGCGLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGGCGLPLT GGGRAGGHCCARALRAGGGQVL RRDVEAHMRDACDARPVGCQGGCGLPLT GGGRAGGHCCARALRAGGGGGTDGARSVDNHD SSSGSYSLUD SSSGSYSLUD GGGRAGGCGGRAAAGGGGLGGRIBTENT RNSSPSPVLDPYLLPELFBSAHEYYPONDY GGBLSRATHLOQAVFAFTAKAGGGTDTA LSNQCKFTFSSALECTDADYLGFPVGCGGTGTDTA LSNQCKFTFSSALECTDADYLGFPVGCGGRGTTDTA LSNQCKFTFSSALECTDADYLGFPVGCGGRGTDTA LSNQCKFTFSSALECTDADYLGFPVGCGGRGTDTA LSNQCKFTFSSALECTDADYLGFPVGCGGRGTDTA LSNQCKFTFSSALECTDADYNTSDIDKRRERLSDITE.P	}		1			1	/=possible indicating defending ( possible
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AMVDGNYTLYVLDNONLOQLGSWVAARI PVOKKYYAFAPRIACLEHIYNLEEVTGTRGKQN KAEINPERNIGBRAACQTRTLRFYSNYTEAGRAN LILRWERYEPLEARDLISIVYYYKESPFONATE HVGPDACGTQSWNLLDVELPLSRTQEFGYAA ASKLYPTQYAVPVARUTLITEEDSPHQGAQS PIVYLRTLPAAPTVPQOVISTSNSSSILLVRW KPPTQRONGLTYYLVLWQRLAEGGLYVLND YCHRGILLFTSNNOPRFDGEDGDPEAFMEN KPPTQRONGLTYYLVLWQRLAEGGLYVLND YCHRGILLFTSNNOPRFDGEDGDPEAFMEN CCPCQHPPPGGVPPLEAQGASPGKFENEH NATTIPISPWKVTSINKSSPQDSGRHRRAAGPL RIGGNSDFELGGENYPERGARSGKFENEH HATTIPISPWKVTSINKSSPQDSGRHRRAAGPH RIGGNSDFELGGENYPERGARSGKFENEH HATTIPISPWKVTSINKSSPQDSGRHRRAAGPH RIGGNSDFELGGENYPERGARSGKFENEH HATTIPISPWKVTSINKSSPQDSGRHRAAGFTGE HATTIPISPWKVTSINKSSPQDSGRHRAAFTGE HATTIPISPWKVTSINKSSPQDSGRHRAAGFTGE HATTIPISPWKVTSINKSSPQDSGRHRAAGFTGE HATTIPISPWKVTSINKSSPQDSGRHRAAGFTGE HATTIPISPWKVTSINKSSPQDSGRHRAAGFTGE HATTIPISPWKVTSINKSSPQDSGRHRAAGFTGE HATTIPISPWKVTSINKSSPQDSGRHTAAFTGE HATTIPISPWKVTSINKSSPQDSGRHTAAFTGE HATTIPISPWKVTSINKSPGVVLEV HATTIPISPWKVTSINKSPGVVLEV HATTIPISPWKVTSINKSSPQDSGRHAAGRAFTGE HATTIPISPWKTSTHILDSIQEE HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEV HATTIPISPWKTSINKSPGVLEGGE HATTIPISPWKTSINKSPGVLOGRENEH HATTIPISPWKTSINKSPGVLOGRENEH HATTIPISPWKTSINKSPGVLOGRENEH HATTIPISPWKTSINKSPGVLOGRENEH HATTIPISPWKTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSPGCMTTSINKSP					1		CLARTITGEL KIKHSFALVSLGFFKNLKLIRGD
PVGKIYTAFPRICLEHIYRLEVIGINGKY KAENPRINGBRACQTRILRYSNNTEADRI LIRWERYEPLEARDILSFIVYYKESPFONATEADRI LIRWERYEPLEARDILSFIVYYKESPFONATEADRI LIRWERYEPLEARDILSFIVYYKESPFONATEADRI LIRWERYEPLEARDILSFIVYYKESPFONATEADRI LIRWERYEPLEARDILSFIVYYKESPFONATEADRI HVGPDACGTOSWILDVELPLEARGEGOLYLAV KPITORNORLTYYL VLWORLAEDGOLYLAV VCHEGURI RIPSTRYNDERFOEDGOEPPEARMESD CCPCQHEPPGGVLPPLEAGEASGKFERAMESD CCPCQHEPPGGVLPPLEAGEASGKFERAMESD CCPCQHEPPGGVLPPLEAGEASGKFERAMESD CCPCQHEPPGGVLPPLEAGEASGKFERAMESD CCPCQHEPPGGVLPPLEAGEASGKFERAMESD CCPCQHEPPGGVLPPLEAGEASGKFERAMESD RICHMANAFTY CSCAALTPY CAPACHA ANTIPISPWKYTSTSKSPKDASGKRERAAGPL RICHMANAFTY CSCAALTPY CAPACHA ADGEPKVAWA ASSINSYLLRWLEPPDHOL ILKYERY RRILGEBAV CACACACACACACACACACACACACACACACACACAC		1		l .			ANADGNYTLYVLDNONLOOLGSWVAAGLTI
KAEINPRINGBRAACQTRILREYSINTIADUL LRWEYSPELRADLISIPIVYYKESPRONATE HVGPDACGTQSWNLLDWEIPLSRIQEPGVA HVGPDACGTQSWNLLDWEIPLSRIQEPGVA ASKEPTQVAVEVRAITLITEEDSPHQGAQS PIVYLRTLPAAPTVPQDVISTSNSSILLVRW KYPTQRONLTYYLVJWQRLAEGGDLYLND YCHRGLEIPTSNNDPRFDGEDGDPEAPBEAGE CCPCQIEPPGQVLPPLEAQEASPCKKFENEH NAITIPISSWKVTSINKSPQBDSGRIBRAAGDL RLGGNSSDFEIQEDKVPREAVLSGLRHFTEY RIDHACNHAAHTVGCSAATFVFARTMPHEE ADGIPGKVAWEASSKNSVLLRWLEPPDPNGL ILKYERYRRLGEGATVLCVSRLRTAKFGOV HLALLPPGNYSARVAATSLAGNGSWTDSVKYFENEH ADGIPGKVAWEASSKNSVLRWLEPPDPNGL ILKYERYRRLGEGATVLCVSRLGTLITIVAAA LGFFYGKKRRRTLYASVNEYFSASDMYVEGLARGLE AGEESTPVALKTVNELASPRECEFLKRASKY VILGFEEDAGGLAVLLTATRVGTLILIVAAA LGFFYGKKRRRTLYASVNEYFSASDMYVEGLARGLE AGEESTPVALKTVNELASPRECEFLKRASKY KAFKCHVVNELIGVVSQGQPTLUMELMTR GOLKSHLRSLRFEAENPGLPQFALGEMQM AGEIADGMAYLAANKFVIREDGTLINGAARGLE AGEESTPVALKTVNELASPRECEFLKRASKY COLKSHLANKFVIREDGTLINGAARGLE PLOYDGGGATGLARGE PLOYDGGATGLEIGTTISDVWSGGVVLWEIV TLASQPYOGLSREQVLKVVMDGGVLEELEG PLOYDGFGRAGSLPTTDAEPDSST TYROCSPQNGFTRASTFHILDSIQEE PLOYDFPSVKIFMESVQSDPQNGHICIARKR SSSWSYSL AUGUSTATA ALGORITATION AGE TO THE					ļ.		DUCKIVE A ENPRI CLEHIYRLEEVI GIRGRON
LIRWERYEPLEARDLLS:IVYYKESPHUNGEN HVGPDACGTGSWILDUEPLIS:RTGEFGYTL ASI,KPWTQYAVFVRAITLITEEDSPHQGGVIL ASI,KPWTQYAVFVRAITLITEEDSPHQGAG PIVYLITI.PAAPITYPO,WISTINSSILLVRW KPPTORNORLTYYLV.WORLAEDGOLYTU YCHRIGLITENDOPPAGEMEND CCPCQHPPPGQVLPPLEAQEASTQKKFERAMEND CCPCQHPPPGQVLPPLEAQEASTQKKFERAMEND CCPCQHPPPGGVLPPLEAQEASTQKKFERAMEND HAITIPSPWKVTSINKSPQHDSGAFRAAGHL RIGHNSDFEIQEDKVPRERAVLSGLRHFTEY RIDHACHHAAHTYGCAAITFYARTHYBE ADGIPGKVAWEASSKNSVLLRWLEPPDHOR ADGIPGKVAWEASSKNSVLLRWLEPPDHOR ADGIPGKVAWEASSKNSVLLRWLEPPDHOR RIKYELSYLVGEASTAVLAGGSWTDSWA YILGEEEDAGGLHVLLTATPYGGASTLIVALAA YILGEEEDAGGLHVLLTATPYGGASTLIVALAA YILGEEEDAGGLHVLLTATPYGGASTLIVALAA YILGEEEDAGGLHVLLTATPYGGASTLIVALAA YILGEEEDAGGLHVLLTATPYGGASTLIVALAA UGFFYGKRRNRTLIASVPEYEASDMYYEGLARGLE ROGERFYGAKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRRTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRTRAGGASTLIASVPEYEASDMYYEGLARGLE ROGERFYGKRTRAGGASTLIASVPEYEASDMYTHOLASVPEYEASDMYTHO			1			1	VARINDR TNGDRAACOTRTLRFVSNVTEADKI
HIVGPDAGGTGSWNILDVELPILSRINGLEGG ALEXPWTQAAVFVARATITEEDSPHQGAQS PIVYLRTLPAAPTVPQDVISTISNSSILLVRW KPPTQRINGILTYYLVLWQBLAEDGGLYLND VCHRGLRLPTSNNDPRFDGEGDPFAAMESD CCPCQHPPPGQALPELAGGASFQKKFENEHL NATIPISPWKVTSINKSPQRDSGRIRRAAGPL RLGGNSSDFEIDGEWVPERAFAVLSGLRHFTSY RIDBIACNIAAHTVGGSAATFVFARTMPIRE ADGIPGKVAWEASSKNSVLLRWAKFGGV HLALLPPGNYSARVRATSLAGNGSWTDSVARA VTLGPEEDDAGGHVLLTATPVGLTILLIVLAA LGFFYGKKRNRTLYASVNPEYFSASDMYVED EWEVPREQSISIRELGGGSFGMVYEGLAGGLE AGESTFVALKTVNELASPRECIEFLKRASVM KAFKCHHVVRLLGVVSQGQTLVIMELMTR GGLKSHLRSLRPEAENNPGLPQALGEMQM AGEIADGMAYLAANKFYNEDLAARNCMVSK DFTVKIGDFGMTRDVVFTDYYPKRGGGLPV VVRMAPESLKGGITHTIABFSTHLLDSSDWSFGVVLWFT TLAEQPYQGLSNEGVLKFVMDGGVLEELGG PLQLGEMSKGWPNPRLRFSTHLLDSSVS TPRDCSPQNGGFGH LAWIDNIEFEKKETDKKRKKGAHEDG ERSPELLSFYYSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGGFGH LAWIDNIEFEKKETDKKRKKGAHEDG ERSPELLSFYYSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGGFGH LAWIDNIEFEKKETDKKRKKKGAHEDG ERSPENLSFYVSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGFGFGH LAWIDNIEFEKKETDKKRKKKGAHEDG ERSPENLSFYNSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGFGFGH LAWIDNIEFEKKETDKKRKKKGAHEDG ERSPENLSFYNSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGFGFG LAWINNIEFEKKETDKKRKKKGAHEDG ERSPENLSFYNSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGFGFG LAWINNIEFEKKETDKKRKKKGAHEDG ERSPENLSFYNSPECRGARGSCULWVVQCGSGCARGGGGALLTTGGHVAGAGGGAVL RAYGKFTEYSARLDSLSRCVAAPRGGGAGAGAGAGGAVL RAYGKFTEYSARLDSLSRCVAAPRGGGGAGAARGAGGAVL RAYGKFTEYSARLDSLSRCVAAPRGGGGAGAARGAGGAVL RAYGKFTEYSARLDSLSRCVAAPRGGGGAGAARGAGGAVL RAYGKFTEYSARLDSLSRCVAAPRGGGAGAARGAGAARAHNGALQARLGALMA KKEALRAGKRESLVAQLAAAQLSLQM ALRYGKFTEYSARLDSLSRCVAAPRGGGAGAARGAGAARAHNGALQARLGALMA KKEALRAGKRESLVAQLAAAQLSLQM ALRYGKFTEYSARLDSLSRCVAAPRGGGAGAARGAGAARGAGAAAAAAAAAAAAAAAAAA	Ì	]	Ì	}			I I DWEDVEDLEARDLLSFIVYYKESPFQNAIL
ASILEPWTQYAVFVRATILITELISHIQAGS PIVYLRTLPAAPTVPQOVISTSNSSSHLLVRW RPPTQRIGHLTYYLVI WQRLAEDGIDLYIND YCHRGLALPTSNNDPRFDGEDGPEAEMESD CCPCQHPPGQVLPPLEAQEASFQKEFMLH NATTRISPWKYTSINKSPGNDSGRIRRAAGPL RLGGNSSDFEIQEDKVPRERAVLSGLRHFTEY RLDIHACNHAAHTVGCSAATFVARTGAW AWABSKNSVLLRWLEPPDPNGL ILKYEKYRRLGEATVLCVSRLRYAKFGGV HLALLPPGNYSARVRATSLAGNGSWTDSVAF YULGPEEDAGGLHVLLATPVGLTLLIVLAA LGFFYGKRRNRTLYASVNPEYFSASDMYVER EWEVPREQISIIRELQQGSFGMYYEGLARGLE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVVRLLGVVSQGQFTLVMEIMTR GDLKSHLRSLRPEAENNFGLPQALGEMQM AGEIADGMAYLAANKFVHRDLAARNCMVS DFTVXLGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGIFTHSDVWSFGVVLWEN TLAEQPYQGLSNEQVLKYPMDGGVLELEL LAWDDNILPEKEKKETDKKRKRKGAHEDCI PVRWMAPESLKDGIFTHSDVSSFGVLWEN TLAEQPYQGLSNEQVLYSDPQNGHCLARKR SSSWSYSL AGGRSRFVWAASWGGRGRPAARRRPRGLA ATMGFELDRFDGDVDPLKCALCHKVLEDP LTTPCGHVPCAGCVLPWVGDGVCELEL GEQFAPPSVKLPMESVQSDPQNGHCLARKR SSSWSYSL AGGRSRFVWAASWGGRGRPAARRRPRGLA ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPCGHVPCAGCVLPWVGDCGCGLPLT GEGRAGGHCCARLLARHGALQARACLEL ALKKEALRAGKEKSLVAQLAAAQLELQMI ALKYGALRAGKEKSLVAQLAAAQLELGKACKACACCACCACACATACCACCACCACACATACCACCACCAC		ļ	}				HUGPDACGTOSWNILDVELPLSRTQEPGVIL
PINYLRTLPAAPTVPQDVISTSNSSSHLVAW RPPTQRIGNLTYYLVLWQALADGGDLYLND YCHRGLRLPTSNNDPRFDGEDGDPAAMESD CCPCQHPPPGQNLPPLEAQGASTQKKFENEH. NAITIPISPWKVTSINKSPQRDSGRIRRAGEL RLGGNSSDFELGEEKVPRERAVLSGLRHFTEY RIDHACNHAAHTVGCSAATFVFARTMPIRE ADGIPGKVAWEASSKNSVLTAGMSWTDSVAR ADGIPGKVAWEASSKNSVLLAKGGV HLALLPPGNYSARVATSLAGMSWTDSVAR VTLGPEEDAGGLHVLLTATPVGLTLLVLAA LGFFYGKKRNRTLYASVNPEYFSASDMYVPD EWEVPREQISIBRELGQSFGMVYEGLARGLE AGESTFVALKTVNELASPRECIELLKASVM KAFKCHHVVRLLGVVSQGFULVIMELMTR GGLKSHLRSLRPEAENNPGLPQFALGEMQM AGEIADGMAYLAANKFYHRDLAARNCMVSS DFTVVLIODFGMTRDVVETDYYPKSGGGLP VRWMAPESLKDGIFTTHSDVWSFGVVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDVWSFGVLEELGG PLQLQELMSRCWOPNPRLSDLGGFG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSLUELGG PLQLQELMSRCWOPNPLSCAACGGGGGAPAGGGGAPAGGGGAPAGGGGAPAGGGGAPAGGGAPAGGGAPAGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGGAPAGA			1	1	1	)	A ST V DWTOVA V F V RAITLITEED SPHQGAQS
RPTORNGNLTYYL.VLWORLAEDUGLYND YCHRGLALPTSNNDPRFDGEDGDPEAEMESD CCPCQHPPGQVLPPLEAQEASFOKKFPNLH NATTPISPWKYTSNNSPRFDGEDGBPEAEMESD CCPCQHPPGQVLPPLEAQEASFOKKFPNLH NATTPISPWKYTSNNSPRFDGEDGBPEAEMESD CCPCQHPPGQVLPPLEAQEASFOKKFPNLH NATTPISPWKYTSNNSPRFDGSGRHRRAAGPL RLGANSSDFELQEBKYPRERAVLSGLRHFTEY RIDHACNHAAHTVGCSAATPVARTMPHRE ADGIPGKVAWEASSKNSVLLRWLEPPDNGL ILKYEIKYRRLGEBATVLCVSRLRYAFGGV HLAALPPGNYSARVRATSLAGNGSWTDSVAF YULGPEEDAGGLHVLLATPVGLTLIVLAA LGFFYGKKRNRTLYASVAPEYFSASDMYVEP EWEVPREQISIRELQGGSFGMYYEGLARGLE AGEESTPVALKTVNELASPRECIFELKEASVM KAFKCHHVVRLLGVVSQGQFTLVMEINT GGLKSHLRSLRYSPERCRAGGGPQHALEMT GGLKSHLRSLRYSPERCRAGGSPTPALEMT GGLKSHLRSLRYSPERCRAGGSPTPURAGMY AGEIADGMAYLAANKFVHRDLAARNCMVS DFTVXIGDFGMTRDVYETDYMGGVGLELD VRWMAPESLKDGIFTHSDVWSFGVVLWEIN TLAEQPYQGLSNEQVLKPMGTVAGGGELP VRWMAPESLKDGIFTHSDVWSFGVVLWEIN TLAEQPYQGLSNEQVLKPMGTVAGGGELP VRWMAPESLKDGIFTHSDVWSFGVVLWEIN TLAEQPYQGLSNEQVLKYMGGGGEPAGE PLQLQELMSRCWQPNPRLRPSTHLDAEDQE RPSFRLLSFYYSPESCRAGRSLPTIDAEDQES RPSFRLLSFYYSPESCRAGRSLPTIDAEDQES PROMPT AMAGEN SSSWSYSL  AGGRRSFPVWAASWGGRGRPAARRRFRGLA ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPGGHVAGCGCLPWVGSDPQNGHELARCR SSSWSYSL  AGGRRSFPVWAASWGGRGRPAARRRFRGLA ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPGGHVAGCGCLPUTH GEQRAGGHCCARALRAHNGALQARLGALH ALKKEALRAGKRESIJ VAQLAAAQLELQMI ALRYGKFTEYSALDSLSRCVAAPPGGKGI EYKSLTJVLHRDSSGLGFNIGGRFSVDNHDX SSSGGIFVSKIVDSGPAAKSGGLQHDRIEVN GRDLSSATTHDAAVAFATSUNQALAR PRTKMTTPSESQLVDTGTQTDITFEHMALT KMSSPSPVLDAYLLHBDSSGLGFNIGGRFSVDNHDX SSSGGIFVSKIVDSGPAAKSGGLQHDRIEVN GRDLSSATTHDAAVAFATSUNQALAR PRTKMTTPSESQLVDTGTQTDITFEHMALT KMSSSPSPVLDPVLLFEEIPSAHEYYDPNDY GDHQEMDRELELEEVDLYRMMSQDKLGL VCYTTDDEDDIGIVSEEDPSNIAAKDGREG DRIATASSTPLAGGRACHTOMDLL EQHHQAMQFTASVLOQKKHDEDGGTTDTA ILSNQHENDSCOGRTDESTRNDESSEGENNC DDATASSNPLAGGRACTCSQDTLGSGDLFF NESFISADCTDADVLGIPVDECEFREBALELK CQVKSATPYGLYFSGPLAGGSSDPSCLOR LELLREGERSPANATSIDYRRHELSDITELP LELLREGERSPANATSIDYRRHELSDITELP LELLREGERSPANATSIDYRRHELSDITELP LELLREGERSPANATSIDYRRHELSDITELP	1	l		[			DIVIVI DTI PA A PTVPODVISTSNSSSHLLVKW
YCHRGIRLPTSNNDPRFDGEDGPLAEMESS) CCPCQHPPGGVLPPLEAQEASFQKKFRNFLH NATTPISPWKYTSNKSPQRDSGRIRRAGGH. RLGGNSSPEIQEDKVPRERAVLSGLRHTEY RIDHACNHAAHTYGCSAATFVFARTMPHRE ADGIPGKVAWEASSKNSVLISWLEPPPPNGI. LIKYEKYRRIGEFATVLCVSRLRYAKFGGV HLALLPPGNYSARVRATSLAGNGSWTDSVAF YILGFEEDDAGGLHVLLTATPVGLTLLIVLAA LGFFYGKKRNRTLYASVMPEYFSASDMYVED EWEVPREGUSIRLELGGGSFGMVYEGLARGLE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVYRLLGVVSGGFGMVYEGLARGLE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVYRLLGVVSGGFGMVYEGLARGLE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVYRLLGVVSGGFGMVYEGLARGLE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVYRLLGVVSGFGVTLWEN TLAGGPYGGLSNEQVLKFVMDGGVLEELGG PLQLOELMSRCWOPNPRLRPSTFILDSIGEEL RPSFRLLSFYYSPECRARGSLPTTDAEPDSS TPRDCSPQNGGPGH TLAGGPYGGLSNEQVLKFVMDGGVLEELGG PLQLOELMSRCWOPNPRLRPSTFILDSIGEEL RPSFRLLSFYYSPECRARGSLPTTDAEPDSS TPRDCSPQNGGPGH AWDINIPEEKKETDKKRKKKGAHEDCT EEPQPFPSVKIPMESVQSDPQNGHICIARKR SSSWYSL  723 2073 A 5672 1 216 LAWDNIPEEKEKETDKKRKKKKGAHEDCT EEPQPFPSVKIPMESVQSDPQNGHICIARKR SSSWYSL TLAGGPYGGLSTPTTAAEPDSS TPRDCSPQNGGGGARGSLPTAARREFGGL ATMGFELDRTDGDVDDLKCALCHKVLEDP ATMGFELDRTDGDVDDLKCALCHKVLEDP TTPCGHVPCAGGCVLPWVVQGGSCPARCRG LSAKELNHVLPLKRLLIKDIBKCAYATRGCG VXKLQQUFELLECTOPAPRCRHAGCGGVL RRDVEAHNRDACDARPVGCQGCGGLPLT GEDRAGGHCCARLARNGALQARLGALH ALKKEALRAGKRESI.VAQLAAQLELQM ALRYQKKFTEYSARLDSLSRCVAAPPGGKG ETKSLTLVLHRDSGSLGFNIGGRFSVDNHDX SSSEGIFVSKIVUSGPAAKEGGLQHDRIEVM GRDLSRATHDQAVEAKTATECTOPHD GDHQEMDREELELEEVDLYRNMSQDKLGL VXKLQDLPEHLERCDFSNYSOLUL KMSSPSPVLDFYLLIPEEHPSAHEYYDPNDY GDHQEMDREELELEEVDLYRNMSQDKLGL VXXLTDEDDIGIGISEDPNIAAKDGREG DRATASSPPLAGGRKALTCSQDTLGSDLPFS NESSISADCTDADYLGIPVDECREFRELLEIK CQVKSATPYGLYYYSGPLDAGKSDPESVDK LELLNEELRSIELECLSVRAHKMQOLKEGY VXXLD DDATASSPPLAGGRKLTCSQDTLGSGDLPFS NESSISADCTDADYLGIPVDECREFRELLEIK CQVKSATPYGLYYYSGPLDAGKSDPESVDK LELLNEELRSIELECLSVRAHKMQOLKEGY VXXLD ALMGGFRINVYSIDVRRHELSDITELP			1		ļ		VDDTOPNIGNI TYYLVLWORLAEDGDLYLND
NAITIPISPWKYPRRAVI.SGLRIFTEY RIGHNSDFEIQEDKVPRRAVI.SGLRIFTEY RIDHACNHAAHTVGCSAATIFVARTMPHRE ADGIPGKVAWEASSKNSVLRWLEPPPPNGL ILKYEIKYRLGEEATVLCVSRLKYAKPGGV HLALLPPGNYSARVRATSLAGNGSWTDSVAF YILGPEEDAGGLHVLLTATPVGLILLIVLAA LGFFYGKKRNRTLYASVMPEYFSASDMYVPD EWEVPREGISIRELGGGSFGMVYEGLARGLE AGEESTPVALKTVNELASPRECIELKEASVM KAPKCHHVVRLLGVVSGGPTLVIMEIMTR GDILSHLRSLRPEAENNPGLPQPALGEMIQM AGELADGMAYLAANKTRDLAARNGMVSG DFIVKIGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGIFTTHRDLAARNGMVSG DFIVKIGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGIFTTHRDLAARNGMVSG PLOGELMSRCWQPNFRLRPSTHILDSIQEE RPSFRLLSFYYSPECRGARGSLPTTAAEPDSSI TPRDCSPONGGPGH  1.AWUDNIPEREKKETDKKRKKKKGAHEDCI EEPQFPPSVKIFMESVQSDPQNGHICLARKR SSSWSYSL  ARGRRSRFVWAASWGGRGRPAARRPRGL ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKCALCHKVLEDP ATMGFELDRFDGDUDPDLKAALAGAGGGCGCLPL GRORAGGHCCARLARANGALQABLQMT ALKKEALRAGKRESI VAQLAAQLELQMT ALKKEALRAGKRESI VAQLAAQLELQMT ALKYEALRAGKRESI VAQLAAQLELQMT KMSSPSPVLDPYLLPEEHPSAHEYYDPNDY GDHQEMDREEL ELEEVDLYRNMSQDKLGL KMSSPSPVLDPYLLPEEHPSAHEYYDPNDY GDHQEMDREEL ELEEVDLYRNMSQDKLGL VCYRTDDEDDIGIYISEDPNIAAKDGREC DRIQNIGEVQNREEAVALLTSEERNKYSLL ARAELQLDEGWMDDDRRDFLDDLHMDML ARAELQLDEGWMDDREDLELEERNKYSLL ARAELQLDEGWMDDREDLEDLEHMSMORIEC DRINGBEVQNREEAVALLTSEERNKYSLL ARAELQLDEGWMDDREDLEDLEHMSMORIEC DRINGBEVQNREEAVALLTSEERNKYSLL ARAELQLDEGWMDDREDLEDLEHMSMORIEC DRINGBEVQNREEAVALLTSEERNKYSLL ARAELQLDEGWMDDREDLEDLEHMSMORIEC DRINGBEVQNREEAVALLTSEERNKYSLL ARAELQLDEGWMDDRENDFLDDLHMDML EQHHQAMQFTASVLQKKHDEDGGTTDTA ILSNQHEKDSGVGRTDESTRKDSESGENNKS COVKSSTYPGLTYYSPGPLDAGKSDESVDKL ALLENEELSSELECLSIVRAHKMQULKEGY VENDELMELMSERDENNYSLDTERHELDITELP	-	1 .			1		VCURGI RI PTSNNDPRFDGEDGDPEAEMESD
RILGGNSSDEFIQEDKVPRERAVI-SILRH RIDHIACNHAAHITVGCSAATFVFARTMPHER ADGIPGK VA WEASSKINSVLIRWLEPPDPNOL ILKY EIKYRIL GEEATVLCVSRIR YAKFGGV HLALLPPGNYSARVRATSLAGNGSWTDSVAF YILGFEEEDAGGLHVLLTATPVGLTLLIVLAA LGFYGKKRNRITLYASNNEYFSASDMYVPD EWEVPREQISIIRELGQGSFGMYVEGLARGLE AGESTPVALKTVNELASPRECIEFIKASVM KAFKCHHVVRILGVVSQGGPTLVIMELMTR GDLKSHLRSLRPEAENPGI-PQPALGEMQM AGELADGMAYLAANKFVIRDLAARNGMVSG DFTVKIGDFGMTRDVYETGDYTRKGKGGLLP VRWMAPESLKOGISTTHISDVWSFGVVLWFUNDGSVLEELGG PLQLQELMSRC WOPPNRLRSTFHILDSIQEEI RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSI TPROCSPONGPOFE RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSI TPROCSPONGPOFE RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSI TPROCSPONGGPGPARGMEN AGELADGWAYLAVANKFVIRDLAARNCMVSK DFTVKLGDEFORD AGENGARGEN AGENGAL AGENGAL ART SSSWYSL ARGREDATED AGENGAL AGENGAL AGENGAL AGENGAL AT MGFELDRFDGDVDPDLKCALCHKVLEDP LTTPCGHYFCAGCVLPWVVQGSCPARCRG LSAKELNIVLPLKRLIIKLDIKCAYATRGCGI LSAKELNIVLPLKRLIIKLDIKCAYATRGCGI LSAKELNIVLPLKRLIIKLDIKCAYATRGCGI LSAKELNIVLPLKRLIIKLDIKCAYATRGCGI LSAKELNIVLPLKRLIIKLDIKCAYATRGCGI LSAKELNIVLPLKRALRAMGALQARLGALH ALKKEALRAGKREKSLVAQLAAQLELQMI ALKYGAGGHCCARALRAMNGALQARLGALH ALKKEALRAGKREKSLVAQLAAQLELQMI ALKYGAGGHCCARALRAMNGALQARLGALH ALKKEALRAGKREKSLVAQLAAQLELQMI ALKYGAGGHCCARALRAMNGALQARLGALL KMSSSPVLDPYLLPEEHPSAHEYYDPNDY GROLSRATHDQAVEARKTAKEPVVOVLRR. PRTKMFTPSESQLVDTGTQTDTTFEHMALT KMSSSPVLDPYLLPEEHPSAHEYYDPNDY GROLSRATHDQAVEARKTAKEPVVOVLRR. PRTKMFTPSESQLVDTGTQTDTTFEHMALT KMSSSPVLDPYLLPEEHPSAHEYYDPNDY GROLSRATHDQAVEARCHACHONISEN DRIIQNINGIEVONREEAVALLTSENNNFSLLL VLARELCELEVDLYRNNSQDLL VCYRTDDEDDIGIVSEDIPNSIAAKDGGRIRE DRIIQNINGIEVONREEAVALLTSENNNFSLLARAELDEGWANDTNISDIDNSIALDHAMML EQHHQAMQFTASVLQQKKHDEGGTTDTA ILSNQHEKDSGVGRTDESTRNDESSEGENNG DDATASSNPLAGGRKLTCSQDTLGSGDLPFS NIESFIADCTDADVLIGPCDECRRELLELK CQVKSATPYGLTYFTSPDLAGSGDLPPS NIESFISADCTDADVLIGPCDECERRELLELK CQVKSATPYGLTYFTSPDLAGSGDLPPS NIESFISADCTDADVLIGPCDECRRELLELK CQVKSATPYGLTYFTSPDLAGSGDLPPS NIESFISADCTDADVLIGPCDECRRELLELG DRIPS NIESFISADCTDADVLIGPCDECRRELLELK CQVKSATPYGLTYFTSPDLAGSGDLPPS NIESFISADCTDADVLIGPCDECRRELLELK CQVKSATPYGLTYFTSPTSNTSDISS			1				CCDCOHPPPGOVLPPLEAGEASFQKKFENFLH
RIDIHACNHAAHTVGCSAATFVARIUMPURNEL ADGREKVAWEASSKNSVLLRWLEPPDPNOL ILKYEIKYRRIGERATVLCVSRIRYAKFGGV HIAALLPPGNYSARVASVLAGORSVTDSVAF YILGFEEDAGGLHVLLTATPVGLTLLIVLAA LGFFYGKKRRKTLYASVNPEYFSASDMYVPD EWEVPREQISIIRELGGSSFGMYVEGLARGLE AGESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVRLLGVVSQGQFTLVMEIMTR GDLKSHLRSLRPEAENNPGLPQPALGEMQM AGELADGMAYLANKFVHRDLAARNGMYSG DFTVKIGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGIFTTHSDWSFGVVLWEIN TLAEQPYGGLSNEGVLKFVMDGGVLEELEGG PLOLQELMSRCWQPMPRLRPSTHILDSIQEEL RPSFRLLSYYSPECFGARGSLPTTDAEPDSSY TPROCSPQNGGPGH LAWIDNILFEKEKETDKKKKGAHEDCI EEQPFPPSVKLPMESVQSDPQNGHCIARKR SSSWSYSL  AGRRSRPVWAASWGGRGRPAARRRPRGLA ATMGFELDREPDGDVDPDLKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQEGSCFARCRG LSAKELNHVLPLKRLILKLDIKCAYATRGGG VVKLQQLPEHLBRCDFAPARCRHAGCGVL RRDVEAHMRDACDARPVGRCGEGGDPLTI GEQRAGGHCCARALRAHNGALQARLGALH ALKKEALRAGKEKE VAQLAAQLELQM ALRYQKKFTEYSARLDSLSRCVAAPPGGKG ETKSLTLVLHRDSGSLGFNINGGRPSVDNHDK SSSGIFVSKIVDSPAAKEGGLQHENIEVM GRDLSRATHDQAVEAFKTAKEPIVVQVLES PRTKMFTPPSSESLVAGDTGTQTDTTFHMALT KMSSPSPPVLDPYLLPEEIPSAHEYYDPNDY GDIHQEMBREELELEEVDTL PRANSODKLGL VCYRTDDEDDIGIYISEIDPNSIAAKDGRIRG DRIQNINGEVQNREEAVALLTSEENINFSLIL ARAEL_OLDEGWMDDRIFLDLHMDML EQHHQAMQFTASVLQQKKHDEDGGTTDTA ILSNQHEKDSGVRTDESTRNDESSEQENNC DDATASSNPLAGQRKLTCSQDTLGSGDLPF NESSISADCTDADVLIGIPDGEERRELLELK CQVKSATPYGLYYPTSGPLDAGKSDPESVDK LELLNEELRSIELECLSIVRAHKMQQLKEQV	ļ		1			1	NAITIPISPWKVTSINKSPQKDSGKHKKAAGPL
ADGIPGKVAWEASSKNSVLIKWELPHPINGE  ILKYEEKYRRIGEGEATVLCVSRLRYAKFGGV HLALLPPGNYSARVRATSLAGNGSWTDSVAF YILGPEEDAGGLHVLLTATPYGLTLLIVLAA LGFYYGKKRNRTLYASVNPEYFSASDMYVPD EWEVPREQISIIRELGQGSFGMYTEGLARGLE AGESTPVALKTVNELASPRECIEFIKASVM KAFKCHHVVRILGVVSQGOPTLVIMELMTR GDLKSHLRSLRPEAENNPGLPPALGEMIQM AGELADGMAYLAANKFVHRDLAARNGMVSG DFTVKIGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGITTHSDWSFGVVLWEIN TLABQPYOGLSNEGVLKFVMDGGVLEELGG PLQLQELMSRCWOPPRLRSFTHILDSIQEEI RSFRILSSYYSPECRGARGSLPITDAEPDSSI TPRDCSSPQNGGPGI PSFRILSSYYSPECRGARGSLPITDAEPDSSI TPRDCSSPQNGGPGI AGRISKETDKRFKKETDKRKKKGAHEDCI EEPQFPPPSVKIPMESVQSDPQNGHCIARKR SSSWSYSL ARGRESRPVWAASWGGRGRAARRERGL ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQEGSCPARCRG LSAKELNHVLPLKRLILKLDIKACATATRGCG VVKLQQLPHLERCDFAPARCHAGCGQVL RDVVEAHMRDACDARPVGRCGEGGGPLTI GEQRAGGHCCARALRAHNGALQALLAGALH ALKKEALRAGKREKSLVAQLAAAQLELQMI ALKYGKFTEYSARLDSLSRCVAAPPGGKG ETKSLTLVHRDSGLGFNIGGRRSVDNHDX SSSEGIFVSKIVDSGPAAKEGGLQHDRIENI GROLSRATHDQAVEAFKTAKEPIVVQVLRR PRTKMTFTPSESQLVDTGTTGTDTTEHIMALT KMSSPSPVLDPYLLPEEIFSAHEYYDPNDY GDHQEMDRELELELEEVDLYRNMSQDKLGL VCYRTDDEDDIGIYISEIDPNSIAAKDGRLEG DRIIQNIGGEVQNREAVALLTSENKNFSLLI ARAELQLDEGWMDDDRNDFLDDLHMDML EQHHQAMQFTASVLQQKKHDEDGGTTDTA ILSNQHEKDSCURATDSTRNDESSEQENNG DDATASSNPLAGQRKLTCSQDTLASGDLPF NESFISADCTDADVLIGPVDECERFRELLELK CQVKSATPYGLYYPSGPLDAGKSDPESVDK LELINEELRSIELECLSIVRAHKMQQLKEQV VENDU BNSGFBNYNTSIDVRRHELSDITELP		1	1			1	RLGGNSSDFEIQEDKVPKEKAVLSGLKAFTET
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LGFFYGKKRNRTLYASVIPEGLARGLE  BWE VPREQISIRELGQGSFGMYYFGGLARGLE  AGESTPVALKTVNELASPRECIEFILKEASVM  KAFKCHHVYRLLGVVSQGQPTLVIMELMTR  GDLKSHLESLRPAEANNFGLPQPALGEMIQM  AGEIADGMAYLAANKFVIRDLAARNCMVSC  DFTVKIGDFGMTRUVETDYYRKGGKGLLP  VRWMAPESLKDGIFTTHSDVWSFGVVLWEIV  TLASQPYQGLSNEQVLKFVMDGGVLELEGG  PLQLQELMSRCWQPNPRLRPSTHILDSIQEEI  RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSI  TPRDCSPQNGGPGH  LAWIDNILPEKEKKETDKKRKKKGAHEDCI  EPOPPPSVIKIPMESVQSDPQNGHICLARKR  SSSWSYSL  ARGRESRPWAASWGGRGRPAARREPRGLA  ATMGFELDRRDGDVDPDLKCALCHKVLEDP  LTTPCGHVFCAGCVLPWVVQEGSCPARCRG  LSAKELNHVLPLKRLLIKLDIKCAYATRGCGI  VVKLQQLPEHLERCDFAPARCRHAGCGGVL  RRDVEAHMRDACDARPVGRQEGGGLPLTT  GEQRAGGHCCARALRAHNGALAGARGALH  ALKKEALRAGKREKSLVAQLAAAQLELQMM  ALKYQKKFTEYSARLDSLSRCVAAPPGGKGI  ETKSLTLVLHRDSGSLGFMIIGGRPSVDNHDV  SSSEGIFVSKIVDSGPAAKEGGLQHEDRIEVN  GRDLSRATHDQAVEAFKTAKEPIVQVLRR  PRTKMFTPPSESQLVDTGTQTDTIFEHIMALI  KMSSPSPPVLDPYLLPEEHPSAHEYYDVNDY  GDIHQEMDREELELEEVDL VRMNSQDKLGL  VCYRTDDEDDIGIYISEIDPNSIAAKDGRIRE  DRIQINGIEVQNREEAVALTSSEENKFSLLL  ARAELQLDEGWMDDDRNDFLDDLHMDML  EQHHQAMOFTASVLQQKHDEDGGTTDTA  ILSNQHENDSGVGRTDESTRNDESSEQENKO  DDATASSNPLAGQRKLTCSQDTLGSGDLPFS  NESFISADCTDADYLGIPVDECERFRELLEIK  CQVKSATPYGLYYSGPLDAGKSDPESVDK  LELLNEERSIELECLSVVAHKMQQLKEQY  FENDAR HNSGFRELSDITTLEY  LELLNEERSIELECLSVVAHKMQQLKEQY				İ			VII CREEED AGGL HVI LTATPVGLTLLIVLAA
### EWEVPREQISIRELGGGSFGMYVEGLARGLE AGESTPVALKTYNELASPRECIEFLKEASVM KAFKCHHVYRLLGVVSQGQPTLVIMELMTR GDLKSHLRSLRPEAENNDGLPQPALGEMIQM AGEIADGMAYLAANKFVHRDLAARNCMVSC DFTVKIGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGIFTTHSDVWSFGVVLWF TLAEQPYQGLSNEQVLKFVMDGGVLELEGG PLQLOELMSRCWQPNPLRPSTTHLDSIQEEI RPSFRLLSFTYSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGGPGH LAWIDNILPEKEKKETDKKRKKKGAHEDCI EEPOFPPSVKIPMESVQSDPQNGHCHCARKR SSSWSYSL  ARGRESRPVWAASWGGRGRPAARRPRGLA ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQEGSCPARCRG LSAKELNHVLPLKRLILKLDIKCAYATRGCG VVKLQQLPEHLERCDFAPARCRHAGCGQVL RRDVEAHMRDACDARPVGRCQEGCGPLTT GEQRAGGHCCARALRAHNGALQARLGAH ALKKEALRAGKREKSI.VAQLAAAQLELQMT ALKYQKKFTEYSARLDSLSSRCVAAPPGGKG ETKSLTLVLHRDSGSLGFNIIGGRJSVDNHDX SSSEGIFVSKIVDSGPAKEGGLQHDRIIEVN GRDLSRATHDQAVEAFKTAKEPIVVQVLRR PRTKMFTPPSESQLVDTGTQTDIFFEHIMALT KMSSPSPVLDPYLLPEEHPSAHEYYDPNDY GDIHQEMDREELELEEVDLYRMNSQDKLGL VCYRTDDEDDIGITISEIDPNSIAAKDGRIREC DRIIQNGIEVQNREEAVALLTSEENKNFSLL ARAELQLDEGWMDDDRNDFLDDLHMDML EQHHQAMQFTASVLQQKHDEDGGTTDTA LISNQHEKDSGVGRTDESTRNDESSEQENNG DDATASSNPLAGGRKITCSQDTLGSGDLPPS NESSISADCTDADYLGIPVDECERFRELLELK CQVKSATPYGLYYPSGPLDAGKSDPESVDK LELLNEELRSIELECLSIVRAHKMQQLKEQY FENDRA LBASGERYNYTISIDVRHELSDITTELP	ł		}		1		I GEEVEKKRNRTI VASVNPEYFSASDMYVPD
AGESTPVALKTYNELLSPRECIEFLKEASVM KAFKCHHVYRLLGVVSQGQPTLVIMELMTR GDLKSHLRSLRPEAENNPGLPQPALGEMQM AGEIADGMAYLAANKVHRDLAARNCMVSG DFTVKIGDFGMAYLAANKVHRDLAARNCMVSG DFTVKIGDFGMAYLAANKVHRDLAARNCMVSG DFTVKIGDFGMAYLAANKVHRDLAARNCMVSG PLQLOELMSRCWQPNPRLRPSTTHLDSLGEG PLQLOELMSRCWQPNPRLRPSTTHLDSLGEG PLQLOELMSRCWQPNPRLRPSTTHLDSLQEEI RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSI TPRDCSPQNGGGH LAWIDNILPEKEKKETDKKRKKGAHEDCI EEPQPPPSVKIPMESVQSDPQNGHCIARKR SSSWSYSL ARGRRSRPWAASWGGRGPAARRPRGLA ATMGFELDRFDGDVDPLIKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQGGSCPARCRG LSAKELNHVLPLKRLILKLDIKCAYATRGCGI VVKLQQLPEHLERCDFAPARCRHAGCGQVL RRDVEAHMRDACDARPVGRCQEGCGLPLTI GEQRAGGHCCARALRAINGALQARLGALH ALKKEALRAGKREKSLVAQLAAQLELQH ALKKEALRAGKREKSLVAQLAAQLELQH ALKKEALRAGKRESLVAQLAAQLELGLY SSSEGIFVSKIVDSGPAKEGGLQHDRIIEVN GROLSRATHDQAVEAFKTAKEPIVVQVLRR PRTKMFTPFSESQLVDTGTQTDITFHIMALT KMSSSPPVLDPYLLPELHPSAHETYDPNDY GDHQEMDREELELEEVDLYRMNSQDKLGL VCYRTDDEDDIGIYTSEIDPNISAAKDGRIEG DRIIQNGIEVQNREEAVALLTSEENKNFSLL ARAELQLDEGWMDDDRNDFLDDLHMDML ALRAGLQLDEGWMDDDRNDFLDDLHMDML ALRAGLQLDEGWMDDDRNDFLDDLHMDML ARAELQLDEGWMDDDRNDFLDDLHMDML ARAELQLDEGWMDDDRNDFLDDLHMDML ARAELQLDEGWMDDDRNDFLDDLHMDML SINGHEKDSGVGRTDESTRNDESSEQENNG DDATASSNPLAGGRKLTCSQDTLGSGDLPF NESFISADCTDADYLGIPVDECERFRELLEIK CQVKSATTYGLYYTSGPLDAGKSDPESVDK LELLNEELRSELECLSIVRAHKMQQLKEQY FENDRA HANGERSTANTSINDVRHELSDITTELP	-	· · ·	1		1		EWEVEREOISTRELGOGSEGMVYEGLARGLE
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GDI.KSHLRSI.RPEAENNFOL.PQPALGEMIQNA AGEIADGMAYI.AANKFVIRDI.AARNCMVSK DFTVKIGDFGMTRDVYETDYYRKGGKGI.LP VRWMAPESI.KDGIIFTHISDWSSGVVLWEIN TLAGPYVGGLSNEQVI.KFVMDGGVI.EELEGG PL.QLQELMSRCWQPNPRLRSFTHILDSIQEIE RPSFRILISFYYSPECRGARGSLPTTDAEPDSSI TPRDCSSPONGGPGH LAWIDNILPEKEKKETDKKRKRKKGAHEDCI EEPQFPPSVIKIPMESVQSDPQNGIHCIARKR SSSWSYSI.  724 2074 A 5704 4235 940 ARGRESPVWAASWGGRGFPAARRFRGI.A ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQEGSCPARCRGI LSAKELNHVLPLKRLILKLDIKCAYATRGCGI VVKLQQLPEHLERCDFAPARCRHAGCGGVI. RRDVEAHMRDACDARPVGRCQEGCGLPLTH GEQRAGGHCCARALRAHNGALQARLGAHT ALKYGKKFTEYSARLDSLSRCVAAPPGGKGI ETKSLTLVLHRDSSLGFNIGGRSVDNHDK SSSEGIFVSKIVDSGPAAKEGGLQHIDRIIEVN GRDLSRATHDQAVEAFKTAKEPIVVQVLRR. PRTKMFTPPSESQLVDTGTQTDITFEHIMALT KMSSPSPPVLDPYLLPEEHPSAHEYYDPNDY GDIHQEMDREELELEEVDLYRMNSQDKLGL VCYRTDDEDDIGIYISEIDPNSIAAKDGRIREC DRIIQINGIGIEVQNREEAVALLTSEENKNFSLLI ARAELQLDEGWMDDDRNDFLDDLHMDML. LSNQHEEXDSGVGRIDESTRNDESSEQENIG DDATASSNPLAGGRRLTCSQDTLGSGDLPFS NESFISADCTDADYLGIPVDECERFRELLELK CQVKSATPYGLYYPSGPLDAGKSDPESVDK LELLNEELRSIELECLSIVRAHKMQQLKEDITELP							VARKCHHVVRLLGVVSOGOPTLVIMELMIK
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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Agneric Acid F=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		E=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		į .	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uchee	İ	1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
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	l	1	1			CINSCTSMFAGFVIFSIVGFMAHVTKRSIADV
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						LLMLGIDSQFCTVEGFITALVDEYPRLLRNRR
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	1		1			ASGMSLLFLVFFECVSISWFYGVNRFYDNIQE
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	1		}		}	LATE TMGNYVEPKWGOGVGWLMALSSMVL
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726	2076	Α	5711	156	423	PONTFLGTIIRKFEGONKKFILANARVONCAII
	1		1			YCNDGFCEMTGFSRPDVMQKPCTCD
	ì	1	1			HASEYFFKLCSFQVFLSFPLATIVIDVGLVVIP
727	2077	A	5716	3	274	LVKSPNVHYVYVLLLVLSGLLFYIPLIHFKIRL
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Į.	l					AWFEKMTCYLQLLFNICLPDVSEE
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[						ALQNVQARIRMVLAYLFAQLSLWSRGVHGG
				1		LLVLGSANVDESLLGYLTKYDCSSADINPIGO
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		1		[		ISKIDLKAF VQFCIQKFQLFALQSIDLAI ATAL
1	1					LEPLADGQVSQTDEEDMGMTYAELSVYGKL
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1		1				KVKRFFSKYSMNRHKMTTLTPAYHAENYSP
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[		Į.				AEPOSLDGVD
		1			1.076	DGCAARI SRARAPGPGAAGAGRKRLADPGP
729	2079	A	5741	1	5976	PASRRLRAPGSRPRLAPCTRRAAQPAHARMA
		1	1			PRAAGGAPLSARAAAASPPPFQTPPRCPVPLI
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		-				LLLLLUAAKAUALEIQKKFFSFFFFFINNFALDO
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1						PVPDSPLCHAPQLPQASCEHPRRLTDNYNKII
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	İ	1		- 1		AVREPPAAPPAEPVTVFPSMLNVAANHPNAS
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	ļ	1				PRNRSLEDHRFENTPEIAIRSLDTRGDLAKLF

NO. of model	airo ID	CCO ID	Nat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,							
in cucleotide could peptide could provided the country of the coun	SEQ ID	SEQ ID	Met	1 ~			D=Aspartic Acid, E=Glutamic Acid,							
Tiss Notes of the corresponding of the correspondin			noa				F=Phenylalanine, G=Glycine, H=Histidine,							
outce of the control		,	}	1	i .		I=Isoleucine K=I vsine I.=Leucine							
914 agino and nce petide sequence peti	cotide	seq-		1			A-Mathionine N-Asparagine P=Proline							
amino acid residue of peptide requence propried sequence of peptide sequence peptide sequen	seq-	uence		1			M=Methodine, N=Asparagne, r= rioline,							
aminio acid residue of peptide sequence	-	1		914	ng to first		Q=Glutamine, K=Arginine, S=Serine,							
Peptide sequence    Poptide   Poptide   Including insertion			1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,							
nucleotide insertion  FDLNFSDDNILKIRQGAKEQHKLGFVSAFLIP  SDPPFGAQSYAYLALNSEARAGDKESQARSL LARICLPHGAGGDAKKLTESYIQLGQCAGG AGRGDLYSRLVSYFPARERLFAVFERPQGSPA ARAPAALCAPREADWAAIRAARTACFVEP APDVVAVLDSVVQGTGPACERKLNIQLQPEG LDCGAAHQHHSLIQPLATTVYRAFGGTSV AVASVNNYTAYEGFVHMVQEPDADSYLY LMTSHQMARVKVAACNYHSTCGDCVGAAD AYCGWCALETRCTLQODCTNSQQOHFWTSA SEGPSRCPAMTVLPSEDVRQEYFGMILQIGSS LPSLSGMEMACDVGNIRITVARVPDADSYLY LMTSHQMARVKVAACNYHSTCGDCVGAAD AYCGWCALETRCTLQODCTNSQQOHFWTSA SEGPSRCPAMTVLPSEDVRQEYFGMILQIGSS LPSLSGMEMACDVGNIRITVARVPGAFGHG LAYCHLPRDQFPFFPNQDHYTVEMSVRVN GRNIVKANFTTUDEGSTQAVYHTACTSCLSA QWPCFWCSQQISCVSNQSRCEASFNFTSPQD CYRTLLSPLAPVPTGGSQNILVLANSVVRCDQVVLH TYRKSQVFPLSLQLKGPARFLDSPFPMTVM VYNCAMGSPDCSQCLGREDLGHLCMWSDGC RRGPLOPMAGTCPAPERALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG LLTIRGRNLGRRLSDVAHGWWIGGVACEPLP DRYTVSEHVCVTGAPERPALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG LLTIRGRNLGRRLSDVAHGWWIGGVACEPLP DRYTVSEHVCVTGAPFGRAFGAGFGNISTLTVAHSKE GSSRDRFSYVLPLVSISLEPTMGPKAGGTRTIT HGNDLLGVSLGQVALVADIOPETELMRITDTSI ACTMPEGALPAPVPCVVEFERRGCVHGNLTT WYMONSMAVHHGREPTLCKVLNSTLTICPSI GALSNASAPVDFFRINGRAYADEVAVAEELLD PEEAGRGSRFRLDYLPFPGFSTARREWIKH HGEPLTLVHVSTKGAGAKEQDISLGUSHEY RVKIGQVSCDIQIVSDRIHCSVNFSLGAVAGC LDTITOVGFNROTIATLQLGGSTATIAVISVICSS LLLLSVVALFVFCTKSRRAERYWQKTLLQMB EMSSQIREBRKGFAGAGGGDDLTGKLINSVINCSS LLLLSVVALFVFCTKSRRAERYWQKTLLQMB EMSSQIREBRKGFAGAGGTDLTGKLINSVINCSS LLLLSVVALFVFCTKSRRAERYWQKTLLQMB EMSSQIREBRKGFAGAGGDDLTGKLINSVINCSS LLLLSVVALFVFCTKSRRAERYWGKTLLQNGTKSCGDATAG RSLSLLTALHAGKAGKEQDISLTGKLINSVINCSS LLLLSVVALFVFTKSRFAERYWGKTLDLDTSV VEDGRKKLNTLAHYKPTGASLAMBLLDKND NTLGRWCDLDTENYFHLVLTPTELLEPKCHSTLYVSICAS GPFLEYKHFVTRTFFPKCSSLYERRYVLSKNTSGGGG MDSLSVRAMDTDTILTOVKEKLLERACKNYPY SQWPRAEDVDLEWFASSTGSVILRDLDDTSV VEDGRKKLNTLAHYKPTGASLAMBLLDKND NTLGRWCDLDTENYFHLVLTSTGTLGCGCC MASILSVRAMDTOTTLYVEKELBEARCKNTPY SQWPRAEDVDLEWFASSTGSVILRDLDDTSV VEDGRKKLNTLAHYKPTGASLAMBLLDKND NTLGRWCDLDTENYFHLVLTTFTPLECSCLAFCRHED KARPYNALKRYPEGASLAMBLLOKND NTLGRWCDLDTENYFHLVLTTPTDELAEPKASH RYPRQMAALEA		(	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,							
nucleotide insertion  FDLNFSDDNILKIRQGAKEQHKLGFVSAFLIP  SDPPFGAQSYAYLALNSEARAGDKESQARSL LARICLPHGAGGDAKKLTESYIQLGQCAGG AGRGDLYSRLVSYFPARERLFAVFERPQGSPA ARAPAALCAPREADWAAIRAARTACFVEP APDVVAVLDSVVQGTGPACERKLNIQLQPEG LDCGAAHQHHSLIQPLATTVYRAFGGTSV AVASVNNYTAYEGFVHMVQEPDADSYLY LMTSHQMARVKVAACNYHSTCGDCVGAAD AYCGWCALETRCTLQODCTNSQQOHFWTSA SEGPSRCPAMTVLPSEDVRQEYFGMILQIGSS LPSLSGMEMACDVGNIRITVARVPDADSYLY LMTSHQMARVKVAACNYHSTCGDCVGAAD AYCGWCALETRCTLQODCTNSQQOHFWTSA SEGPSRCPAMTVLPSEDVRQEYFGMILQIGSS LPSLSGMEMACDVGNIRITVARVPGAFGHG LAYCHLPRDQFPFFPNQDHYTVEMSVRVN GRNIVKANFTTUDEGSTQAVYHTACTSCLSA QWPCFWCSQQISCVSNQSRCEASFNFTSPQD CYRTLLSPLAPVPTGGSQNILVLANSVVRCDQVVLH TYRKSQVFPLSLQLKGPARFLDSPFPMTVM VYNCAMGSPDCSQCLGREDLGHLCMWSDGC RRGPLOPMAGTCPAPERALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG LLTIRGRNLGRRLSDVAHGWWIGGVACEPLP DRYTVSEHVCVTGAPERPALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG RRGPLOPMAGTCPAPERALEPLSQCDGG LLTIRGRNLGRRLSDVAHGWWIGGVACEPLP DRYTVSEHVCVTGAPFGRAFGAGFGNISTLTVAHSKE GSSRDRFSYVLPLVSISLEPTMGPKAGGTRTIT HGNDLLGVSLGQVALVADIOPETELMRITDTSI ACTMPEGALPAPVPCVVEFERRGCVHGNLTT WYMONSMAVHHGREPTLCKVLNSTLTICPSI GALSNASAPVDFFRINGRAYADEVAVAEELLD PEEAGRGSRFRLDYLPFPGFSTARREWIKH HGEPLTLVHVSTKGAGAKEQDISLGUSHEY RVKIGQVSCDIQIVSDRIHCSVNFSLGAVAGC LDTITOVGFNROTIATLQLGGSTATIAVISVICSS LLLLSVVALFVFCTKSRRAERYWQKTLLQMB EMSSQIREBRKGFAGAGGGDDLTGKLINSVINCSS LLLLSVVALFVFCTKSRRAERYWQKTLLQMB EMSSQIREBRKGFAGAGGTDLTGKLINSVINCSS LLLLSVVALFVFCTKSRRAERYWQKTLLQMB EMSSQIREBRKGFAGAGGDDLTGKLINSVINCSS LLLLSVVALFVFCTKSRRAERYWGKTLLQNGTKSCGDATAG RSLSLLTALHAGKAGKEQDISLTGKLINSVINCSS LLLLSVVALFVFTKSRFAERYWGKTLDLDTSV VEDGRKKLNTLAHYKPTGASLAMBLLDKND NTLGRWCDLDTENYFHLVLTPTELLEPKCHSTLYVSICAS GPFLEYKHFVTRTFFPKCSSLYERRYVLSKNTSGGGG MDSLSVRAMDTDTILTOVKEKLLERACKNYPY SQWPRAEDVDLEWFASSTGSVILRDLDDTSV VEDGRKKLNTLAHYKPTGASLAMBLLDKND NTLGRWCDLDTENYFHLVLTSTGTLGCGCC MASILSVRAMDTOTTLYVEKELBEARCKNTPY SQWPRAEDVDLEWFASSTGSVILRDLDDTSV VEDGRKKLNTLAHYKPTGASLAMBLLDKND NTLGRWCDLDTENYFHLVLTTFTPLECSCLAFCRHED KARPYNALKRYPEGASLAMBLLOKND NTLGRWCDLDTENYFHLVLTTPTDELAEPKASH RYPRQMAALEA						,	/=possible nucleotide deletion, \=possible							
FDLNPSDDNILKIKGGAKEOHKLOFVSAFILIP SPPPGAGSYAYLALNSEARAGDKSQARSI LARICLPHGAGGDAKKLTESYIQLGLQCAGG AGRGDLYSRI VSVPRARERI FAVERPGOSPA ARAAPALCAFRADVRAARRAARTACFVEP APDVVAVLDSVVGGTOPACERKINIQLOFEG LDCGAAHLQHRISLIQPLATPVFRAPGLTSV AVASVAVLDSVVGTOPACREKINIGLOFEG LDCGAAHLQHRISLIQPLATPVFRAPGLTSV AVASVAVLDSVVGTOPACREKINIGLOFEG LDCGAAHLQHRISLIQPLATPVFRAPGLTSV AVASVAVLDSVVGTOPACREKINICOPEG LDCGAAHLQHRISLIQPLATPVFRAPGLTSV AVASVAVLDSVVGTOPACREKINICOPEG LDCGAAHLQHRISLIQPLATPVFRAPGLTSV AVASVANCTAMICOPEGCAGAA ATCGGCALETRCTLQODCTNSSQOHFWTSA SEGFSRCPAMTVLPSEDVROEPFRAGCVGAA ATCGGCALETRCTLQODCTNSSQOHFWTSA SEGFSRCPAMTVLPSEDVROEPFRAGCVGAA ATCGGCALETRCTLQODCTNSSQOHFWTSA SEGFSRCPAMTVLPARVPFRAGSVAN GRNIVKANFTDVCSRTAQVPHACTSCLS ACCOUNTY THA CITICAT GRNIPACT ARE ACCOUNTY THA CITICAT GRNIVKANFTDVCSRTAQVPHACTSCLOVER ATCGCCACCA ALECSGOLEFFRA VAMPESVYRCEQOVLH TTRKSQVFPLSQUK, GEPARELDSFEPNTIVM VYNCAMGSPOESQCLGREDLGHLGMWSDGG ALECSGOLEFFRA VAMPESVYRCEQOVLH TTRKSQVFPLSQUK, GEPARELDSFEPNTIVM VYNCAMGSPOESQCLGREDLGHLGMWSDGG ALECSGOLEFFRA VAMPESVYRCEQOVLH TTRKSQVFPLSQUK, GEPARELDSFEPNTIVM VYNCAMGSPOESQCLGREDLGHLGMWSDGG ALECSGOLEFFRA VAMPESVYRCEQOVLH TTRKSQVFPLSQUK, GEPARELDSFEPNTIVM VYNCAMGSPOESQCLGREDLGHLGMWSDGG ALECSGOLEFFRA VAMPESVYRCHGOVLCFPL DRYTYSEEIVCYTGPAGPLSCVCHGNLTF VYNCAMGSPOESQCLGREDLGHLGMWSDGG ALECSGOLEFFRA VAMPESVYRCHGONLTCHS GRSRDFSTYLLVHSLEPTMGFKAGGTRITT HGNDLFVGSQCLGVCHGNLTTAGERFF MYNGNYSMAVHHGREPTLCXVLNTLTGCSS GRSRDFSTYLLHUMSTLTCTSS GRSRDFSTYLLHUMSTLTGCSS GRSRDFSTYLLHUMSTLTGCSS GRSRDFSTYLLHUMSTLTGCSS GRSRDFSTYLLHUMSTLTGCSS GRSRDFSTRAGSVCGGCTTTAGGERFT MYNGNYSMAVHHGREPTLCXVLNTLTGCSS GRSRDFSTRAGTLTAGGERFF MYNGNYSMAVHHGREPTLCXVLNTLTGCSS GRSRDFTTAGGTAAAGEVANCE ANAMALLAGERFTAGATAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAG		1	1	ĺ										
SIPPPGAQSYAYIALINSEARAGDKESQARSL LARICLPHOAGGDBAKKITESYIQLOCAGG AGGBLYSRLYSYFPAERIFAYFERPOGSPA ARAPAALCAPRADWAAITASHTACFYEP APDVVAVI.DSVVQGTGPACERKINDLOPEG LDCGAAH.QHEISLIQPILATPYFRAFGITSY AVASVANNYAYFIGTYNCRILKININESMQ VYSRRYVTAVAGEPYHMVQGPDADSYLY LMTSHQMARYKVAACNYHSTCGDCVGAAD AYCGWCALETRCTI-QODCTNSSQOFFWTSA SGGPSRCPAMTVLPSEDVROEYPGMILQISGS LPSISGMEMACDYSNIBETVARVPGAPGHG IAYCALLERCTI-QODCTNSSQOFFWTSA SGGPSRCPAMTVLPSEDVROEYPGMILQISGS LPSISGMEMACDYSNIBETVARVPGAPGHG IAYCALLERCTI-QODCTNSSQOFFWTSA SGGPSRCPAMTVLPSEDVROEYPGMILQISGS LPSISGMEMACDYSNIBETVARVPGAPGHG IAYCALLSPLAPYPTGGSQNILVPLANTAFFQQ CPRTILSPLAPYPTGGSQNILVPLANTAFFQQ AALECSGALEFIERAWNSSVXCHOQVVLH TTRKSQVFPLSQLKGGRAFHIDSPEMTVVM VYNCAMGSPCSQCGREDLGHLGMWSDG RIRGPLQPMAGTCPAPEIRALEPLSGPLDGVT TTRKSQVFPLSQLKGGRAFHIDSPEMTVM VYNCAMGSPCSQCGAREDLGHLGMWSDG RIRGPLQPMAGTCPAPEIRALEPLSGPLDGVT BORTYSEERIVCVTGPAGPLSGVYTVNASKE GKSRDRFSYVLLVISLEPTMGPKAGGGRITI HGNDLHVGSELQVLVNDITIPCTELMRIDTSI ACTMPEGALPAPVPCVEFERRGCVGGRIF WYMQNPVTAISPRRSSVSGGRITTVAGERFH WYMGNPTHYTYTGCSCLAPERCWIGHLT HOPPOTATION TO WEEKEN WYMGNPTHYTYTGCSCLAPERCWIGHLT HOPPOTATION TO WEEKEN GREENERGERGFAGGRITTGATT WYMGNPTHOAUTHOATT RAGGRITTATATOATT RAGGRITTATATATATATATATATATATATATATATATATATAT		Ļ <u>.</u>	<del> </del>		sequence									
LARICLPHIGAGGDAKKLTESYIQLGIQCAGG AGRGDLYSRLVSVPPAREBLFAVPERPQOSPA ARAAPAALCARRFADVRAARRARTACTVEPP APDVVAVLDSVVQGGGACERKINIQUPEQ LDGGAAHLQHPLSLQPLKATTVFRAPGLTSV AVASVNNYTAVLGTVNGGLLKINESMQ VVSRRVVTVAYGEPVHHVMQFDPADSGYLY LMTSHQMARVXAACKVHSTGCOVGAAD AYCGWCALETRCTLQQDCTNSSQQHFWTSA SEOPRCPAMTVLPSEIDVRQCPVGMLQISGS LPSLSGMEMACDYGNIRTVARVPGPAGIGIG LAYCALLETRCTLQQDCTNSSQQHFWTSA SEOPRCPAMTVLPSEIDVRQCPVGMLQISGS LPSLSGMEMACDYGNIRTVARVPGPAGIGIG LAYCALLETROCPPPPPNQDHVTVEMSVRVN GRAIVXANFTTYDCSSTAQVYPHTACTSCLSA QWPCFWCSQQHGCVSNGNGRCENGVBVGNAV AYCGWCALETRCTLOQDCTNSSQQHFWTSA SEOPRCPAMTVJCSSTAQVYPHTACTSCLSA QWPCFWCSQQHGCVSNGNGRCENQOVLH TTKLSQVPPLSLQLKGRARFLDSPEPMTVM VYNCAMGSPDCSCQLGREDLGLMSWDGG ALLESGGLEEFERAVWNESVCQOVLH TTRKSQVPPLSLQLKGRARFLDSPEPMTVM VYNCAMGSPDCSQCLGREDLGLMSWDGG ALLESGGLEEFERAVWNESVCQOVLH TTRKSQVPPLSLQLKGRARFLDSPEPMTVM VYNCAMGSPDCSQCLGREDLGLMSWDGG ALLESGGLEEFERAVWNESVCQOVLH TTRKSQVPPLSLQLKGRARFLDSPEPMTVM VYNCAMGSPDCSQCLGREDLGLMSWDGG ALLESGGLEEFERAVWNESVCGOVLH TTRKSQVPPLSLQLKGRARFLDSPEPMTVM VYNCAMGSPDSQCLGREDLGLMSWDGGV RLRQPLAYDVCVPREFAGGGRITTYAGERFF MYQNNSMAVHHGGREPTLCXVLTSUTGGVACHGNLTF AVTMQNPVTTAISPRSSPVGGRTTTVAGERFF MYQNNSMAVHHGGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLTGFSS GRAVTLNEHGREPTLCXVLTSLMSELLDVDLD ASAAKNFRLMLRTESVCKRALLDVDMS CKSCAACHTHLLGCKCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		}	1	1	İ	İ	SDDDDC AOSVAVI AI NSEAR AGDKESOARSI.							
AGROBLYSKI-VSEPARERITAVFERPOGEN  ARAPAALCARFADVRAARRARTACTVEP APDVVAVLDSVVQGTGPACERKLINQLOPE APDVVAVLDSVVQGTGPACERKLINQLOPE LDGGAHLOPPLSLQPLKATPVFRAPGLTSV AVASVNINYTAVELGTVNGRLLKININENS VVSRRVTTAVFLGTVNGRLLKININENS VVSRRVTTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS AVASVNINYTAVFLGTVNGRLLKININENS LPSLSGMEMACDYGNHIVTVASQOPHWTSA SECPRECRAMTYLPSEDVRQFYPGMILDING AVACCESTALOPTONSOOPHWTSA SECPRECRAMTYLPSEDVRQFYPGMILDING AVACCESTALOPTONSOOPHWTSA SECPRECRAMTYLPSEDVRQFYPGMILDING AVACCESTALOPTONSOOPHWTSA SECPRECRAMTYLPSEDVRQFYPGMILDING AVACCESTALOPTONSOOPHWTSA GRINDLAPVFGGSCASPAPTSPOOD CPRTLLSFLAPVFTGGSGNTATAFFOC AVACCESTALOPTONSOOPHWTSA GRINDLAPVFGGSCASPAPTSPOOD CPRTLLSFLAPVFTGGSGNTATAFFOC ALECSFGLEEFERAVWNESVVRCDQVVLH TTRKSQVFPLSQLKGRARAFLDSPEPATVH VYNCAMGSPLOSCOLGREDLGHLCMWSDG RLRGPLQPMAGTCAPAFRALERISGPLOGGT LLTIRGRNLGRRLSDVAHOVWTGGVACEPLP DRYTVSEEHVCVTGPAPGPLSGVVTVNASKE GKSRDHSSVVLPVHSLERTMGGVACEPLP DRYTVSEEHVCVTGPAPGPLSGVVTVNASKE GKSRDHSSVVLPVHSLERTMGGVACEPLP DRYTVSEEHVCVTGPAPGPLSGVVTVNASKE GKSRDHSSVVLPVHSLERTMGGGTATITVAGERH MVQNYSMAVHIGGREPTLCKVLNSTLITGPSI GKSRDHSSVVLPVHSLERTMGGGTATITVAGERH MVQNYSMAVHIGGREPTLCKVLNSTLITGPSI GALSNASAPVDEFTNGRAYADEVAVAEELUL DPEAGAGSRFRLDVLPROPGSTAKREKWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLVHIVSTRGAGKEQDSLGLQSHEWIKH HPGEPLTLUHINGGRETLCKVTNSTLITGPSS GKSGSGAQETHPLLGGWKIPSCRPNAV KKIQQVSCDIQUSDRHICSVTPLUSCH KKITTATATATICAPCH KKITTATATATICAPCH KKITTATATATICAPCH KKITTATATATATATATATATATATATATATATATATATA			1				A DICE DICE A CODA VVI TESVIOL GLOCAGO							
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MNAHLAEESRKYQNEFNTNVAMAEIYKYAK RYRPQIMAALEANPTARRTQLQHKFEQVVAL MEDNIYECYSEA  730 2080 A 5744 3 292 QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ VANGKGNQRNMGSPQPSLLAFERNLELQIMO LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD  731 2081 A 5747 1 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC		1	1	1	1		KI I VAKEIDEVRKIVORVYKOIODMTPL SEOF							
RYRPQIMAALEANPTARRTQLQHKFEQVVAL MEDNIYECYSEA  730 2080 A 5744 3 292 QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ VANGKGNQRNMGSPQPSLLAFERNLELQIMO LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD  731 2081 A 5747 1 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC							ANIALI AEEGRKVONEENTNVAMAFIYKVAK							
730 2080 A 5744 3 292 QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ VANGKGNQRNMGSPQPSLLAFERNLELQIMO LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD  730 2081 A 5747 1 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC							MINATE AREA DE LA DESCRIPTA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA  5747 1 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC	1		1			1	
VANGKGNQRNMGSPQPSLLAFERNLELQIMO LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD  733 2081 A 5747 1 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC	1		1		1	1	MEDNIYECYSEA							
VANGKGNQRNMGSPQPSLLAFERNLELQIMO LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD  731 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC	730	2080	A	5744	3	292	QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ							
LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD  382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC	1,30	2000	1	- / · ·	-		VANGKGNORNMGSPOPSLLAFERNLELQIMG							
LKD  182 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC	1	1	1	1 .			LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT							
723 2081 A 5747 1 382 FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC	[	1		1										
731   2081   A   5747   1   382				+	<del></del>	1297	FLKCMRK AFRSSKI LOVGYTPDGKDDYRWC							
TO THE TRANSPORT OF THE PROPERTY OF THE PROPER	731	2081	A	5747	1	382	FRVDEVNWTTWNTNVGIINEDPGNCEGVKRT							

	OFO ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
IO: of	peptide	liou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-		1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutarnine, R=Arginine, S=Serine,
ence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ		peptide	Sequence	/=possible nucleotide deletion, \=possible
	İ	Į	l			nucleotide insertion
	_		<u> </u>	sequence	<del> </del>	I SESI RSSRVSGRHWKNFALVPLLREASARD
		T	1	}		RQSAQPEEVYLRQFSGSLKPEDAEVFKSPAAS
	1	1		ł	1	GEK
	1	1	1		<u> </u>	AQAESSTVASPEATAGPLCTRIPNVPPPTPIRP
732	2082	A	5753	198	3	PGKLQAQLPCPSPVRFTSARIPPASRPQTKS
		1	Į		<u> </u>	AAGPPGLEAEGRAPESAGPGPGGDAAETPGL
733	2083	A	5754	2	2223	AAGPPGLEAEGRAPESAGPGFGGDATETT GE
133	2003	1	1	1	1	PPAHSGTLMMAFRDVTVQIANQNISVSSTAL
	1		ļ	1		SVANCLGAQTVQAPAEPAAGKAEQGETSGR
	1		1	ì		EAPEAPAVGREDASAEDSCAEAGASGAADG
	1		1	}	Ì	ATAPKTEEEEEEETAEVGRGAEAEAGDLEQ
		1	ļ	ļ		LNRTSTSTKSAKSGSEASASASKDALQAMILS
		1			l .	LPRYHCENPASCKSPTLSTDTLRKRLYRIGLN
		· I		1		I ENTENDED & GIOFLISR GFIPD TPIGVAHFLL QKK
	1	ľ			ì	GL SROMIGEFLGNSKKOFNRDVLDCVVDEM
	ł	1	i	1		DESSMEI DEALRKFOAHIRVOGEAQKVERLIE
	1		1			A ESOR Y CMCNPEVVOOFHNPDTIFILAFAILLL
	Ì	Į.	İ			NITOMYSPNIKPDRKMMLEDFIRNLRGVDDG
	1			}		ADIPREL VVGIYERIOOKELKSNEDHVTYVTK
	i		1		j	VEK STUGMKTVLSVPHRRLVCCSRLFEVTDV
	1	1	[	1	1	NKLQKQAAHQREVFLFNDLLVILKLCPKKKS
			1	Ì		SSTYTFCKSVGLLGMQFQLFENEYYSHGITLV
	1	İ	-	ļ		TPLSGSEKKQVLHFCALGSDEMQKFVEDLKE
	1		1	1	ļ	SIAEVTELEQIRIEWELEKQQGTKTLSFKPCGA
	l	1	)	}	}	QGDPQSKQGSPTAKREAALRERPAESTVEVS
	1	ļ.		-		QGDPQSKQGSPTARREALIG ALST VERY HNRLQTSQHNSGLGAERGAPVPPPDLQPSPPF
	ł	l		1	Ì	HNRLQ1SQHNSGLGAERGAI VIII DEQIBITA
	ì	1	Ţ	1		QQTPPLPPPPPTPPGTLVQCQQIVKVIVLDKPC
	1		1			LARMEPLLSQALSCYTSSSSDSCGSTPLGGPG
					1	SPVKVTHQPPLPPPPPPYNHPHQFCPPGSLLH
	1	1				GHRYSSGSRSLV
	2004	HA	5788	8	362	SSVMGDLVGQGLEEQIVARDENSWLIDGGTF
734	2084	A	3788	١		IDDVMRVLDIDEFPQSGNYETIGGFMMFMLR
	l	ļ	ŀ			KIPKRTDSVKFAGYKFEVVDIDNYRIDQLLV
	j	1	[	1		PIDSKATALSPKLPDAKDKEESVA
_	<u> </u>			<del></del>	1257	MVESAVITAFHTGTSNTTFVVYENTYMNILL
735	2085	A	5827	1	1237	PPPEOHPDLSPLLRYSFETMAPTGLSSLTVNS
			İ			AVETTEAAFKSLNLPLOITLSAIMIFILFVSFLC
	l l		j			NLVVCLMVYQKAAMRSAINILLASLAFADM
	[		1			LLAVLNMPFALVTILTTRWIFGKFFCRVSAM
						FWLFVIEGVAILLIISIDRFLIIVQRQDKLNPYR
	Ì	İ				AKVLIAVSWATSFCVAFPLAVGNPDLQIPSR
		1				PQCVFGYTTNPGYQAYVILISLISFFIPFLVILY
				1		SFMGILNTLRHNALRIHSYPEGICLSQASKLG
			-	Į.		SHMGILNI LKHNALKING I FEOICESQASKEO
					1	MGLQRPFQMSIDMGFKTRAFTTILLIFAVFIV
					1	WAPFTTYSLVATFSKHFYYQHNFFEISTWLL
ĺ	1	1	1			WLCYLKSALNPLIYYWRIKKFHDACLDMMF
1	1	- 1		1		KSFKFLPQLPGHTKRRIRPSAVYVCGEHRTV
			5070	3	268	CTPSDFLARHYRTHTGEKRFSCPLCPKQFSK
736	2086	A	5870	1 3	200	DHI TKHARRHPTYHPDMIEYRGRRRTPRIDE
ļ				1		1 TSEVESSASGSGPGPAPSFTTCL
						1 TWPOLELETT PELLHMSRPAEDGPSPGALV
737	2087	A	5871	2	521	RSSSLGYISKAEEYFLLKSRSDLMFEKQSERI
			1	1		GLARRLTTARRPPASSEQAQQELFNELKPAV
			1			DGANFIVNHMRDQNNYNEEKDSWNRVART
						DUANTIVNIMICULARIA INC.
]				1		VDRLCLFVVTPVMVVGTAWIFLQGVYNQPI
						QPFPGDPYSYNVQDKRFI
	0000		5881	- <del> </del> 1	1160	LVVTAITAILAFPNEYTRMSTSELISELFNDC
738	2088	A	2001			I I DSSKI CDYENRFNTSKGGELPDRPAGVG
ţ		1			i	VSAMWOLALTLILKIVITIFTFGMKIPSGLFIP
	1			1		MAVGALAGRLLGVGMEQLAYYHQEWTVFN
						MAVGAIAGRLLGVGMEQLAYYHQEWT

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-A enertic Acid E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	l	ł	ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	<u> </u>	Į.	peptide		nucleotide insertion
	}	ł		sequence		WCSQGADCITPGLYAMVGAAACLGGVTRMT
	<del> </del>		1			VSLVVIMFELTGGLEYIVPLMAAAMTSKWVA
	İ		1			VSLVVIMFELIGGLETIVFLIVAAANTSKW VX
	1	l				DALGREGIYDAHIRLNGYPFLEAKEEFAHKTL
	1	l	İ	1		AMDVMKPRRNDPLLTVLTQDSMTVEDVETII
	ļ	l	1	•	Ì	SETTYSGFPVVVSRESQRLVGFVLRRDLIISIE
	1		1		1	NARKKQDGVVSTSIIYFTEHSPPLPPYTPPTLK
		Ì	}	1	{	I DATE DE SPETVIDE. TPMEIVVDIFKKLULKQU
		Ì	1	1		LVTHNGRLLGIITKKDVLKHIAQMANQDPDSI
		1	1		1	I EN
	Ì	1	J		1016	TI OLA A SVPEFAISLISW WLPESAR WLIINGKP
739	2089	Α	5892	2	916	DOALOFI RKVARINGHKEAKNLTIEVLMSSV
	1	1	]	i	}	KEEVASAKEPRSVLDLFCVPVLRWRSCAMLV
		1		1		VNFSLLISYYGLVFDLQSLGRDIFLLQALFGA
			1			VNFSLLIST IGEVIBEGERTIQAGSQAMAGL
		1	1			AILANMLVPQDLQTLRVVFAVLGKGCFGISL
		1	- (	1		TCLTIYKAELFPTPVRMTADGILHTVGRLGA
	· [		ļ		<b>\</b>	MMGPLILMSRQALPLLPPLLYGVISIASSLVVL
		1				MMGPLILMSRQALPELFFELT GVISIASSEVVE
	İ		İ		1	FFLPETQGLPLPDTIQDLESQKSTAAQGNRQE
	1	1	1			AFTVESTSLLEIVALHGAL
	2000	A	5900	2	426	RPIKTLGIGFHFSVDGVHFLTQREVQNLWKE
740	2090	A	3900	1 ~		NLIILDTAKKHGYEVVDTFTITMGRYKEFLQG
	ı			1		KCGCHFHEVVKSKLSKEYNFIKMKRSRNHIM
	ŀ		1	1	j	GRYFSNQSKLQQGTVTNFRSPYHVRGPINQV
		1	1	1		CSEILLSRMCANKRTM
		<del></del>	- 6010	<del></del>	412	DMPESTI I IICENGYILEAPLPTIKQEEDDHDV
741	2091	Α	5910	3	412	VEVETEDMCIKCEHESSVKSKILRLIEIEKRER
		ł				- LODGE VEVIDEEDRNKI AAFMGEDGEKEFUEE
			1	ŀ	1	EEEKEEEEEEPLPEIFIPSTPSPILCGFYSEPG
						KEWV
						MCCRITCCVVFCLLOAGPLDTAVSQTPKYLV
742	2092	A	5936	1	482	TOMONDKSIKCEONLGHDTMYWYKQDSKK
	)	1		-	1	FLKIMFSYNNKELIINETVPNRFSPKSPDKAHL
		}				NLHINSLELGDSAVYFCASSQDTALQSHCIPV
	1	-	]			HKPPGSARKLQGSVCTCTQGSSLHSLMASDG
Ì		l l	1			HKPPGSAKKLQG5VC1C1QGG5LL1021.2100
	1	- 1	1	1	l	VPVC CONCRETE STATE OF THE ACRES
747	2093	A	5938	1	1566	MNSFFGTPAASWCLLESDVSSAPDKEAGRER
743	2093	^	3,55	1 -		RALSVQQRGGPAWSGSLEWSRQSAGDRRRL
ļ		1		1		GLSRQTAKSSWSRSRDRTCCCRRAWWILVPA
1		1				ADR ARRERFIMNEK WDTNSSEN WHIPI WN YN
}		ŀ	ì	1	1	DIKHHI YSDINTTYVNYYLHQPQVAAIFIIS I
ļ			1		l	I JEEL CMMGNTVVCFIVMRNKHMHTVTNLFI
l					1	LATEATS DE L'AGRECMPITLLDNILAGWPFGNIN
1				}	}	CVISCI VOGISVAASVETLVAIAVDREQCVV)
			{			DEKPKI TIKTAFVIIMIIWVLAITIMSPSAVMLI
1			Į		1	VOEEKAARTNISONKTSPVYWCKEDWPNO
1				1		EMRKIYTTVLFANIYLAPLSLIVIMYGRIGISL
}	-					RAAVPHTGRKNQEQWHVVSRKKQKIIKMLL
]					1	VALLFILSWLPLWTLMMLSDYADLSPNELQI
ł	İ			[		NIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRO
						NIVIPPEAHWLAFUNSSVIPHTIOFFIAENTRO
1		1	l	1		FQEAFQLQLCQKRAKPMEAYALKAKSHVLII
1			ĺ			TSNQLVQESTFQNPHGETLLYRKSAEKPQQE
						I VMEELKETTNSSEL
			- + 6000	149	327	SHVCVSHYAGSSGCPAGAGAGAVALGISAV
744	2094	A	5966	149	321	1 VDVOGGRLGVARGAWYMEAPDIRQGUM
		[			0.57	CAPHTDWAWAPTPMSGLGSGRGRQGTLAS
745	2095	A	5970	413	856	DI CI DI LI AGVTGILATELEDOMARPAACMV
1			ļ			CGALMWIMLILVGLGFPFIMEALSHFLYVPFI
1						GVCVCGAIYTGLFLPETKGKTFQEISKELHRI
	1	1	1		1	GVCVCGALLIGETERGELIGETER
		1		1		NFPRRAQGPTWRSLEVIQSTEL

	650 ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-		ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	neuce	[	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		]		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
		Ì	1	sequence	}	nucleotide insertion
		<del> </del>	6071	3	1343	AOTARRIGLELDTEGHRLFVAFSGCIVYLPLS
746	2096	Α	5971	3	1343	RCARHGACORSCLASODPYCGWHSSRGCVDI
		ļ			1	RGSGGTDVDOAGNOESMEHGDCQDGATGSQ
			1		1	SGPGDSAYGVRRDLPPASASRSVPIPLLLASV
						AAAFALGASVSGLLVSCACRRAHRRRGKDIE
			}			TPGLPRPLSLRSLARLHGGGPEPPPPSKDGDA
		1				VQTPQLYTTFLPPPEGVPPPELACLPTPESTPE
	[		ļ		1	LPVKHLRAAGDPWEWNQNRNNAKEGPGRSR
	1	1	}			GGHAAGGPAPRVLVRPPPPGCPGQAVEVTTL
		1				EELLRYLHGPQPPRKGAEPPAPLTSRALPPEP
						APALLGGPSPRPHECASPLRLDVPPEGRCASA
		1	ļ		}	PARPALSAPAPRLGVGGGRRLPFSGHRAPPAL
	1		i			LTRVPSGGPSRYSGGPGKHLLYLGRPEGYRG
	ł	1	1	1	İ	RALKRYDVEKPQLSLKPPLVGPSSRQAVPNG
	Ì	ļ	Į			
		1		J		GRFNF DHASLPCSWNHRFDVETRHVFIGDHSGQVTI
747	2097	A	5998	2	754	LKLEQENCTLVTTFRGHTGGVTALCWDPVQ
		1				RVLFSGSSDHSVIMWDIGGRKGTAIELQGHN
						DRVQALSYAQHTRQLISCGGDGGIVVWNMD
		1	1			VERQETPEWLDSDSCQKCDQPFFWNFKQMW
	1	1	1		1	DSKKIGLRQHHCRKCGKAVCGKCSSKRSSIPL
			ļ			MGFEFEVRVCDSCHEAITDEERAPTATFHDSK
		1	1			HNIVHVHFDATRGWLLTSGTDKVIKLWDMT
	1	}	i			
		}				PVVS AMVFGGVVPYVPQYRDIRRTQNADGFSTYV
748	2098	A	6001	2	747	CLVLLVANILRILFWFGRRFESPLLWQSAIMIL
' ' ' '		1	1			TMLLMLKLCTEVRVANELNARRRSFTAADS
		ļ	1			TMLLMLKLCIEVKVANELNAKKSI TAADS
		1	ł			KDEEVKVAPRRSFLDFDPHHFWQWSSFSDYV
	1	ł	1		1	QCVLAFTGVAGYITYLSIDSALFVETLGFLAV
		1	ı			LTEAMLGVPQLYRNHRHQSTEGMSIKMVLM
	1				}	WTSGDAFKTAYFLLKGAPLQFSVCGLLQVLV DLAILGQAYAFARHPQKPAPHAVHPTGTKAL
			Ì			DLAILGUAYAFARHPURFAFRA ON TOTRAL
749	2099	A	6002	2	447	GRPDRSELVRMHILEETFAEPSLQATQMKLK
142	2077		1		1	RARLADDLNEKIAQRPGPMELVEKNILPVDSS
	-		l			VKEAIIGVGKEDYPHTQGDFSFDEDSSDALSP
}	1		1			DQPASQESQGSAASPSEPKVSESPSPVTTNTP
	1	-	1			AQFASVSPTVPEFLKTPPTAD
750	2100	A	6004	2	427	LLTQAMLVLPHRPQWFTPGPRLQAQGPCQEC
130	2100	1 '	500.		1	WRWELRLRNYVPEDEDLNKRRVPQAKPDAV
ŀ		1				QEKVKEQLEAAKPEPVIEEVDLAKLAPRKPD
[		1	1	1	1	WDLKRDVAKKLEKLLKRTQRAIAELIRERLK
				1		GQEDSLDSAVDAATEHKTC
700	2101	A	6007	33	1280	TDOAKVDNOPEKLVRSAEDVSTVPTQPDNPF
751	2101	A	0007	55		SHPDKLKRMSKSVPAFLODESDDRETDTASE
		Ì		1		SSYOLSRHKKSPSSLTNLSSSSGMTSLSSVSGS
l		İ	1	1		VMSVVSGDFGNLEVKGNIQFAIEYVESLKEL
[		1	1			HVFVAOCKDLAAADVKKQRSDPYVKAYLLP
J		-	1	1		DKGKMGKKKTLVVKKTLNPVYNEILRYKIER
[	ļ					OILKTOKLNLSIWHRDTFKRNSFLGEVELDLE
1				1		TWDWDNKONKOLRWYPLKRKTAPVALEAE
1		1				NRGEMKLALQYVPEPVPGKKLPTTGEVHIWY
1	l			1		KECLDLPLLRGSHLNSFVKCTILPDTSRKSRQ
1	1					KTRAVGKTTNPIFNHTMVYDGFRPEDLMEAC
			1			VELTVWDHYKLTNQFLGGLRIGFGTGKSYGT
						EVDWMDSTSEEVALWEKMVNSPNTWIEATL
1						
1	į.	1	1	l		PLRMLLIAKISK KEIFSPFELISVKPLCLLLGVTCSQSMAFEELL
}	1			1.00	1283	T K FIFSPELLIS V KPLULLLU V I US QSIMATEELL
752	2102	A	6028	108	1203	THE ST COPPORTED AND THE POST AND THE PARTY OF THE PARTY
752	2102	Α	6028	108	1283	SQVGGLGRFQMLHLVFILPSLMLLIPHILLENI AAAIPGHRCWVHMLDNNTGSGNETGILSEDA

70.10	CEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID NO: of	Met   hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
iO: of	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	ļ	1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ		l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ.	1	1	peptide	5042	/=possible nucleotide deletion, \=possible
		1	ļ	sequence		nucleotide insertion
		<b></b>	<del></del>	Sequence		LLRISIPLDSNLRPEKCRRFVHPQWQLLHLNG
	ļ	1			ì	TILISTSE ADTEPCVDGWVYDOSYFPS11V1KW
	1		1			DLVCDYOSLKSVVQFLLLTGMLVGGIIGGHV
	ì	Ì		1		SDREGRREILRWGLLOLAITDTCAAFAPITPV
		1	i			VCVLRELAGESSMIIISNNSLPITEWIRPNSKAL
	1	ì			Ì	VVII SSGALNIGOIILGGLAYVFRDWQTLHVV
		}	Y			ASVPFFVFFLLSRWLVESARWLIITNKLDEGL
		1				KALRKVARTNGIKNAEETLNIEVVRSTMQEE
		\	ļ			LDAAQTKTTVWDLFRNPSMRKRICILVFLRK
		1				KNLKEKA
	i		Į.		<u> </u>	DSFESILRLIFEIHHSGEKGDIVVFLACEQDIEK
753	2103	A	6043	1	1470	VCETVYQGSNLNPDLGELVVVPLYPKEKCSL
		1	1		1	FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN
	1	1	1	1	1	SVRFVIDVGVERRKVYNPRIRANSLVMQPISQ
	1	1		1	1	SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTT
		1				LKPAEMQEANLTSMVLFMKRIDIAGLGHCDF
						MNRPAPESLMQALEDLDYLAALDNDGNLSE
	İ		1			FGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA
	)	1	- 1	}		AMVTAPNCFSHVPHGAEEAALTCWKTFLHPI
	l		1			GDHFTLISIYKAYQDTTLNSSSEYCVEKWCRI
	l	}	1			YFLNCSALRMADVIRAELLEIIKRIELPYAEPA
	1		ı			FGSKENTLNIKKALLSGYFMQIARDVDGSGN
			ł			YLMLTHKQVAQLHPLSGYSITKKMPEWVLF
	1	1				HKFSISENNYIRITSEISPELFMQLVPQYYFSNI
	1	1	1	1		PPSESKDILQQVVDHLSPVSTMNKEQQMCET
	Ì	1			]	PPSESKUILQQV VDHLSF VSTVIIVILQQIVOZX
	İ	1	•		1	CPETEQRCTLQ YYALHHWPFPDLLCQTTGAIFQMNMYGSCII
754	2104	A	6055	2	394	LMLINVDRYAAIVHPLRLRHLRRPRVARLLC
134	210.	1	1			LGVWALILVFAVPAARVHRPSRCRYRDLEVI
		]	ļ	1		LCFESFSDELWKGRLLPLVLLAEALGFLLPLA
1		}				
	i	1				AVVYSS LGLGSGTLLSVSEYKKKYREHVLQLHARVK
755	2105	A	6059	3	1795	RNARSVKITKRPTKLLIAPESAAPEEALGPAE
133	1 2.02	1 - "				PEPGRARRSDTHTFNRLFRRDEEGRRPLTVV
	ı			1		QGPAGIGKTMAAKKILYDWAAGKLYQGQV
ļ	1	1		-		OGPAGIGKIMAAKKILIDWAAGKEIQOQ
	1	-	į		Ì	FAFFMPCGELLERPGTRSLADLILDQCPDRGA
	1	1		İ		PVPQMLAQPQRLLFILDGADELPALGGPEAA
1	l	İ	1			CTDPFEAASGARVLGGLLSKALLPTALLLVT
	1					RAAAPGRLQGRLCSPQCAEVRGFSDKDKKK
1						YFYKFRDERRAERAYRFVKENETLFALCFV
	1					PFVCWIVCTVLRQQLELGRDLSRTSKTTTSV
					1	TI FITSVLSSAPVADGPRLOGDLRNLCRLAR
			i			GVLGRRAQFAEKELEQLELRGSKVQTLFLSH
1		1	1			KEI POVI ETEVTYOFIDOSFOEFLAALSYLLI
		Ì			1	DGGVPRTAAGGVGTLLRGDAQPHSHLVLTI
1	i	- {				DELEGI I SAERMRDIERHFGCMVSERVKQE
1	- 1	1		1		I RWVOGOGOGCPGVAPEVTEGAKGLEDTE
		1		Ì		PEFFEEGEENYPLELLYCLYETQEDAFYRQ
		1				T CREPELALORVRFCRMDVAVLSYCVRCCP
1						GQALRLISCRLVAAQEKKKKSLGKRLQASL
						GG
					126	SCRPTRPAKPTGOGMGRFMLTLVCQGSIMN
756	2106	A	6060	12	436	ADDI IMNNI TELOPGLEHHLRELEELRLSGN
1		- 1			]	I SHIPGOAFSGLYSLKILMLHNNQLGGIPAQ
1		1	į.	[		LWELPSLQSLRLDANLISLVPERSFEGLSSLR
		1				LWLDDNALTEIPS
1		.				ITPLGLGAADMCAFPWLLLLLLQEGSQRR
757	2107	A	6063	54	419	WRWCGSEEVVAVLQESISLPLEIPPDEEVEN
	1	1		1	i	WKWCGSEE4 AWAFARSTON DERY SEE ABO
		- 1				WSSHKSLATVVPGKEGHPATIMVTNPHYQ

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	иепсе	}	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
			ļ	sequence		QILTMLLRSLQQPSASWPRDCSSSCSW
			1000	106	438	IGISCPATIFVPMFSHSLIGIGEEYQLPYYNMV
758	2108	A	6066	125	430	PSDPSYEDMREVVCVKRLRPIVSNRWNSDEC
	Ì	1				LRAVLKLMSECWAHNPASRLTALRIKKTLAK
		1				MVESODVK!
		<u> </u>	1000	1	650	PGRRERPAALEERAMEKLREKVPFQNRGKGT
759	2109	Α	6072	3	030	I SSIIPNNSDTRKATETTSLSSKPEYVNPDFRW
						SKDPSSKSGNLLETSEVGWTSNPEELDPIRLA
					]	LLGKSGLSCOVGSATSHPVSCQEPIDEDQRISP
	1	1	ł		1	KDKSTAGREFSGOVSHOTTSENQCTPIPSSTV
		1	ļ			HSSVADMONMPAAVHALLTQPSLSAAPFAQ
		Į	ł			RVI GTLPSTGSTTLPOCHAGNATVW
	0110	$\frac{1}{A}$	6077	3	730	PLRLTLMEEVLLLGLKDREGYTSFWNDCISSG
760	2110	^	10077		1	LRGCMLIELPLRGRLQLEACGMRRKSLLTRK
			1			VICKSDAPTGDVLLDEALKHVKETQPPETVQ
		1				NWIELLSGETWNPLKLHYQLRNVRERLAKNL
						VEKGVLTTEKQNFLLFDMTTHPLTNNNIKQR
		1		ļ		LIKKVQEAVLDKWVNDPHRMDRRLLALIYL
				1		AHASDVLENAFAPLLDEQYDLATKRVRQLLD
		ļ				LDPEVECLKANTNEVLWAVVAAFTK
761	2111	+ <u>_</u>	6078	833	390	IVSFHLSGFKKFVRPFSFLSVHGLQVDEYHSV
/61	2111	^	00,0			HQKLSADMADHSNLIRSLLVGAEDARLMRD
					}	MKTMKSRYMELYDLNRDLLNGYKIRWNNH
1		1	Ì			TELLGNLKAVNQAIQRAGRLRVGKPKNQVIT
						ACRDAIRSNNINTLFKIMRVGTASS
762	2112	A	6079	2	2686	KKAITCGEKEKQDLIKSLAMLKDGFRTDRGS
102	2112	1				HSDLWSSSSSLESSSFPLPKQYLDVSSQTDISG
	1	1				SFGINSNNQLAEKVRLRLRYEEAKRRIANLKI
1				ļ	į	QLAKLDSEAWPGVLDSERDRLILINEKEELLK EMRFISPRKWTQGEVEQLEMARKRLEKDLQ
ŀ		1			1	AARDTQSKALTERLKLNSKRNQLVRELEEAT
İ						RQVATLHSQLKSLSSSMQSLSSGSSPGSLTSSR
İ						GSLVASSLDSSTSASFTDLYYDPFEQLDSELQ
ļ						SKVEFLLLEGATGFRPSGCITTIHEDEVAKTQ
1	ļ		İ			KAEGGGRLQALRSLSGTPKSMTSLSPRSSLSS
1	ĺ	1			ĺ	PSPPCSPLMADPLLAGDAFLNSLEFEDPELSA
i					İ	TLCELSLGNSAQERYRLEEPGTEGKQLGQAV
				i	i	NTAQGCGLKVACVSAAVSDESVAGDSGVYE
	1		1			ASVQRLGASEAAAFDSDESEAVGATRIQIALK
			}	}		YDEKNKQFAILIIQLSNLSALLQQQDQKVNIR
		1	1			VAVLPCSESTTCLFRTRPLDASDTLVFNEVFW
1						VSMSYPALHQKTLRVDVCTTDRSHLEECLGG
						AQISLAEVCRSGERSTRWYNLLSYKYLKKQS
1		-		1	1	RELKPYGYMAPASGPASTDAVSALLEQTAVE
}					1	LEKRQEGRSSTQTLEDSWRYEETSENEAVAE
		1			1	EEFEEVEEEGEEDVFTEKASPDMDGYPALK
1		1	1			VDKETNTETPAPSPTVVRPKDRRVGTPSQGPF
		-				LRGSTIIRSKTFSPGPQSQYVCRLNRSDSDSST
1	1	1	1	-		LSKKPPFVRNSLERRSVRMKRPSPPPQPSSVK
1	1					SLRSERLIRTSLDLELDLQATRTWHSQLTQEIS
						VLKELKEQLEQAKSHGEKELPQWLREDERFR
}			1		`	LLLRMLEKRMDRAEHMGELQTDKMMRAAA
						KDVHRLRGQSCKEPPEVQSFREKMAFFTRPR
		1				MNIPALSADDV
	1				<del></del>	PHPIRFSKLCVSFNNQEYNQFCVIEEASKANE
1			(0.00	3	1558	LULIKLOUTCA OLIMIA CATTOLICA TOTALIA
763	2113	A	6082	1 -	1	VI ENTITOCKMOLVPGKTRKLLFKFVAKTED
763	2113	A	6082			VLENLTQGKMCLVPGKTRKLLFKFVAKTED
763	2113	A	6082			VGKKIEITSVDLALGNETGRCVVLNWQGGGG
763	2113	A	6082			VLENLTQGKMCLVPGKTRKLLFKFVAKTED VGKKIEITSVDLALGNETGRCVVLNWQGGGG DAASSQEALQAARSFKRRPKLPDNEVHWGSII IQASTMIISRVPNISVHLLHEPPALTNEMYCLV

كالله فينه فيها فيما طيلا الرسداسة

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  VTVQSHEKTQIRDVKLTAGLKPGQDANLTQK THVTLHGTELCDESYPALLTDIPVGDLHPGEQ LEKMLYVRCGTVGSRMFLVYVSYLINTTVEE KEIVCKCHKDETVTIETVFPFDVAVKFVSTKF EHLERVYADIPFLLMTDLLSASPWALTIVSSE
					1402	LHLAPSMTTVDQLESQVDNVILQTGESASECF CLQCPSLGNIEGGVATGHYIISWKRTSAMENI PIITTVITLPHVIVENIPLHVNADLPSFGRVRES LPVKYHLQNKTDLVQDVEISVEPSDAFMFSG LKQIRLRILPGTEQEMLYNFYPLMAGYQQLPS LNINLLRFPNFTNQLLRRFIPTSIFVKPQGRLM DDTSIAAA AAADLANSNAGAAVGRKAGPRSPPSAPAPAP
764	2114	A	6093		1422	PPPAPAPPTLGNNHQESPGWRCCRPTLRERN ALMFNNELMADVHFVVGPPGATRTVPAHKY VLAVGSSVFYAMFYGDLAEVKSEIHIPDVEPA AFLILLKYMYSDEIDLEADTVLATLYAAKKYI VPALAKACVNFLETSLEAKNACVLLSQSRLF EEPELTQRCWEVIDAQAEMALRSEGFCEIDR QTLEIIVTREALNTKEAVVFEAVLNWAEAEC KRQGLPITPRNKRHVLGRALYLVRIPTMTLEE FANGAAQSDILTLEETHSIFLWYTATNKPRLD FPLTKRKGLAPQRCHRFQSSAYRSNQWRYRG RCDSIQFAVDRRVFIAGLGLYGSSSGKAEYSV KIELKRLGVVLAQNLTKFMSDGSSNTFPVWF EHPVQVEQDTFYTASAVLDGSELSYFGQEGM TEVQCGKVAFQFQCSSDSTNGTGVQGGQIPE LIFYA
765	2115	A	6099	1	1150	RPVKAPGTFHMVHGKCMCKHNTAGSHCQH CAPLYNDRPWEAADGKTGAPNECRTCKCNG HADTCHFDVNVWEASGNRSGGVCDDCQHN TEGQYCQRCKPGFYRDLRRPFSAPDACKPCS CHPVGSAVLPANSVTFCDPSNGDCPCKPGVA GRRCDRCMVGYWGFGDYGCRPCDCAGSCD PITGDCISSHTDIDWYHEVPDFRPVHNKSEPP WEWEDAQGFSALLHSGKCECKEQTLGNAKA FCGMKYSYVLKIKILSAHDKGTHVEVNVKIK KVLKSTKLKIFRGKRTLYPESWTDRGCTCPIL NPGLEYLVAGHEDIRTGKLIVNMKSFVQHWK PSLGRKVMDILKRECK
766	2116	A	6103	2	384	CVLTERGLQLFEAKGTGGRPKELSFARIKAVE CVESTGRHIYFTLVTEGGGEIDFRCPLEDPGW NAQITLGLVKFKNQQAIQTVRARQSLGTGTL VS SGSSHASDGSGFQELRICSEDQTPLIAGMCSLP
767	2117	A	6106	1	542	SGSSHASDGSGFQELRICSEDQIFLIAGINGSEI MARYYIIKYADQKALYTRDGQLLVGDPVAD NCCAEKICTLPNRGLDRTKVPIFLGIQGGSRC LACVETEEGPSLQLEDVNIEELYKGGEEATRF TFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQ PVQLTKESEPSARTKFYFEQSW FILQAVLQLSSQEARYKAFGTCVSHIGAILAF
768	2118	A	6109	3	292	YTPSVISSVMHRVARCAAPHVHILLANFYLLF PPMVNPIIYGVKTKQIRDSLGSIPEKGCVNRE RHEPSCSNGVASTKSKQNHSKYPAPSSSSSSS
769	2119	A	6110	1	711	RHEPSCSNGVASTKSKQNHSKTFAF333333 SSSSSSSPSSVNYSESNSTDSTKSQHHSSTSNQ ETSDSEMEMEAEHYPNGVLGSMSTRIVNGAY KHEDLQTDESSMDDRHPRRQLCGGNQAATE

EQ ID IO: of ucl- otide eq- ence	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
ucl- otide eq-	peptide	hod	LID NU: I		nucleotide	1 ) EASTMILE ACID, E-CIDAMINE 11010,
otide eq-			-	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
eq-	seq-		in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
-	1	Į	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ence	uence	1	09/496	ng to first	acid residue	Glutamine R=Arginine, S=Serine,
		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			]	residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
			1	peptide	Sequence	/=possible nucleotide deletion, \=possible
		1		sequence	ļ.	nucleotide insertion
		<del> </del>	<b>├</b> -	scquence		RIII FGRELOALSEOLGREYGKNLAHTEMLQD
					]	ARSITAYSDPWSCPVGOOLDPIQREPVCAAL
	1	1	1			NSAILESQNLPKQPPLMLALGQASECLRLMA
		1		1	}	RAGIGSCSFARVDDYLH
		<del> </del>	6125	2	570	VEGLNI HVOHLGNNVFLLQTLFGAVILLANC
770	2120	A	0123	2	""	VADWALKYMNRRASOMLLMFLLAICLLAIIF
						VPOFMOMLREVLATLGLGASALANTLAFAH
	ļ	1	1			CNEVIPTIRARAMGINATFANIAGALAPLMM
		1			ļ	II SVYSPPLPWIIYGVFPFISGFAFLLLPETRNK
	1	į			i	PI FOTIODEKNERKDPREPKQEDPRVEVTQF
		·	(126	909	353	DSEVI DTASAICNYNAHYKNHPKYWCRGYF
771	2121	Α	6126	909	333	RDYCNIIAFSPNSTNHVALRDTGNQLIVTMSC
					1	I TKEDTGWYWCGIORDFARDDMDFTELIVI
						DDKGTLANDFWSGKDLSGNKTRSCKAPKVV
						PK ADRSRTSIL IICILITGLGIISVISHLTKRRRS
	1	1			1	ORNERVONTLKPFSRVLTPKEMAPTEQM
			6148	17	810	EVI CIT AT SHTISPEMNK FFPASFPNROYOLLE
772	2122	A	0146	'	070	TOGSGENKEEHNYEFDTKDLVCLGLSSIVGV
	1			1		WYLLRKHWIANNLFGLAFSLNGVELLHLNN
	l	I	1	Í		VSTGCILLGGLFIYDVFWVFGTNVMVTVAKS
	1			1		FFAPIKI.VFPODLLEKGLEANNFAMLGLGDV
		1				VIPGIFIALLERFDISLKKNTHTYFYTSFAAYIF
		1				GLGI TIFIMHIFKHAOPALLYLVPACIGFPVLV
	l		1		1	ALAKGEVTEMFSYEESNPKDPAAVTESKEGT
	ļ					EASASKGLEKKEK
		<del>                                     </del>	6161	3	1088	CQPMLVTRKNHPKLLLRRTESVAEKMLTNW
773	2123	A	0101	"		FTELLYKELKESAGEPLEMLYCALKHQMEKU
	l l	4				PIDAITGEARYSLSEDKLIRHLIDYKTLTLNCV
	-		1	l		NPENENAPEVPVKGLDCDTGTQAKEKLLDA
		l	1	1		AYKGVPYSQRPKAADMDLEWRQGRMARIIL
	ł	Ì				QDEDVTTKIDNDWKRLNTLAHYQVTDGSSV
	-	Ì				ALVPKQTSAYNISNSSTFTKSLSRYESMLRTA
		-	1	1		SSPDSLRSRTPMITPDLESGTKLWHLVKNHDI
	1	1		]		LDQREGDRGSKMVSEIYLTRLLATKGTLQKF
	Í					VDDLFETIFSTAHRGSALPLAIKYMFDFLDEQ
	1	İ				ADKHQIHDADVRHTWKSNCLPLRFWVNVIK
		Ì			_	NPQFVFDIHKNSITDACLSVV
771	2124	-	6163	860	125	KTAVKKRNLNPVFNETLRYSVPQAELQGRVI
774	2124	1	"""		ļ	SLSVWHRESLGRNIFLGEVEVPLDTWDWGSE
		1	1			PTWLPLQPRVPPSPDDLPSRGLLALSLKYVPA
	1		1	1		GSEGAGLPPSGELHFWVKEARDLLPLRAGSL
	1	1	1			DTYVQCFVLPDDSRASRQRTRVVRRSLSPVF
		[	}		1	NHTMVYDGFGPADLRQACAELSLWDHGAL
	1		1	1		NRQLGGTRLSLGTGSSYGLQVPWMDSTPEEI
				1		QLWQALLEQPCEWVDGLLPLRTNLAPRT
771	2125	A	6191	12	392	ARGIGSLGRDHSGSGGGTGMAGAWVRKAA
775	2123	^	0191	-		YVRSKDFRDYLMSTHFWGPVANWGLPIAAI
				<b>\</b>		DMK\KSPEIISRRMTFAL*CYSLTFVRFAHYV
			j	1		PWNWLMLGCHTAVDFDQLISSMPCISHGMT
	(	- (		{		ASASAI.
L			6217		827	FRGYWGVREAFTDASWSGGLGPGKPGMKIT
776	2126	A	021/	'	32,	ROKHAKKHLGFFRNNFGVREPYQILLDGTFC
}			1			OAAL RGRIOL REOLPRYLMGETQLCTTRCVL
1						VELETLICK DLYGAKLIAOK COVRNCPHEKN
		!				VSGSECLLSMVEEGNPHHYFVATQDQNLSV
1						VKKKPGVPLMFIIONTMVLDKPSPKTIAFVK.
]			1			VESG/RLSOCMRKKVSNISKRNRV**KTLNRG
1		1				RRKKRKKISGPNPLSCLKKKKKAPDTQSSAS
1					<b>.</b>	KKRKRKRIRNRSNPKVLSEKQNAEGE
776	2126	A	6217	1	827	RQKHAKKHLGFFRNNFGVREPYQILLDG QAALRGRIQLREQLPRYLMGETQLCTTR KELETLGKDLYGAKLIAQKCQVRNCPHI VSGSECLLSMVEEGNPHHYFVATQDQNI VKKKPGVPLMFIIQNTMVLDKPSPKTIAI VESGIRLSOCMRKKVSNISKRNRV**KTL

			1000	Predicted	Predicted end	Amino acid sequence (A=Aianine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D—Aspertic Acid E=Glutamic Acid,
NO: of	NO: of	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I-Isoleucine K=Lysine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		i	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	} '	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	2127	A	6236	1038	1402	YYQISSLPSIVGNGIFLWLLICIFLAKQGGSRL*
777	212/	1	0230		1	FQPFGRPRGGGHLRSGVLGQPGQHGETP/SFF
			1	1		YNSKISPALWGPPVIPSALGGEAGKSL*PRRQ
		1	ļ	1		RFQRGGIAPLPSRVRGRAKLFLKKK
770	2128	A	6237	422	913	ASFFHHHRGAFLLLLAIPGS*GQDQSLIHWSN
778	2120	1	020.	1	1	ASSPHILITION OF THE AVENUAL PROPERTY OF THE AVENUAL PR
		1		İ		PQVL\SEPN*RSGGCFSAPSFEVPPWTGEVKP/
	1	1		1		SPQRDGGALG\QGPLGIPSDSILALLKKQT*RA LLNWPLGSLRRSSCFGGQDGQDLKPRSGLGC
			ļ			
					l	NSFRYRR ARAPSPSFSVRDVELSDPARERGEMPVAVGP
779	2129	A	6249	420	36	YGQSQPSCFDRVKMGFVMGCAVGMAAGAL
119	1212)	1				FGTFSCLSSILVSSSG/SGMRGRELMGGIGKTM
		1		1		MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH
		ľ		1		MOSGGIFGIFIANGMONG THEFT TE
		1				QSQPMY RIMRMCDRGIQMLITTVGAFAAFSLMTIAVG
780	2130	A	6263	415	1380	TDYWLYSRGVCRTKSTSDNETSRKNEEVMT
100		1				HSGLWRTCCLEGAFRGVCKKIDHFPEDADYE
		}				QDTAEYLLRAVRASSVFPILSVTLLFFGGLCV
		-				A A SEFHESE HNVILS A GIFFVS A GLSNII GILV II
	1	ŀ	ł	Ì	1	S\ANAGRTPGQR\DSKKSYSYGWSF/YFSGAFS
		1		į	ļ	FILED/IIC*GVGLPWHIYIEKHQQLKAKSHSEF
		1				I V V STEAR I PPYRYRFRRRSSSRSTEPRSKDLS
	1			1	Ì	DISK GEHTIPSTDISMFTLSRDPSKITMGTLLNS
	1		Ì		1	DRDHAFLQFHNSTPKEFKESLHNNPANRRTT
			ļ	i	1	DV
			(0.71	832	318	PULVEDI KOTLAIKTAYPRCKCLVEMDQIFH
781	2131	A	6274	632	310	LOVKOKOLACLCTWOARDPDCPPSTKVVL/L
		1.				VCDCMCCMVALFODSIAWSNKSMPSSLSAIS
		1		]		QSPCQVQAPEGPSSFHLPTLSFTTCLSWQGGD
İ		Į				LEFLGDLKGCSELKNFQELITQSALVHPKADV
						WWYCGRPLLGTLPSN
	-	+	6281	1324	393	WISLPSSLLCRKNGSSAEDDRR/GEPSAEEAEG
782	2132	^	0281	132.		EREDWGIGSA*SVGAVSKVPSARF*RTYPS\E
		1			}	DEEEVTHOKSSSSDSNSEEHRKKKTSRSRNK
		-	-	1		KKRKNKSSKRKHRKYSDSDSNSESDTNSDSD
		l		İ		DDKKRVKAKKKKKKKKKKKKKKKKKKKKKKKKKKK
ļ				ł	ļ	ESSDSSCKDSEEDLSEATWMEQPNVADTMDL
		1				IGPEAPUHTSQDEKPLKYGHALLPGEGAAMA
1		- 1	- (			EYVKAGKRIPRRGEIGLTSEEIGSFECSGYVM SGSRHRRMEAVRLRKENQIYSADEKRALASF
	1			1		SGSRHRRMEAVKLRKENQIISADEKKALASI
1		- 1				NQEERKRESKILASFREMVHKKTKGKDDK
702	2133	- A	6305	201	1032	WDDYPQGALRRREAAEGLHFLGPPGRVRGQ LRGITGPAWYCHSPSHSLLSAFCHLPTPSRCP
783	2133	1 '`	1 3333			LRGITGPAWYCHSPSHSLLSAFCHLF IT SICH AMARPPVPGSVVVPNWHES/RRGQGVPGLHS
1		1	1			AMARPPVPGSVVVPNWHES/RROQGVVGEIS AQEPPAGVWAA*AASAAAA\LSIDTASYKISV
						SGKSGVGKTALVAKLAGLEVPVVHHETTGIC
İ						SGKSGVGKTALVAKLAGLEVTVVIIIDTTO
						TTVVFWPAKLQASSRVVMFRFEFWDCGESA LKKFDHMLLACMENTDAFLFLFSFTDRASFE
		)		ĺ		DLPGQLARIAGEAPGVVRMVIGSKFDQYMF
[		1				DLPGQLAKIAGEAPGVVKVIVIGSKI DQTVI
		Į.				DVPERDLTAFRQAWELPLLRVKSVPGRRLG DVPERDLTAFRQAWELPLLRVKSVPGRRLG
204	2134	-	6308	86	96	GSSPDPASLITMKNQDKKNGAAKQSNPKSSP
784	2134	^	0300	1		GOPEAGPEGAQERPSQAAPAVEAEGPGSSQA
1	į					PRKPEGAQARTAQSGALRDVSEELSRQLEDII
1			1			STYCVDNNQGGPGEDGAQGEPAEPEDAEKS
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1	1	ļ	1	1		QSDEVGDRDHRRPQEKKKAKGLGKEITLLM
1						
						QTLNTLSTPEEKLAALCKKYAELLEEHRNSQ KQMKLLQKKQSQLVQEKDHLRGEHSKAVLA

NO. of nucle- order peptide group tenore  wence with the pertial control of the pertial con			<del></del>	1-050	D 11 11 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nociente conde conteste contes	SEQ ID	SEQ ID	Met	SEQ	Predicted		D-Aspertis Asid E=Glutamic Asid
i cortice ponding of first a mine and of peptide residue of peptide residue of peptide sequence    Sequence   Part	NO: of	1	hod	L		1	E-Phenylalanine G-Glycine H=Histidine
corresponding tenice uni	nucl-	peptide	1				remenylatanine, G-Grychie, it institute,
uence unce part of the property of the propert	eotide	seq-	i	USSN	location		l=Isoleucine, K=Lysine, L=Leucine,
uence    914   an gto first animo acid residue of peptide residue of peptide sequence   T-T-Inconine, V-V-Nine, W-Tryptophan, Y-Tyrosine, X-Unknown, **-Siep codon, Y-Tyrosine, X-Unknow			)	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
### anino acid residue of peptide residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per per per per per per per per per pe				914		acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of poptide sequence	ucha	1		1		of peptide	T=Threonine, V=Valine, W=Tryptophan,
### Peptide sequence   ### peptide sequence   ### s	,			l .			Y=Tyrosine, X=Unknown, *=Stop codon,
	·	l .	1	1	1	Joquena	/=possible nucleotide deletion. \=possible
RSKLESI.CRELQRIMNESI.KEEGVQRAREE   RREVTSHIPQYLTNDIQU,DMEQHERNS   QEMMEL AERLIKKLIEQYELREEHIDKVFK   DLQQQLVDAKLQQAGEMIKAEREHOR   PILKBAVESQRMCELMKQQETHLKQQL, TEKFEEFQNTI.SKSSEVFTIFKQEMEKMI   KKLEKFTITMYRSKYESSINALLEMAEE   RDKELEGI,QVKIQRLEKLCRALQTIGAQ*   GQRWGSIRTSAVRIFS   RDKELEGI,QVKIQRLEKLCRALQTIGAQ*   GQRWGSIRTSAVRIFS   SPOGPILERSVSPVSAGASSVTPGGAQPGV   PSLVAVAPAFGSAGPAAGWQ*HAGCT   KLPWSWGMRFMKIFFSESTRSISTINSBID   EKCTOPAKPLSMRTGSSSSPGPJLVKW   RREFRNSGTRVVSSCCGMSCMYSFIGHE   GDLPLHYDVDWGPPLGFTVGRPGLF   TTPCOKLVYDDLDWA   TTPCOKLVYDDLDWA   RREFRNSGTRVVSSCCGMSCMYSFIGHE   GDLPLHYDVGWPPLGFTVGLRPGLF   TTPCOKLVYDDLDWA		1		1			nucleotide insertion
RKREVTSHFQVTLNDIQU_MEQHHERQ NEW OF DLQQQLVDAKLQQAQEMLKEAERHDKVFK DLQQQLVDAKLQQAQEMLKEAERHDKVFK DLQQQLVDAKLQQAQEMLKEAERHDKVFK DLQQQLVDAKLQQAQEMLKEAERHDK MERERGATTLSKSSEVFITFKQEMEST MAGER FLKEAFESFQNTI_SKSSEVFITFKQEMEST MAGER RDKELEGQLQVKIQRLEKLCRALQT/GAQ*** GQRWGSHRTSAVRIFS**  785 2135 A 6319 1493 889 SPQGPLLRSVSFVSAGASSVTPGGAQPGV PPSLVAVAPAPGSAAGPAAGWQ*** IAGGCT KLPWSWGMPMKIFFSEEVFSTSTRISHDLEKCTQPAKPLSMRTGSSVSFGGPLVKWGMPKIFFSEFSTSTSTRISHDLEKCTQPAKPLSMRTGSSVSFGGPLVKWGMPKRFFRNSGTCWSCCGMSCMYSFLGHCQDLPLYHVDVGWQPPLGPTVGLRFGLLFTPCQKLVYDDLDWA**  786 2136 A 6320 551 135 RWILPVAECDSSCVGCTGEGPGNCKES**  FTPCQKLVYDDLDWA**  787 2137 A 6330 1693 227 RWILPVAECDSSCVGCTGEGPGNCKES**  FTPCQKLVYDDLDWA**  788 2137 A 6330 1693 227 DYVLTAELHRGRSFGVSFGLSVFNLMMAS**  SGILGLAYWAMNTOVFGFSFLLLTVALM**  SGILGLAYWAMNTOVFGFSFLLLTVALM**  SGILGLAYWAMNTOVFGFSFLLLTVALM**  SGILGLAYWAMNTOVFGFSFLLLTVALM**  FLEFLQSL*NSL*NATSYEDLGLFAFGLI**  FLEFLQSL*NSL*NATSYEDLGLFAFGLI**  FLEFLQSL*NSL*NATSYEDLGLFAFGLI**  FLEFLQSL*NSL*NATSYEDLGFAFGLI**  FLEFLQSL*NSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYEDLGJFAFGLI**  FLEFLQSL*NATSYE	_	i		<u> </u>	sequence		DOLL DEL CORT OF THE CANADAR SEE SE
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DLQQQLVDAKLQQAQEMLKEAEERHQQL   FLIKEAVESQRMCEIMKQQCHTILKQQL   TEKFEFEQNTI_SKSSEVFITTKQEMENT   KELEACITMYRSWESSNALLEMAEER   RDKELEGLQVKQRLEKLCRALQT/GAQ*    GQRWGSHRTSAVRIF*    FOOTPILESSEVFITTKQEMESNISTRISHD    FOOTPILESSEVFITTKQEMESNISTRISHD    EKCTQPAKPLSMIRTGSSVSRGPIVKYSICGREY   FPSLVAVAPAPGSAAGPAGNQ* HAGGE   KLPWSWGMRPMKIFFSEFSTSISTRISHD    EKCTQPAKPLSMIRTGSSVSRGPIVKYSICGREY   REFERNSGITVSSCCGMSCMYSFLGHC   GDJEPLVHYDVGWQPPLGPTVGLRFGLF    TTPCQKLVVDIDDWA    RWIPVAECDSSCVGCTGEGPGNCKECIS    REHGQCADVDECSLAEKTCVRKNOSCMYSFLGHC   GDJEPLVHYDVGWQPPLGPTVGLRFGLF    TTPCQKLVVDIDDWA    RWIPVAECDSSCVGCTGEGPGNCKECIS    REHGQCADVDECSLAEKTCVRKNOSCMYSFLGHC   GDJEPLVHYDVGWGPPLGPTVGLAGAGG*    RWIPVAECDSSCVGCTGEGPGNCKECIS    REHGQCADVDECSLAEKTCVRKNOSCMYSFLGHC   STATE		ì				ļ	KKKEVISHPQVILINDIQLQMEQHNEANSALK
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RIKELEGLQVKIQRLEKLCRALQT/GAQ* GQRWGSHRTSAVRIPS  REGREGRITSAVRIPS  A 6319 1493 889 SPQGPLLRSVSPVSAGASSVTPGGAQPGV PPSLVAVAPAPGSAAGPAAGWQ*HAGCH KLPWSWGMRPMKHFSESYRSISTRISHD EKCTQPAKPLSMIRITGSSVSPG/PLVKWN RREFRNSGTRVVSSCCGMSCMYSFLGHC QDLPLVHVDVGWQPPLGPTVGLRPGLLF TTPCQKLVVDDLDWA  RWLPVAECDSSCVGCTGEGPGNCKECIS REHGQCADVDECSLAEKTCVRKNENCY GSYVCVCPDGFETFRACLCAAGRG*SHF PDTAALPRRPVMCRTYPLNYSEGGPVEN RMPSPAVDSGGERLPAL  787 2137 A 6330 1693 227 DYVLTAELHRQRSPGVSFGLSVTLMMA SGIGLAVMANTGVFGFSFLLLTVALL VHLLLSMCIQTAYLGP*TNYFMVLPAH*I PLEFLQSL*NSLW*AVTSYEDLGLFAFGLI VVAGTIIIGNIGAMSSYLLIKTELPAAIAE GDYSRYWYLDOQTLLIICVGIVFPLALL FLGYTSSLSFFFMMFFALVVIIKKWSPECT NYVEKGFQISNVTDDCKPKLFHFSKESA TMAFSFLCHTSILPYCLSPSKKKMON TAIALSFLIYFISALFGYLTFDVGTTKAQ VTCHRIKDKVESELKG***IP*SHDWYN KLCILFAVLLVTPLHFPARKAVTMMFF FSWIRHFLITLALNIIVLLATYVPDIRNYF GASTSTCLIFFFGLFTVLKSREDFLSWKK GCCALSFKTSILRNSLSVYILLPASKSIS VVQGPTSAFLFFFVTEEDPILSSFSKCLK LGFWRRDGPRERREL *FFWGGEDPVLL TMTYQKKKMECGRMDFPMAVLCSK NLLERCLMRNRVVRIJGKWFVKFYEKDEI LGFWRRDGPFRREL* *FFWGGEDPVLL TMTYQKKKMECGRMDFPMAVLCSK NLLERCLMRNRVVRIJGKWFVKFYEKDEI KSSHLSCSFTFFLHGDSNVCTSVCLKEI EKQEDMDWEDDSLAAVEVLVAGVRMT FVLVPOSDIFTPSPVGSTCSLRSCLIGHT AFKMSDSATKKLIGEWKQFYPISCCLKEI EKQEDMDWEDDSLAAVEVLVAGVRMT FVLVPOSDIFTPSPVGSTCLSHGSNCLKHON LISEHTITLAQGSNSFPTSHSSSCLGVHQ TRDPAMSSVTLTPTSPEEVQTVDQSV VKFSSVSDOFNDSTSTHHGKIFRKLANI DRVWQECTMRRAQNKRKYSASSGGLC AAKVASWDFVEATGRTHSOCLHKKINL AGQQGQAPSLGQQQQLPKHKTNEKQEI PQKRPLTFFHHRVSVSDDVGMDADSAS VISAPDSGVRYNFSININIDVAKITPCMH MANSPQPPLSPFPPCDVVDEGVTKTSTI	ł	1		}		}	KKLEKETTMYRSRWESSNKALLEMAEEKTV
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	!	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
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1				peptide		nucleotide insertion
				sequence		RONSEREAGKKHKVEDGTSSVTVLSHEEDA
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		ļ				VSYTDLDNLFNSDEDELTPGSKRSANGSDDK
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		1				CIYRQSWTVGKLELLSSGPSMPFIKEGDGSNM
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1						
				-		EQKTELVCELQKLQYCVGMCGDGANDCGAL KAADVGISLSQAEASVVSPFTSSMASIECVPM

NO: of N nucleotide s	SEQID NO: of peptide	Met hod	SEQ ID NO: in	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl- peotide s		hod				D 71 - Islania C-Clusine H=Histidine
eotide s	peptide		l in			1 F=Phenvialanille (1-()[vcii]o, 11 11131101110,
				nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
SET 110	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	Q=Glutamine, K=Arginine, S=Scille,
delice				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Ī		ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i			1	peptide	,	/=possible nucleotide deletion, \=possible
1		1	1	sequence	1	nucleotide insertion
				sequence		VIREGRCSLDTSFSVFKYMALYSLTQFISVLIL
		1	ļ	,		YTINTNLGDLQFLAIDLVITTTVAVLMSRTGP
l.		i	ļ			ALVLGRVRPPGALLSVPVLSSLLLQMVLVTG
1						ALVEGRARI TI A ODMENDI METVA APONI PNY
ļ		1	1	ļ		VQLGGYFLTLAQPWFVPLNRTVAAPDNLPNY
			1	1		ENTVVFSLSSFQYLILAAAVSKGAPFR\RPLTN
		i				NVPFLLASAL*SSVLVVLVLSPGLLHGPLALR
j			ł		1	NITDTGFKLLLVGLVTLNFVGGLHAGERARP
1			1			VPPRLPAPPPAQAG\SKKRFKQLERELAEQPW
1				ļ	•	PPLPAGPLR
ļ			L			SSAGSARKLQVMALAARLWRLLPFRRGAAP
790	2140	A	6380	76	1059	GSRLPAGTSGSRGHCGPCRFRGFEVMGNPGT
		1			1	GSKLYAG I SUB-COMMONICO A A TOTAL A TA
1		1	1		[	FKRGLLLSALSYLGFETYQVISQAAVVHATA
1		1	1	1	1	KVEEILEQADYLYESGETEKLYQLLTQYKESE
		1	1		1	DAELLWRLARASRDVAQLSRTSEEEKKLLVY
l l		1		1	1	FAI FYAKRA/L/EKNESSFASHKWYAICLSDV
						GDYEGIKAKIANAYIIKEHFEKAIELNPKDATS
. 1		ì	Ì			THI MGIWCYTFAEMPWYORRIA*NACLQLPP
1			İ			*FPPYEKALG\YFHRAEQVDPNFYSKNLLLLG
l 1		1				KTYLKLHNKKLAAFWLMKAKDYPAHTEED
1 1		1	1			KI I LKLINKKLAAL WEME EEST I
		1	1			KQIQTEAAQLLTSFSEKN
791	2141	A	6434	3	1460	IALLIVDGLAWDDQGGLALLHISPSKLIL*QDS
1/91	2141	1.7	0.5.			SGMS/YVMVRCTITRAFFKSLLCHICQYSIGPQ
1 1		ł	1			*VT\CPGQDACKE*KSTAN*GG*RE**PQVLFF
! !				1	}	AFT SNPAVKFGRMSKKORDSLYAEVQKHQQ
1						RLOEOROOOSGEAEALARVYSSSISNGLSNLN
1						NETSGTYANGSVIDLPKSEGYYNVVSGQPSP
1		İ	1			DQSGLDMT\GIKQIKQEPIYDLTSVPNLFTY\SS
1		1	ļ	i		FNN/GQLAPGIT/MTEIDRIAQNIIKSHLETCQY
]			1			TMEELHQLAWQTHTYEEIKAYQSKSREALW
l j			ļ			QQCAIQITHAIQYVVEFAKRITGFMELCQNDQ
ļ ļ		1	1			QQCAIQITHAIQYVVEFARRITOFMELCQNDQ
1				1	İ	ILLKSGCLEVVLVRMCRAFNPLNNTVLFEG
]		1	1	ļ		KYGGMQMFKALGSDDLVNEAFDFAKNLCSL
1 1	·			1		QLTEEEIALFSSAVLISPDRAWLIEPRKVQKLQ
1		ì	1		1	EKIYFALQHVIQKNHLDDETLAKLIAKIPTITA
			1			VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF
1 1		1				NPDCATACK
]	1					SRGTFRCFCRDFFPCFSNMRLFLWNAVLTLFV
792	2142	A	6440	92	781	TSLIGALIPEPEVKIEVLQKPFICHRKTKGGDL
'	1		1	ì		MLVHYEGYLEKDGSLFHSTHKHNNGQPIWFT
	1	1		1	1	WLAHAEG I TEVTAGTELUS I UVULUNGALANI
] !	1			1		LGILEALKGWGPGA*K/DMCVGEKRKLIIPPA
1				1	]	LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH
}	l			1		ESFQEMDLNDDWKLSKDEVKAYLKKEFEKH
		1			1	GAVVNESHHDALVEDIFDKEDEDKDGFISAR
1			ļ		1	FFTYKHDEL
	1				1.52	PRLKRLVVTEEDGGARPEALGKIAPRTPAELG
793	2143	A	6446	3201	152	ARADQELVTALMCDLRRPAAGGMMDLAYV
'	1	1				AKALUELY IALIVIODERA AAGGINIDATI
į į		1				CEWEKWSKSTHCPSVPLACAWSCRNLIAFTM
1	1			ļ		DLRSDDQDLTRMIHILDTEHPWDLHSIPSEHH
1	1				}	EAITC\LEWDQSGFPGFLFSRWPTGQIK\CWS
1	1	1	1			MGVSTLA\NSWE\SSVGSL\VEGGPHLWALS\
						WLH\NGVKLALHVEKSGASSFGEKFSR\VKFS
	}					P\SLTLF\GGNAMEGWIAVTVSGLVTVSLLQ\P
	1	1				SGQVL\TST\ESLCRLRARVALADIAFTGGGNI
			1			SGQVE/151/ESECKERARY ALADIA 1000M
						VVATADGSSA\SPVQFYKVCVSVVSEKCRIDT
				1		DILPSLFMRCTTDLNRKDKFPAITHLKFLARD
		1	) .	J		MSEOVILCASSOTSSIVECWSLRKEGLPVNNI
(		1	1			FOOISPVVGDKOPTILKWRILSATNDLDRVSA
	1			1.		VALPKLPISLTNTDLKVASDTQFYPGLGLAL
			1		ĺ	A FUDGSVHIVHRI SLOTMAVFYSSAAPRPVD
						AFHDGSVHIVHRLSLQTMAVFYSSAAPRPVD EPAMKRPRTAGPAVHLKAMQLSWTSLALVG

			CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	i -	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	i	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	1	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	ļ	İ	residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		/=possible nucleotide deterion, (* possible
	1	Ī		sequence		nucleotide insertion
			1			IDSHGKLSVLRLSPSMGHPLEVGLALRHLLFL
	1	1	1		1	LEYCMVTGYDWWDILLHVQPSMVQSLVEKL
	İ	1	1			HEEYTRQTAALQQVLSTRILAMKASLCKLSP
						CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT
	1	1			1	PDKSPGDRLTEICTKITDVDIDKVMINLKTEEF
	1	1		İ		VLDMNTLQALQQLLQWVGDFVLYLLASLPN
		1	l	1		OPCPTSEPCPTSEPSPTSEPSPTSEPSSP*SLC/G
		1	1			SLLRPGHSFLRDGTSLGMLRELMVVIRIWGLL
		1				KPSCLPVYTATSDTQDSMSLLFRLLTKLWICC
	İ	1	Ì			RDEGPASEPDEALVDECCLLPSQLLIPSLDWL
		1				PASDGLVSRLQPKQPLRLQFGRAPTLPGSAAT
		1				LQLDGLARAPGQPKIDHLRRLHLGACPTEEC
			1			KACTRCGCVTMLKSPNRTTAVKQWEQRWIK
	1	1	1		Ì	NC/LVRWALVAGAPQLPLSPAAPQLLLSYPSA
	1	1	1			APEPGCCKSHRSPWTLLGAVNLSPPCRAVEG
i		1			1	APEPGCCKSHRSPWILLUAVNESFICKAVED
		1	1		1	RGPDACVTSRASEEAPAFVQLGPQSTHHSPRT
			1			PRSLDHLHPEDRP
794	2144	A	6490	418	585	NGDKADLENESCRAQVLMPVVPALWEAEGG
194	2144	1 ^	10.50			GSIEPRDLRLQ*AVITPL\TPAWVTQ
705	2145	A	6499	395	1027	KLLWLPPHSEQKRSPLYHPQGPSGTTPSAP\FS
795	2145	^	0422	3,50		SHSPPPSLLQAVPSIAAFLRTHGHISASGPLRMP
			1			FPH/H*NAFLLVFPGQRSQLTS/PSHYLCREVFP
	]		ļ	1	· ·	DHHHHLCRLSLESSPLFHHRVLFCVPKQNVN
						STRAOIFCLEVHIVGCRCINTFPLHLFRLHLWL
	i i	İ	1	i		HFLQIPLCKKNKSVKLGKTVVGRGCQSAAGS
	1	1	1	1		DTRVRAAVGAPGLPVEPLV
			<del></del>		936	HSALLTHSSFCVFTLCODFFTYSSMSEEVTYA
796	2146	A	6503	68	936	DLQFQNSSEMEKIPEIGKFGEKAPPAPSHVWR
l	1	ł		Į.	ſ	PAALFLTLLCLLLLIGLGVLASMFHVTLKIEM
Ì		1				KKMNKLQNISEELQRNISLQLMSNMNISNKIR
						NLSTTLQTIATKLCRELYSKEQEHKCKPCPRR
	ļ		1		1	WIWHKDSCYFLSDDVQTWQESKMACAAQN
	j	}	Į	1		ASLLKINNKNALEFIKSQSRSYDYWLGLSPEE
			- 1			DS/YSWYESG*YNQ\PSAWVIRNAPDLNNMY
			ļ	ļ	1	CGYINRLYVQYYHCTYKQRMICEKMANPVQ
ļ	]		1	ł	1	
1		]				LGSTYFREA
797	2147	A	6507	1	881	PGSTHASARSQVPRSAGEAAPHSRPPGLLPH PGSTHASARSQVPRSAGEAPHSRPPTAGEAPHSRPPTAGEAPHSRPPTAGEAPHSRPPTAGEAPHSRPPTAGEAPHSRPPTAGEAPHSRPTAGE
1		1				APRAASAQLEERMRDPHPGMTLQEGDCRGS
ŀ		1	Ì	1		QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ
İ	l	-	l l			ESALAKLLLTCCSALRPRATQARGSSRLLVAS
			1			WVMQIVLGILSAVLGGFFYIRDYTLLVTSGA
i			1	}	1	AIWTGAVAVLAGAAAFIYEKRGGTYWALLR
	J	}				
{						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS
			-			TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTOSPEEVRRLHLCTSFM
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMI KALFRTLOAMLLGVWILLLLASLTPLWL
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SI /RGECSOPKG*VPKKRDQKEMLEVSGI*PG
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSOVPRSAGEAAPHSRRPPGLLPHAP
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAOLEERMRDPHPGMTLQEGDCRGSQT
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAOLEERMRDPHPGMTLQEGDCRGSQT
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPOHTHIDVHIHQES
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES A1 AKILLTCCSALRPRATOARGSSRLLVASW
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMOIVLGII SAVLGGFFYIRDYTLLVTSGAAI
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTOSPEEVRRLHLCTSFMDM
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM LKALFRTLQAMLLGVWILLLASLTPLWLYC
						TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM LKALFRTLQAMLLGVWILLLASLTPLWLYC WRMFPTKGVSP
			4620	912	2287	TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTQSPEEVRLHLCTSFMDM LKALFRTLQAMLLGVWILLLASLTPLWLYC WRMFPTKGVSP
798	2148	A	6528	912	2287	TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM LKALFRTLQAMLLGVWILLLASLTPLWLYC WRMFPTKGVSP

			1.000	D disad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ĺ	in	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
eotide	seq-	}	USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	1	ng to first	acid residue	C=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}	]		residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
		1			Sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
			<u> </u>	sequence		EVEDEGTCI PLPHSDLPTSWCGHSLOCGSQSS
			1			EDDAIHENAFIVEIASSLGHMLLTCILWRLTKK
	ļ	i				HTVSQE\DGLSLAGAPRQPRRKSRTSVLRIRV
				ļ	İ	MVRWELSSNGNPGRGVLGLGLGLGNKLRVV
					1	CONT. GL * HCVWVVWETGE*KRWRLQMGIL*
		<b>,</b>	1	Ì	1	GVASRRQ*VRNSVRGLVCHNSSAPPMYMGFF
		1		1		SPTVFGGGVGG*LHVTFILHPPEVEAAGIPLLL
		1	1	1	1	GPSLPQRQGREHIVVILAAPACAPFHDR*WEP
	1			1		REIRPSP*ELGLRGEPTLSYPASCRVIRQPIP*D
	Į.		}	4		RKSYSWKQRLFIINFISFFSALAVYFRHNMYC
		1	ł			EAGVYTIFAILEYTVVLTNMAFHMTAWWDF
		İ			İ	GNKELLITSQPEEKRF
		Ì				FFFFQRINFIEHSGSVSLLALACDLGWCEDWS
799	2149	A	6529	1	874	CCLVQGGGDLVDVVQTNHGEDEAGGDTDSV
177		1	ł	ļ	1	DEARCKESQUEAQENLREDLCLESFAKDKIL
			ļ			QIIEGSEREHEETRTKQAALDGEPLGGGQLTA
		1	ľ			VHLHPSKEQQGQEGGERQRGARTHHWRGW
		-	1			EKGRRVRLRPPSGKLRADQPVRKLGGPTPS/T
					1	ELPGLQPHAPTPHTA/PATPTYSPAPDTPNPPV
		- [				RWKCPLPVEPRTRQLCRERTRKACPPKPRPPL
	ļ					GLPGDPTGPVTHHAPPVSPTGASGQERRAEP
• •		-	1	ı		GLPGDPIGPVIHHAFF VSI TOASOQUIAGE
	İ		· ·			GAVSYAHASATK SAQRWAAVAGRWGCRLLALLLLVPGPGGAS
800	2150	A	6544	2	662	EITFELPDNAKQCFYEDIAQGTKCTLEFQVITG
800	2130	1		İ		GHYDVDCRLEDPDGKVLYKEMKKQYDSFTF
1	İ	1	1			TASKNGTYKFCFSNE\FSTFTHKTVYFDFQVG
		l l				TASKNOTYKEUTSNEUTSTETTIKT VITBI QVO
ł		-		1		E\THLCFLVR/DRVSALTQMESACVSIHEALKS
		- [		j		VIDYOTHFRLREAQGRSRAEDLNTRVAYWSV
l	-	1		1	<u> </u>	GEALILLVVSIGQVFLLKSFFSDKRTTTTRVGS
801	2151	A	6556	1	1319	TPCMECIKGEGLREPQNLSGSQREPQTEGSM
901	2131				•	DGWRRMPRWGLLLLLWGSCTFGLPTDTTTF
		1	l			KRIFLKRMPSIRESLKERGVDMARLGPEWSQI
			1	1		MKRLTLGNTTSSVILTNYMDTQYYGEIGIGTF
	1	- 1	İ	<b>\</b>		POTFKVVFDTGSSNVWVPSSKCSRLYTACVY
		İ				HKLFDASDSSSYKHNGTELTLRYSTGTVSGFI
	1	1 .	İ			SQDIITVGGITVTQMFGEVTEMPALPFMLAEF
Ì				1		DGVVGMGFIEQAIGRVTPIFDNIISQGVLKED
İ			ļ			VFSFYYNRDSENSQSLGGQIVLGGSDPQHYE
	}		1	İ		GNFHYINLIKTGVWQIQMKGVSVGSSTLLCE
1	1	-		1	İ	DGCLALVDTGASYISGSTSSIEKLMEALGAKI
1						KRLFDYVVKCNEGPTLPPTFLFLLGGKDTPLT
						SADYLFQESYSSKKLSTLAHAMYIPPPTGPTI
1		- 1			\	\ALGATF\IRKFYTEFDRGNNPHGFALAR
000	0150	A	6567	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGS
802	2152	^	0307	1	1	LAVVVLLALPVAWGQCNAPEWLPFARPTNI
		l	1		1	TDEFEFPIGTYLNYECRPGYSGRPFSIICLKNS
						VWTGAKDRCRRKSCRNPPDPVNGMVHVIKC
	ļ		i			IOFGSOIK YSCTK GYRLIGSSSATCHSGDTVIV
1				1		DNETPICDRIPCGLPPTITNGDFISTNRENFHI
	1					GSVVTYRCNPGSGGRKVFELVGEPSIYCISN
1		1		1		DOVGIWSGPAPOCIIPNKCTPPNVENGILVSD
1	Į.					NRSI ESI NEVVEFRCOPGFVMKGPRRVKCQA
						I NIK WEPET PSCSRVCOPPPDVLHAERT QRUK
	1	1		}		DNIESPGOEVEYSCEPGYDLRGAASMRCTPQ
		Į			1	DISTRICT THE PROPERTY OF THE P
					1	DWSPAAPICEVKSCDDFMGQLLNGKVLITV
						NI OLGAK VDF V CDEGFOLKGSSASY CVLAG
						NI OLGAK VDF V CDEGFOLKGSSASY CVLAG
						DWSPAAPTCEVKSCDDFMGQLLNGRVLFPV NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESLWNSSVPVCEQIFCPSPPVIPNGRHTGKP LEVEPEGKAVNYTCDPHPDRGTSFDLIGESTI
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESLWNSSVPVCEQIFCPSPPVIPNGRHTGKF LEVEPFGKAVNYTCDPHPDRGTSFDLIGESTI
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- eotide seq-	peptide	hod	i	beginning	nuciconac	
eotide seq-				. 1	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-			in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
- 1	seq-		USSN	location		M=Methionine, N=Asparagine, P=Proline,
- 1	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
Į.		l	1	amino acid	of peptide	T=1 hreonine, V=Vaine, W-Tryptoprian,
1		1	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i		1		peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
			ļ	Sequence		SITCLDNLVWSSPKDVCKRKSCKTPPDPVNG
			1		1	MVHVITDIQVGSRINYSCTTGHRLIGHSSAECI
						LSGNAAHWSTKPPICQRIPCGLPPTIANGDFIS
1			1		1	TNRENFHYGSVVTYRCNPGSGGRKVFELVGE
ı	i		1			PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV
			1			ENGILVSDNRSLFSLNEVVEFRCQPGFVMKGP
	1	1	1		ļ	ENGIL VSDNRSLFSLNEV VERKCQFOI VIVIKOI
	1	1	1			RRVKCQALNKWEPELPSCSRVCQPPPDVLHA
	ł	{	1			ERTQRDKDNFSPGQEVFYSCEPGYDLRGAAS
	1					MRCTPQGDWSPAAPTCEVKSCDDFMGQLLN
		1	ļ	1	1	GRVLFPVNLOLGAKVDFVCDEGFQLKGSSAS
						YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG
	1				1	RHTGKPLEVFPFGKAVNYTCDPHPDRGTSFD
			1		}	LIGESTIRCTSDPQGNGVWSSPAPRCGILGHC
		1			1	QAPDHFLFAKLKTQTNASDFPIGTSLKYECRP
		1				EYYGRPFSITCLDNLVWSSPKDVCKRKSCKTP
						ETTUKTOTICLUILT WOODKU CONGOCKIT
	1		1	1	1	PDPVNGMVHVITDIQVGSRINYSCTTGHRLIG
						HSSAECILSGNTAHWSTKPPICQRIPCGLPPTI
	i	1				ANGDFISTNRENFHYGSVVTYRCNLGSRGRK
	1	1	1	1	1	VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN
		1	1			KCTPPNVENGILVSDNRSLFSLNEVVEFRCQP
	1					GFVMKGPRRVKCQALNKWEPELPSCSRVCQ
	1	1	ļ			PPPEILHGEHTPSHODNFSPGQEVFYSCEPGY
i		1				DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF
Ì	1	1	1			LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL
i.		l l			<b> </b>	KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN
				j	,	PPAILNGRHTGTPSGDIPYGKEISYTCDPHPDR
I		{	1			GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE
			i		1	GMTFNLIGESTIRCTSDITIONO WOOTH ROS
			1			LSVRAGHCKTPEQFPFASPTIPINDFEFPVGTS
l	1	İ	1		1	LNYECRPGYFGKMFSISCLENLVWSSVEDNC
ŀ			1	1	Į	RRKSCGPPPEPFNGMVHINTDTQFGSTVNYSC
1						NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII
l		-	Ì	1		SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH
1				ļ		TGPDGEQLFELVGERSIYCTSKDDQVGVWSS
l		1		Į.		PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI
			i i	ł		IRFRCOPGFVMVGSHTVQCQTNGRWGPKLPH
ļ				1		CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY
					[	SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV
		1		1	1	KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC
1				1	1	DEGFRLKGRSASHCVLAGMKALWNSSVPVC
1					!	EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT
	1	1		1		EQIFCPNPPAILNORGITOTPLODIF TOREVOTE
				i		CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS
[		1		1		SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL
1					1	YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS
		1			}	OLDHYCKEVNCSFPLFMNGISKELEMKKVYH
		1	ĺ	[		VGDYVTLKCEDGYTLEGSPWSQCQADDRWD
	1	1		1		PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI
		1				ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP
1	1					RTLQTNEENSRVLP
						HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL
803	2153	A	6574	2	3233	LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY
		}	1			LLLPPLLLLKG/SHAUNLI VAV VLFLANISI
1			1			PWSWA\RVGPAVELALAQVKARPDLLPGWT
						VRTVLGSSENALGVCSDTAAPLAAVDLKWE
				1		HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL
1						TAGAPALGFGVKDEYALTTRAGPSYAKLGDF
				1		VAALHRRLGWERQALMLYAYRPGDEEHCFF
1				1		LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT
						RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA
1				(		GLCGEDYVFFHLDIFGQSLQGQGPAPRRPW
				1		GLUGEDI VILULDILOGOLQUQUI AI ARI
1		1		1		ERGDGQDVSARQAFQAAKIITYKDPDNPEYL EFLKQLKHLAYEQFNFTMEDGLVNTIPASFH
1	1	1	1		1	TEST VOLVULA VEDENELMELLE VNITVANTH

SEO   D   SEO   D   Met   SEO   D   Met   SEO   D   Met   Seo   Methods   D   Methods   Sequence		_					Amino acid sequence (A=Alanine C=Cysteine,
No. of peptide cold by sequence of peptide color under the color of peptide color of the color o	SEQ ID	SEQ ID	Met	-	1		De A sperie A sid E=Glutamic Acid.
Sequence  13SN   Coation	NO: of		hod	ID NO:		l .	E-Phenylalanine Ge-Glycine H=Histidine.
coulor enrice and polyage correspond to go and the control of the	nuci-	peptide					Interlegian Kell using I = I encine
uence    1914   mg to first ambourd of peptide residue of peptide sequence   peptide sequ	cotide	seq-		USSN			1=180/euclife, A=Lysine, D=Ecounic,
mence soft peptide sequence of peptide sequenc	l .	uence		09/496			M=Metinonnic, N=Assinine S=Serine
residue of peptude sequence products and provide insertion sequence sequenc		1	Į.	914	ng to first	1	Q=Glutamine, K=Arginine, 3-3crine,
## peptide sequence	delies	ì					T=Threonine, V=Valle, w=Tryptophan,
mucleotide insertion  SQUENTICE    DGLL TY/QAVTETLAHGGTV/TDGENITQRMW     NGSFQGYTGYLKIDSSGPRETDFSLWDMDPE     NOARRYVLNYNOTSGELVAVSGRELWPUS     NOARRYVLNYNOTSGELVAVSGRELWPUS     NOARRYVLNYNOTSGELVAVSGRELWPUS     VERYPPDPEKCGFONEDPACNODHLSTLEVLALV     GISLLGLUNSFFTYRMQLEKELASELWAVR     WEDVEPSSLERHLRSAGSRITLSGRGSNYGSL     LTEGGPOYAKATAYKGKLVAVKNYRKR     IELTRKVLFELKHMRDVQNEHLTRFVGACTD     PPNCLITEYCPGRSLQDLENESITLD WMFRY     SI.TNDIVKGMLFLINGACSHGNLKSSNCVV     DGRYLLRIDYGLGESFROLDPEGGHTVYAKK     LUTAPELLRMASPPVRGSQAGDVYSGILLQE     ALRSGYFNVEGLDLSPEGLIDTGGPPR     GIRLTLRKFNENSSINLDNLSSREGGYAN     CLKRGETYQAEAPDSKEILBRVTRGGPPR     PSLALQSHLEELGLIMQRCWAEDPOERPPPC     QIRLTLRKFNENSSINLDNLSSREGGYAN     CLKRGETYQAEAPDSKEILBRVTRGGPPR     PSLALQSHLEELGLIMQRCWAEDPOERPPPC     QIRLTLRKFNENSSINLDNLSSREGGYAN     CLKRGETYQAEAPDSKEILBRVTRGGPPR     PSLALQSHLEELGLIMQRCWAEDPOERPPPC     QIRLTLRKFNENSSINLDNLSSREGGYAN     CLKRGETYQAEAPDSKEILBRVTRGGPPR     PSLALQSHLEELGLIMQRCWAEDPOERPPPC     QIRLTLRKFNENSSINLDNLSSREGGYAN     CLKRGETYQAEAPDSKEILBRVTRGGPPR     PSLALQSHLEEGGVYVTLEDROSTAR     CLKRGETYQAEAPDSKEILBRVTRGGPPR     PSLALQSHLEEGGVYVTLEDROSTAR     CLKRGETYQAEAPDSKIINTPOECHALLY     CLKRGETYQAEAPDS		1		j	residue of	sequence	Y=Tyrosine, X=Unknown,Stop could,
DGILLYIQAVTETLAHGGTVTDGENTIQAMDPE   NGAFRVYLNYNGTSQELVANSGRLINWPIG   NGAFRVYLNYNGTSQELVANSGRLINWPIG   YPPPIPKCGFDNEDPACNQOMLESTLEVLALV   GSLSLLGILVSFFTYRKMQLEKELASELWYL   WEDVEPSSLERH RSAGSAILTSGRGSNYGSL   LTTEGOFQVFAKTAYYKGNLVAVKRVNRKK   RELTRKVLFELKHMBDVQNEHLTRFVGACTD   PPNICILTEVCPRGSLQDLEMESITLDWMFFY   SITNDIVKGMLFLHRAGICSHGNAKSSNCVV   DGRFVLKTIDYGLESFRDLDFEQGHTVYAKK   LWTAFPELLRMASPYRGSQAGDVSFGILQE   IALRSGVFHVEGLDLSFKELIERVTRGEQPFF   PSLALQSHLEELGLMQRCWAEDPQSRPFPQ   QIRLTLRKFNRENSSNILDNILSRMEQVANNI   EELVERTQAYLEEKRKAFALLYQILHSVAE   QLKRGETVQABAFDSVTIYSSDIVGFTLASSA   STPMQVYLLNDLYCTEPAVUDHFDVYKVET   IGDAYMVVSGLPVRNGRLHACEVARMALAL   LDAVRSFRRHRPGPQLRLRIGHTGFVCAGV   VGLKMFRVYLLGERGSTRG   QLKRGETVQABAFDSVTIYSSDIVGFTLASSA   STPMQVYLLNDLYCFFAVUDHFDVYKVET   IGDAYMVVSGLPVRNGRLHACEVARMALAL   LDAVRSFRRHRPGPQLRLRIGHTGFVCAGV   VGLKMFRVYLLGERGSTRG   QUKRGETVQABAFDSVTIYSSDIVGFTLASSA   STPMQVYLLNDLYCFAVUDHFDVYKVET   IGDAYMVVSGLPVRNGRLHACEVARMALAL   LDAVRSFRRHRPGPQLRLRIGHTGFVCAGV   VGLKMFRVYLLGERGSTRG   QUKRGETVQABAFDSVTIYSSDIVGFTLASSA   STPMGVYLLDHACH   STRENGTALT   STRENGT	1	i		1	peptide	l	/=possible nucleotide deterion, /=possible
NRSPGGVTGYLKEDSGDRETDFSLWMDPG NGAFRVUNNYGDQLAVASGKLAWPLG YPPPDIPKCGFDNEDFACNQDHLSTLEVLAJU GSLSLLGILIVSFTPKMQLEKEL SASL WAVR WEDVEPSSLERHLRSAGSRITLSGGSMYGSL LTTEGGFQVYAXTAYYKGNULVAVRAVNRKR IELTRKVLFELKHMEDVQNEHLTRFVGACTOL PPINCIL TEYCPRGSLQDLEMESITLDVMFRY SI.TNDIVKGMLFLHRGAICSHGNLKSSNCVV DGFYLKITDYGLESFRDLDPFDGGHTVYAKK LWTAPELLRMASPPVRGSQAGDVYSFGILL IALRSGYFHVGGLDLSFKEILEVTRGGPPFR PSLALQSHLEELGLLMQRCWAEDPQERPPPG QIRLTIRKFNRENSSNID.DNLSRMEQYANNL EELVEERTQAYLEERKAAALLYQILHSVAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLKRGETVQAABADSTVITYSDIVGFTALSAE QLTVPALLEERGGFELERGDVEMKGKG KYNTYNLLOERGSTRO QLTVPAVLERGGFTELERGDVEMKGKG KYNTYNLLOERGSTRO QLTVPAVLERGGFTELERGDVEMKGKG QLTVPAVLERGGFTGEGEVAYDAANSHLEET REAELKEYNALHGREFTERHINYBEVGEVGEK QLTVPEREALRHAGEKFEFELGGFELG QLTVPEREALRHAGEKFEFELGGFELGGFT AGGGLLTPDAQKGGFTGSGEVKTQELSOPR SHTSLKDELSDVSQGGSKATTPASTANSDV TIPTDTPLKEERGFFVXVTDATNSTGSISKHEV QVAQETTRNYTGSAENEKSEVQAIESTYPL AGGGLLTPDAQKGGFTGSGEVKTQELSOPR SHTSLKDELSDVSQGGSKATTPASTANSDV TIPTDTPLKEERGFFVXVTDATNSTGSAENHEEREELKAE REAELKEYNALNIVANDLIAKAPDENTESL FELSSAGSGLIGDVDEGADALGMGREVENLI LENGQLSGYKGSSTFYKGENAKAPDENTESL FELSSAGSGLIGDVDEGADALGMGREVENLI LENGQLSGYKGVTGVTSVKKRSSTLSQLF QGEKSKSTPKGESTETASLASRERGERGEVQAG GKRSKNSSTPYKGURAKTVK ARPPAMBEKKRSSWQFFSKLYGE VKAHVQKEDGRVVYTRFLEERSSSNTTK KPEPPVNLKYNATTSVKKRSSTLSQLSD GCKKMKNLPYVTYSVKKRSSTLSGLSGTVQGS QVDKASLCGSMTSNSSAGTDSLLGGGTVVGG SAGGVYGGASTPYGDVAGL GELSSLVWICTSTHSATKVLIDAVQPGHALD TGCSKQGRAGDSSDLKLDGGLEKEQQKEKNUN QGELSSLVWICTSTHSATKVLIDAVQPGHALD TGCSKQGRAGDSSDLKDQGLEKEQQKEKNUN QGUYTH-WYTDPLGVQFGEAUS QGUYTH-WYTDPLGVQFGEAUS QGUYTH-WYTDPLGVQFGEAUS QGUYTH-WYTDPLGVQGEAUS QGUYTH-WYTDPLGVQFGEAUS QGUYTH-WYT	Į.			1	sequence		nucleotide insertion
NGAFRYUNYNGTSQELAVSGRKLINWPL  YPPEDPIKCGFUNEDPACKOPOHLSTLEVLALV GSLSLLGHLVSFTYRKMQLEKELASELWYN WEDVEPSSLERH RSAGSLTLSKORGSNYOSL LTTEGOFOVFAKTAYYKGNLVAVKRVINKK HELTRKVLFELKHMDVONEHLTRFVGACTI PPNICHTEYCPFGGLQDLENESITLDWMFRY SILTDDIVKGMLFHRBGACSHORLKSSNCVV DGRFVLKITDYGLESFEDLDFEOGHTVYAKK LWTAPPLLRMSPVRGSQAGDVSFGILQE HALSGVFHVEGLDLSPKEHERVTRGEOPPF PPLALQSHLEELGLMORCWAEDPOFRPPF ORTHER STRONG VTLLADLINTERSUNDLLSRMEQVANILL EELVEFRTQAYLEFRKRAEALJOHENSVA UCJKMBRYCLFGDTVNTASRMESNGLAIKH EELVEFRTQAYLEFRKRAEALJOHENSVA UCJKMBRYCLFGDTVNTASRMESNGCALKH LIDAYMVVSGLPVRNGRHACEVARMALA LIDAYMVVSGLPVRNGRHACEVARMALA LIDAYMSFERNHPPGOLURLIGHTGPVCAGV VGLKMBRYCLFGDTVNTASRMESNGCALKH HASSETRANIPEGGFELERGDVEMKGKG KVRTYMLLGERGSSTRG UCJKMBRYCLFGDTVNTASRMESNGCALKH HASSETRANIPEGGFELERGDVEMKGKG KVRTYMLLGERGSSTRG UCJKMBRYCLFGDTVNTASRMESNGCALKH HASSETRANIPEGGFELERGDVEMKGKG KVRTYMLLGERGSSTRG UCJKMBRYCLFGOTVNTASRMESNGCALKH LSVETYANILEGGGFELERGDVEMKGKG KVRTYMLLGERGSSTRG UCJKMBRYCLFGOTVNTASRMESNGCH LVAVLEBLSVGTOGLELKARNOSILEE LVAVLEBLSVGTOGLELKARNOSILEE LVAVLEBLSVGTOGLELKARNOSILEE LVAVLEBLSVGTOGLELKARNOSILEE RAEKEYNALIGHTFEMINYMEHLERDING UCJTVBERKARLRKHEKFEFFEDSOGCEKK DLQTRVEBGGFELTERJDSVKGCESCATTPSCOWKFGELSOFR KHISLKDELBOYSOGGSKATTPSCOWKFGELSOFR SHTSILKDELBOYSOGGSKATTPSCOWKFGELSOFR KHISLKDELBOYSOGGSKATTPSCOWKFGELSOFR KHISLKDELBOYSOGGSKATTPSCOWKFGELSOFR UCJTVBERGEFFKVTDAPHNSEISKHEV UCJGELERAVKGNALHIGHTFEMINYMEHLERD UCJGELERAVKGNALHIGHTFEMINYMEHLERDING UCJGELERAVKGNALHIGHTFEMINYMEHLERDING UCJGELERAVKGNALHIGHTFENIT LENTQLETTNNSTGSAENEESEVQAIESTPEL DMKKDLSGYKGSSTTYGGENARDENTESL FEELSSAGSGLIGDVBGADLLGGREVENI LENTQLETTNNSTGSAENEESEVGARNESINGF UCJGELERAVKGNALHIGHTFENIT RKHPUTTSVKKRSSTLIGGTLV UCJGELERAVKGNALHIGHTFENIT RKHPUTTSVKKRSSTLIGGTLV UCJGELERAVKGNASHLYTTSVKKRSSTLIGGTLV UCJGELERAVKGNASHLYTTSVKKRSSTLIGGTLV UCJGELERAVKGNASHLYTTSVKKRSSTLIGGTLV UCJGELERAVKGNASHLYTTSVKKRSSTLIGGTLV UCJGELERAVKGNASHLYTTSVKKRSSTLIGGTLV UCJGELWSTYTARETAGRAGRATTRVE MARVLMERROYSERGERGVROWSHYRDVAGL UCJGELSSLVWINGELDSILLSTLICHTAGNACH UCJGELSVVYISSLOGGENITATERSCOWCH UCJGELSSTLOWAGLES		<del> </del>	<del> </del>	+			DGLLLYIQAVTETLAHGGTV1DGENITQKMW
SPEPDIPKCGFONEDPACNQOHLSTLEVILAY	i						NRSFQGVTGYLKIDSSGDRETDFSLWDMDPE
GSLS.L.GILVSFFTYRKMOLEKELASELWRYN WEDVEPSSLERHIRASGASITLTSCRGSNYOSL LTTEGOPGVPAKTAYYKONLVAVKRVNRKR IELTRKVLFELKHMEDVONEHLTRFVGACTD PFNICLTEVCPRGSLQDLEMESITLDWMFRY SLTNDIVKGMLELHRAGICSHONLKSSNCVV DGRFVLKITDYGLESFEDLDFEOGHTVYAKK LWTAPPLLRMASPVRGSQAGDVYSFGIILQE IALRSGVFHVEGLDLSPKEILERVTRGEOPFPF PSLALQSHLEELGLMQRCWAEDPOPERPFP QIRLTLRKFNRENSSNILDNLLSRMEQVANNL EELVERTQAYLEEKRKAEALLYOLDFEDVFKVET IGDAYMVVSGLPVRNORRHACEVARMALA LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPMSTEDGSCOWKFQELSCRB RAELKREYNALHGRITTEMINNYMEHLER LVAVLENLDSVEGGSTATTPASTANSDVA TIPTTDTPLAGENEGFVKVTDAPHXSEISCHEPL AGDGLTTDSVGGGSTATTPASTANSDVA TIPTTDTPLAGENEGFVKVTDAPHXSEISCHEPL QVAQETRNNTGSAENEEKSEVOAIRESTPEL DMKKDLSGVKGSSTTTKGENKAPDRNTESL FEILSSAGSGLIGDVDEGADLLGMGREVSDLI LENTGLLETINALNIVRNDLLAKVDELAKV QVAQETRNNTGSAENEEKSEVOAIRESTPEL DMKDLSGVKGSSTTYGEBKAADRENGEN ARREDDARGKAADDOBDEDTARGREPTEVE MARVLMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW GGENKMNLPVYVARFISHVTFSVKRRSSTLSGUS GOKKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHT GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHT GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHSUCMTVVARFISHVTFSVKRRSS	Į.	l	1				NGAFRVVLNYNGTSQELVAVSGRKLNWPLG
GSLS.L.GILVSFFTYRKMOLEKELASELWRYN WEDVEPSSLERHIRASGASITLTSCRGSNYOSL LTTEGOPGVPAKTAYYKONLVAVKRVNRKR IELTRKVLFELKHMEDVONEHLTRFVGACTD PFNICLTEVCPRGSLQDLEMESITLDWMFRY SLTNDIVKGMLELHRAGICSHONLKSSNCVV DGRFVLKITDYGLESFEDLDFEOGHTVYAKK LWTAPPLLRMASPVRGSQAGDVYSFGIILQE IALRSGVFHVEGLDLSPKEILERVTRGEOPFPF PSLALQSHLEELGLMQRCWAEDPOPERPFP QIRLTLRKFNRENSSNILDNLLSRMEQVANNL EELVERTQAYLEEKRKAEALLYOLDFEDVFKVET IGDAYMVVSGLPVRNORRHACEVARMALA LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPGOLGLRIGHTGPVCAGV VGLKMPRVCLPGDTVNTASRMESNGEALKI LDAVRFFRRHRPMSTEDGSCOWKFQELSCRB RAELKREYNALHGRITTEMINNYMEHLER LVAVLENLDSVEGGSTATTPASTANSDVA TIPTTDTPLAGENEGFVKVTDAPHXSEISCHEPL AGDGLTTDSVGGGSTATTPASTANSDVA TIPTTDTPLAGENEGFVKVTDAPHXSEISCHEPL QVAQETRNNTGSAENEEKSEVOAIRESTPEL DMKKDLSGVKGSSTTTKGENKAPDRNTESL FEILSSAGSGLIGDVDEGADLLGMGREVSDLI LENTGLLETINALNIVRNDLLAKVDELAKV QVAQETRNNTGSAENEEKSEVOAIRESTPEL DMKDLSGVKGSSTTYGEBKAADRENGEN ARREDDARGKAADDOBDEDTARGREPTEVE MARVLMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW ARRUMERNQYRERLMELQEAVR WTHW GGENKMNLPVYVARFISHVTFSVKRRSSTLSGUS GOKKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHT GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHT GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHVTFSVKRRSSTLSGLIGHTVG GGENKMENLPVYVARFISHSUCMTVVARFISHVTFSVKRRSS		1		1	1		YPPPDIPKCGFDNEDPACNQDHLSTLEVLALV
WEDVEPSILERHIRSAGELTLS CROSSNOSL LTTEGGFQVAKATAYYKGNLVAVKRVNRKR IELTRKVLFELKHMRDVQNEHLTREVGACTD PPRICLI TEVCFGGSL,ODLENESITLDWMFRY SITNDIVKGMLFLHNGAICSHONLKSSNCVV DGRPVLKITDVGLESRDLDFGHTVYAKK LWTAPELLRMASPPVRGSQAGDVYSFGILQE IALRSGVPHVEGLDLSPKEIELBEVTRGGOPPFP QRATTARFANENSNILDHLSIRMEQVANNL EELVEERTQAYLEEKRKAEALLYQUIPHSVAE QLKRGETVQAEADSVTIVFSDVGFTALSAE GURGETVQAEADSVTIVFSDVGFTALSAE STFMQVVILLNDLYTCFDAVIDNEDVYKVET IGDAYMVVSGLPVRNGELHACVARMALAL LDAVRSFRIRHRQEQLRLRIGHTGPVCAGV VGLKMPRYCLFODTVNTASRMESNGEALKI HLSSETKAVLEEFGGFELERGDVEMKGKG KVRTYWLLGERGSSTRA KVRTYWLLGERGSSTRA KVRTYWLLGERGSSTRA MSERVSGLAGSIYREFERIJVRYDEEVYKELD LVVAVLENLDSVFAQDGEHQVELELRDDNE QLTTQYEEKALRKHAEEKFEFGDSGEKK DLQTTQYEEKALRKHAEEKFEFGDSGEKK DLQTTQYEEKALRKHAEEKFEFEDSGEKK DLQTTQYEEKALRKHAEEKFEFEDSGEKK DLQTTQYEEKALRKHAEEKFEFEDSGEKK PAGDELLTPDAQKGGETFOSEQWKFQELSOPR SHTSILXDELSDVSGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISCHEV QVAGETRNYSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTTYKGIENKAFDROTESSL FEELSSAGSGLIGDVEGGAUTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISCHEV QVAGETRNYSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTTYKGIENKAFDROTESSL FEELSSAGSGLIGDVEGGAUTPAGELSOPR SHTSILXDELSDVSGGSKKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISCHEV QVAGETRNYSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTTYKGIENKAFDROTESSL FEELSSAGSGLIGDVEGGAUTPAGRKRETESSL FEELSSAGSGLIGDVEGGAUTPAGRKRETESL FEELSSAGSGLIGDVEGGAUTPAGRKRETESL FEELSSAGSGLIGDVEGGAUTPAGRKRETESL GORKKKADPLOSEDVERVENDERFREVE MARVLMERNOYKELMELGEAVKWTEMIR ASRENAMQEKKRSSINOFFSRLFSSSSNTTK KREPPYNLKYNAPTSNTTYBKLEEELKA RAEAEDARGKAKDDDDSDDTTAGRKRRIKUVCA VGVNLSGGKTTROGSVVGSNTYKDVAGLD TEGSKGKASGSSLDKLDELAGEVYRQ VKAHVVKEDGEVQAFGVSLPGYKGVTNG VKAHVVKEDGEVQAFGVSLPGYKGVTNG GGEKKMKNLPPYVLEPLDEKDTSMVKUNCA GGEKGKTASTSTTGASSVPTYDVAGEL SCYDENVTYAEELATATROHLORAV GGEKGTATRSTTGASSVPTYDVAGEL SCYDENVTYAEEAATRATRUDAVQPOTUDIS GTGYTTENVTPDLGVVGPDELSPVYGSSND SDAYKGDISVIPEGOLVAEEAGKKSLLPT MWGAGGGGCTURGPRISILKGT	}	1		1		ſ	GSLSLLGILIVSFFIYRKMQLEKELASELWRVR
LTTEGGFQVFAKTAYYKGNLVAVKRYNRK IELTKRVIFELKHMRDVQMEHLTRFVQACTD PPMICIL TEYCFRGSLQDLENESITLDWRFY SI.TNDTVKGMLFHNGAUGSHONLKSSNCVV DGRFVLKITDYGLESFRDLDFEQGHTVYAKK LWTAPELLRMASPPVRGSQDYSSGILLQE IALRSGYPHVEGIDLSPKEIERVTRGEQPFPR PSLALQSHEBELGLMQRCWADYSSGILLQE IALRSGYPHVEGIDLSPKEIERVTRGEQPFPR PSLALQSHEBELGLMQRCWADYSGILLQE IALRSGYPHVEGIDLSPKEIERVTRGEQPFPR PSLALQSHEBELGLMQRCWADYSGILLQE IALRSGYANNL EELVEERIQA*TLEEKIKAEALLYQLIPHSVAE QLKRGETVQAEAFDSYTITFSDIVGFTALSAE STFMQVVTLLNDLYTCFDAVIDNFDYTKVFT IGDAYMYNSGLVFVNRGH.HACEVARMALAL LDAVRSFRRRRPQEGLRIGHTGPVCAOV VGLKMFRYCLFGDTVNTASRMESNGEALXH LDAVRSFRRRRPQEGLRIGHTGPVCAOV VGLKMFRYCLFGDTVNTASRMESNGEALXH HLSSSETKAVLEEFGGFELELRGDVEWKGK KVRTYWLLGEFGGSTRG KVRTYWLLGEFGGFELELRGDVEWKGK KVRTYWLGEFGGSTRG LOTT VALENDE LOTT VALEN	1	1	1	i			WEDVERSSLERHLRSAGSRLTLSGRGSNYGSL
IELTRKVLFELKHMRDVQKEHLTRRVAGACID PPRICLITEYCPROSLQQLENSTILDWMFRY SI.TNDIVKGMLFLHNGAICSHGNLKSSNCVV DGRPVLKITDYGLESTRDLDGHTVYAKK LWTAPELLRMASPPYRGSQAGDVYSFGILQE IALRSGVFHVEGDLSPKPELIERVTRGEQPPRFQ QIRLTLRKFRRENSSNILDNLSRMEQYANNL ELLVEERTQAYLEERKAEALLYQILFHSVAE QLKRGETVQAEAFDSVTIVFSDIVGFTALSAE STFMQVVILLNDLYTCFDAVJUNFDVVKVET IGDAYMVVSGLPVRNGRLHACEVARMALAL LDAVRSFRIRHRPQGCLLRLRGHTGPVCAGV VGLKMPRYCLFGDTVNTASRMESNGEALKI HLSSETKAVLLEFEGGFELELRGDVEMKGKG KVRTYWLLGERGSSTRG  DAFGRPPVELTWELEGGVYQEEPGGSGAV MSERVSGLAGSTYREFERLIVTYDEEVYKELD LVVAVLENLDSVFADQDEPGVELELRDDNE QLTQYEREKALRKHAEEKFIEFEDSQEGEKK DLQTTYESLESQTTQLELKANNYADQISILEE REAELKEVNALHQRITEMIENYMEHLERT KLHQLSGSDQLESTAHSRIRKERNISLIGHLP AGDGLLTPDAGKGETTOSSCWKFQELSQFN SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPITDTPLKEENGFVKVTDAPNSEISKHEV QVAQETRNVSTGSAEREKSEVQAIEESTPEL DMDKDLSGYKGSTFTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLIGMGREVENLI LENTGLETKKALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRAA RAEADARQKKADDIDSDIPLAGRKEFTEVE MARVLMERNQYKERLIMELQEAVRWTMIR ASRENS-MQEKKRSSIWQFFSRLFSSSNTTK KPEPPYNIK,YNAPTSHYTTSVKKRSSTLSQLP GDKSKAATDFLSET-LASLASRREQKREQTYRQ VKAHVQKEDGRVAGFWSTPKSULDELQEAVRYTMIR ASRENS-MQEKKRSSIWQFFSRLFSSSSNTTK KPEPPYNIK,YNAPTSHYTTSVKKRSSTLSQLP GDKSKAATDFLSET-LASLASRREQKREQTYRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKAHVQKEDGRVAGFWSTPKYRQYTRQ VKASTPKTHDAVQFGMILDS FTVCNSHVLCIASVPGARETDYPAGEDLESG QVDKASLCGGRMTSNSASTEDLLGGTVVGC SAEGVTGAATSPSTNGASPYMDLPPFMAEN SEVDENVPTAEEATEATEGARGSAEDTVDIS GTGYTTENTYDPLGNQGPDLSPQXCKKNQ ESSLVWICTSTHALTXVLIIDAVQPGMILDS GTGYTTENTYDPLGNQGPDLSPQXCKKNG SEVDENVPTAEEATEATEATEGAGSAEDTVDOSD SDAYKDQISVPREQUVRRECHSTRLKU SILSJVHVKGTLVALADGTLAIFHRGVDGW DLSNYHLLDLGPHHSIEKGHTVVHDKVWCG VRNKTYVOPKAARLEKSSPAHPRRSSQURQ LAWGGGGWSRILDDELLALTHAHTYOHOGW DLSNYHLLDLGPHHSIEKGHTVATDKWWCCC VRNKTYVOPKAARLEKSSPAHPRRSSQURQ	1			1			LTTEGOFOVFAKTAYYKGNLVAVKRVNRKR
PPNICIL TEYCPROSLODILENESITLD WIRTY SITNDIVKGMICHINGAICSINGNLKSSNCVV DGRFVLKITDYGLESFROLDPEQGHTVYAKK LWTAPELLRMASPPVRGSQAGDVYSFGIILQ IALRSGVFHVEGIDLSPKEIBERVTRGEQPFPR PSLALQSHLEELGILJMQRCWDQFPRFP PSLALQSHLEELGILJMQRCWANNL EELVEERTQAYLEEKRKARALVIJUFHSVAKE QLKRGETVQAEAFDSVTIVFSDIVGFTALSAE STFMQVVTILNDLYTCFDAVIDNFDVTKVET IGDAYMVVSGLVENGRIHACEVARMALAL LDAVRSFRIRHRVQEQILRIGHTGPVOYAKGK KVRTYWLLGERGSSTRG WKRTYWLLGERGSSTRG DAPGRPVRLPTIMELEGGVVYQEEPGGSGAV MSERVSGLAGSIYEFFRILVRYDEEVVYKELIP LVVAVLENIDSVFAQDQEHQVELELLRDDNE QLITQYEREKARLRHAEEKFEDSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEYNAHAIRHAITEMFENSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEYNAHAIRHAITEMFENSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEYNAHAIRHAITEMFENSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEYNAHAIRHAITEMFENSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEYNAHAIRHAITEMFENSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEKSMAHAIRHAITEMFENSQEQKK DLQTRVESLESGTRQLELKAKNYADQISILEE REALKEKSMAHAIRHAITEMFENSQEQK TIPTDTPLKENBGFVKVTDAPNNSEISKHIEV QVAQETRNVSTGSAEAMEKSSEVQAIBSTPEL DMDKDLSGYKGSSTPKGGENACHAIRHAITE LENTQLLETKNALINVKNDLLAKVDELTCEK DVLQGELEAKVQAKKLEENRELEELRKA RAEAEDARGKAKDDDDSDITTAGRRRPTRVE MARVLMERNGYKERLMELGEAVRWTEMIR ASRENFAMQEKKRSSINOFFSRLFSSSNTIK KPEPPYNLKYNAPTSNTTPSVKKRSSTLSOLP GDKSKAFDFLSEETEASLASRREQKREYRQV VKAHVQKEDGRVQAFGWSLYGKYRQVX VKAHVQKEDGRVQAFGWSLYGKYRQVX VKAHVQKEDGRVQAFGWSLYGKYRQVX VKAHVQKEDGRVQAFGWSLYGKYRQVX VKAHVQKEDGRVQAFGWSLYGKYRQVX VKAHVQKSDGRVQAFGWSLYGKYRQVX VKAHVQKSDGRVQAFGWSLYGGTVAGG SAEGOVTGAATSTNTAGASPYMDAPPEMEAFN SEVDENNYTAEBATEATEGNAGSAETVADG GTGYTTEHVTPDLGVVIPPELSPYVQSSND SDAYKDQISVJRNEQDLVREAQKMSKLLPT MWLGAQNGCVYNSLOGLTALFHRGYDGQW DLSNYHLGLGPHISIKCHATVYHDKWCWG URNKYYVQKALALDGTLAIFHRGYDGQW DLSNYHLGRPHISIRCHATVYHDKWCWG URNKYYVQFKAMKLEKSFOAHPRKSOQVRQ LSNYHVLOGRUPSRILLADGTLAIFHRGYDGQW DLSNYHLLGRERSFOAHPRKSOQVRQ LSNYHVLOGRUPSRILLADGTLAIFHRGYDGQW DLSNYHLLGLGRPHISIRCHATVYHDKWCWG URNKYYVQFKAMALADGTLAIFHRGYDROW	1			ł	1	ĺ	IELTRKVLFELKHMRDVQNEHLTRFVGACID
SLINDIVKGMLEH.NAGACSHGNLKSSNOVV DGRFVLKITDYGLESFRDLDPEGGHTVYAKK LWTAPELLRMASPPVRGSQAGDVYSFGILLQE IALRSGVFHVEGLLJSKERVTRGOPPFR PSLALQSHLEELGLLMQRCWAEDPQERPFO QIRLTLRKFNRENSSNILDISRMEQVANNL EELVEERTQAYLEEKRKABALLYQULPHSVAE QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE STFMQVVTLINDLYTCFDAVIDNFDVTKVET IGDAYMVVSGLPVRNGRLHAGEVARMALAL LDAYRSFRIRHPQFORLRIGHITGFVCAGV VGLKMPRVCLFGDTVNTASSMESNGEALKI HLSSIETKAVLEFRGGFLRRIGHITGFVCAGV VGLKMPRVCLFGDTVNTASSMESNGEALKI HLSSIETKAVLEFRGGFLRRIGHTGFVCAGV VGLKMPRVCLFGDTVNTASSMESNGEALKI HLSSIETKAVLEFRGGFLRRODVEMKGKG KVRTYWHLIGERGSSTRG DAFGRPPVRIPTMELEDGVVYQEEPGGSGAV MSERVSGLAGSIYRFFERLIVRYDGEPGGSGAV MSERVSGLAGSIYRFFERLIVRYDGEVVKELP LVVAVLENLDSVAQDODEHOVELELLRDDNE QLITQYERSKALRKHAEEKFIEFDSQEQEKK DLQTRVESLESOTROLGLKANYADOISILEE REAELKKEYNALHQRHTEMIFNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFIPA AGGGLLTFDAQKGGGTFGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPFNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAHESTPEL DMDKDLSGVKGSSTPTKGENKAFPRNTESL FFELSSAGSGLIGDVDEGADLLGROREVENLI LENTOLLETKNANIVNIALKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEELRAK RAEAEDARGKAKDDDBFTAGRKEFTIVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSINPFTAGRKFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSINPFTAGRENKREPT VKAHPQKERSSSVAGVSKROKTROGVSVATOKAGLD GKSKAFTDFLSEETASLASRRGROREQYRQ VKAHPQKERGSRVAGNSLPCKYRQVTNG QENKMKNLPYPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVASTYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQCKELKNQ USCASHONSASPTNGASPYMDKYAGLD FTVCNSHYLCTASVPGARETDYPAGEDLESEG QVDKASLGCSMTSNSSAETDSLLGGTVVGG SAEGVTGAATSPSTNGASPVMGPKARAND SDAYKDQISVLTGTSTHATKUTDAVQPGONILDS FTVCNSHYLCTASVPGARETDYPAGEDLESEG QVDKASLGCSMTSNSSAETDSLLGGTVVGG SAEGVTGAATSPSTNGASPVMGPKRAFEND SVDENNHLICLASVPGARETDYPAGEDLESEG QVDKASLLGCSMTSNSSAETDSLLGGTVVGG SAEGVTGAATSPSTNGASPVMGPKRAFEND SVDENNHLICLASVPGARETDYPAGEDLESEG QVDKASLGCSMTSNSSAETDSLLGGTVVGG SAEGVTGAATSPSTNGASPVMGPKRAFILDS SVDENNHLICLASVPGARETDYPAGEDLESEG QVDKASLLGCAMSSLLDT MWLGAQAGCCTVHSSVAAVARKCLHSIKLKD SILSIYHVKGGVVASILLDSTLAPHARTOYDLC UN AVVGGVVASILLDSTLAPHARTOYDLL						J	PPNICIL TEYCPRGSLODILENESITLDWMFRY
DGRFVLKITDYGLESFRDLDPEGGHTVYAKK LWTAPELLRMASPPVRSGQAGDVYSFGILQE IALRSGVFHVEGLDLSPKEIERVTRGOPPFR PSI.ALQSHLEGLIGLIMQRGWAEDPQERPPFQ QIRLTLRKFNRENSSNILDNLLSRMEQYANNL EELVEERTQAYLEEKRKAEALLYQILPHSVAE QLKRGETVQAEAFDSVITYSDIVOFTALSAE STEMQVVTLLNDLYTCFDAVIDNFDVTKVET IGGAYMVVSGLPVRNGRHACEVARMALAL LDAVRSFRIRHRPQEQLRLRIGHTGPVCAGV VGLKMPRVCLFGDTVNTASRMESNGEALKI HLSSIETKAVLEEFGFFELELRGDVEMKGKG KVRTYWILGEGGSSTRG VGLKMPRVLFGDTVNTASRMESNGEALKI HLSSIETKAVLEEFGFFELELRGDVEMKGKG KVRTYWILGEGGSSTRG VGLKMPRVLFBEDVGVPGLEEFGGSGAV MSERVSGLAGSIVREFEBLIVRYDEEVVKELD LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQVEREKALRKHAEEKFFFEDSQEQEKK DLQTRVESLESGYTGCLELKAENYADQISILEE REAELKKEYNALHQRHTEMHINYMEHLERT KLHQLSGSDQLESTAHSRKKERPISLGIFPLP AGDGLITTDAQKGGETTGSEQWKYGLSOPR SHTSLKOBLSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPPKSEISKHEV QVAQETERNYSTGSAENESVQAIBSTPEL DMDKDLSGYKGSSTPTKGIENKAPRONTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETTENALNIVKNDLLAKVDELTCEK DVLQGELEAVKQAKI KLEEKNRELEELRKA RAEAEDARGKAKDDDDSDITAGRKFTRVE MARVLMERNQYKERLMELQEAVWTEMIR ASRENPAMGEKKRSSIWGFFSRLSSSSNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSLSQLP GDKSKAFDG SEPT SEETEKALSRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPYPVYLRPLDEKDTSMILWG QGENKMKNLPYPVYLRPLDEKDTSMILWG VKAHVQKEDGRVQAFGWSLKPQKPQKDLNG VKAHVQKEDGRVQAFGWSLKPQKPGLSOPS GDKSKAFDGSSVYOGSVYVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ VKAHVQKEGGRVQAFGWSLKPGLEDLESG QVDKNSALLCHANGAVGEDLESG QVDKNSALLCHANGAVEDLESGLENGEN GGGNTSNSASGTDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMOKRELHSKLKD SLSIVHVKGIVLVALADGTLAIPHRGVDGQW DLSNYHLLDLGRPHINISTALGMAGSPETNVDIS SDAYKDQISVLPREQDL VREEAQKMSSLLPT MWLGAQNGCLYVINSVAQAVRKCLHSKLKD SLSIVHVKGIVLVALADGTLAIPHRGVDGQW DLSNYHLLDLGRPHINISTRLYPHAHTYOPLLQ SAVKGVVSVISILDSTLAIPHRESSVRO UNDENNYHLDLGRPHINISTRLYPHATTYOPLL		ļ		1		ì	SI TNDIVKGMLFLHNGAICSHGNLKSSNCVV
LUTAPELLRMASPYVRGSQAGDVSFGIILQE IALRSVEYHVEGLLISKELIERVTRGEQPPR PSLALQSHLEELGLLMQRCWARDPOGERPPG QIRLTLRKFNRENSSNILDISRMEQYANNL EELVEERTQAYLEEKRKAEALLYQILPHSVAE QLKRGETVQAEAFDSVTIYFSDIVGFALSAE STFMQVVVILNDLYTCFDAVIDNFDVTKVET IGDAYMVVSGLPVRNGRIHACEVARMALAL LDAYRSFRIRHPQFOGLIRLRIGHTGFVCAGV VGLKMPRYCLFGDTVNTASRMESNGEALNXI HLSSUETKAVLEERGGFELLRGDVEMKGKG KVRTYWLLGERGSSTRG  BO4 2154 A 6585 2 3837 DAFGRPFVRIPTMELEDGVVYQEEPCGSGAV MSERVSGLAGSIYREFERLIVRYDEEVVKELIP LVVAVLENLDSVFAQDQEHQVELELRDDNE QLITQYEREKALRKHAEKFIEFEDSQEQEKK DLOTRVESLESGTRQLELKARNYADQISILEE REAELKEYNALHORHTMIYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPL AGDGLLTPDAQKGGETBEQWKFQELSOPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRINNSTGSAENEEKISEVQAILESTPEL DMDKDLSGYKGSSTPTKGIENKAFRNTESL FEELSSAGGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELE AVVQAKLKLEENRELEEELRKA RAEAEDARQKAKADDDSDPTAQRKFTRVE MARVLMERNQYKERLMELOGAVRFTRWE MARVLMERNQYKERLMELOGAVRFTRWE MARVLMERNQYKERLMELOGAVRFTRWE MARVLMERNQYKERLMELOGAVRFTRWE MARVLMERNQYKERLMELOGAVRFTRWE MARVLMERNQYKERLMELOEAVRFTRWE MARVLMERNGYSERLSSENGKRQVRQ VKAHVQKEDGRVQAFGWSLPQKYQVTNG QCENKMKNLPYVYLRJEREDTSMIKJWCA VGVNLSGGKTRDGGSVVGASVYRQVTNG QCENKMKNLPYVYLRJEREDTSMIKJWCA VGVNLSGGKTRDGGSVVGASVYRQVTNG QCENKMKNLPYVYLRJEREDTSMIKJWCA VGVNLSGGKTRDGGSVVGASVYRQVTNG QCENKMKNLPYVYLRJERGELISEED GOVDKASLGCSMTSNSSAETDSLLGGITVVGG SAEGVTGAATSPSTNGASPVMCKPEMEAEA SEVDENVYTAAEATERGNAGSAEDTVDIS GTGVYTEHYTTDPLGVQOPEDLSPVYQSSND SDAYKDQISVLPNEDDLVQPDLSPVYQSSND SDAYKDQISVLPNEDDLVQPDLSPVYQSSND SDAYKDQISVLPNEDDLVQPDLSPVYQSSND SDAYKDQISVLPNEDDLAGATHVYGLG SAEGVTGAATSPSTNGASPVMCKPEMEAEA SEVDENVYTAAEATERGNAGSAEDTVDIS GTGVYTEHYTTDPLGVQOPEDLSPVYQSSND SDAYKDQISVLPNEDDLAGATHVYGLG SAEGVTGAATSPSTNGASPVMCKPEMEAEA SEVDENVYTAAEATERGNAGSAEDTVDIS GTGVYTEHYTTDPLGVQOPEDLSPVYQSSND SDAYKDQISVLPNEDDLAGATHRYDHQUDQ SLSNYHLLDLGRPHINISRCHTVYHDKVWCG YENKIYVYQPKAMKIEKSFDAJFRESSQVRQ USLSNYHLDLGGFTINKSFSCARG	1			1		<b>\</b>	DGREVI KITDYGLESFRDLDPEOGHTVYAKK
IALRSGVFHVEGLDLSPKEILERVTREGEPPFR PSILALGSHLEELGILINGORGWAEDPOERPFPQ QIRLTLRKFNRENSSNILDNLLSRMEQYANNI EELVEERTOAYLEERKAELIYQILPHSVAE QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE STEMQVVTLLNDLYTCFAUNDINFDVYKVET IGGAYMVVSGLPVRNGRLHACEVARMALAL LDAVRSFRIRHBPGEQLRLRIGHHFOPCAGV VGLKMPRYCLFGDTVNTASRMESNGEALWI HLSSETKAVLEEFGGFELELRGDVEMKGKG KVRTYWLLGERGSSTEN  804 2154 A 6585 2 3837 DAPGRPPVRLPTMELEDGVVYQEEPGGSGAV MSERNSGLAGSIYREFERELIVRYDEEVVKELP LVVAVI.ENLDSVFAQDQEHQVELELLRDDNE QLITQVEREKALKGAGSIYREFEREFEDSQCGEK DLQTRVESLESGTRQLELKARNYADQISILEE REAELKKEYNALHORHTEMHINYMEHLERT KLHQLSGSDQLESTAHSRIKRERPISLGIFPLP AGDGLLTTDAQKGGETTGSEQWKYGELSOPR SHTSLKDELSDVSQGGSKATIPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHEV QVAQETENNYSTGSAENESVQAIESTPEL DMDKDLSGYKGSSTPTKGIENKAFRNTESI FELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLLAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAFAEDBARGKAKDDDDSDIPTAQRKRFTRVE MARVLMERRQYKERLMELQEAVRTEMR ASRENPAMGEKRSSIVMFFSRLTSSSSNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GDKSKAFDFLSETETSALSSNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GDKSKAFDFLSETETSALSSNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GDKSKAFDFLSETETSALSKNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GDKSKAFDFLSETETSALSKNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GOKSKAFDFLSETETSALSKNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GOKSKAFDFLSETETSALSKNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GOKSKAFDFLSETETSALSKNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLF GOKSKAFDFLSETETSALSKNTIK KPEPPVNLKYNTHERDFROMFPERAFAN SEVDENVPTABEATETETGMAGSAEDVGNILDG GGVYTENVFTDPLGVQIPEDLSETG GVYTENVFTDPLGVQIPEDLSPCT SAEGVTGAATSPSTNGASPVMDKPPEMEAFN SEVDENVPTABEATETETGMAGSAEDVANSLDF MWLGQQGCKYNTSHLSCARAFTDSLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAFN SEVDENVPTABEATETETGMAGSAEDVANSLDF MWLGQQGCLYVINSVANDRACLHSIKLKD SILSIVHVKGIVLVALADGTLAIPHRGVDGQW DLSNYHLLDLGRPHINISKGRTVAHDKVWCG YRNKIVVYOPKAMKIEKSFDAHFRESQVRQ DLSNYHLLDLGRPHINISKGRTALHYHAHTYQHLQ UNDUSNYHLDLGRPHINISKERFESQVRQ UNDUSNYHLDLAGRTHINISKERFESQVRQ LAVVGKUSWYSIRLDSTRLHYHAHTYQHLQ			1	l.	1	ł	LUZZA DELI PMA SPPVRGSOAGDVYSFGIILOE
PSLALQSHLEELGLLMQRCWAEPQEAPPQEAPPQ QIRATTREKPRENSINILONLISRMEQYANNL EELVEERTQAAJEEKRKAEALLYQILPHSVAE QLKRGETVQAEAFBYITSDIVGTFALISAE STPMQVVTILNDLYTCFDAVIDNPDVYKVET IGDAYMVVSRIPHRIPROELRIGHTGPVCAGV VGLKMPRYCLFGDTVINTASRMESNGEALIXI HLSSUETKAVILEEFGGEFLELRIGHTGPVCAGV VGLKMPRYCLFGDTVINTASRMESNGEALIXI HLSSUETKAVILEEFGGFELLRIGHTGPVCAGV VGLKMPRYCLFGDTVINTASRMESNGEALIXI HLSSUETKAVILEEFGGFELLRIGHTGPVCAGV VGLKMPRYCLFGDTVINTASRMESNGEALIXI HLSSUETKAVILEEFGGFELLRIGHTGPVCAGV VGLKMPRYCLFGBTSTRG DAFGRPPVRLFTMELEGVVVQEEPGGSGAV MSERVSGLAGSIYREFERLIVRYDEEVVKELP LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQYEEKALRKHALEKFIEFEDSQEQEKK DLQTRVESLESGTRQLELKAKNYADQISILEE RAELKKEVNALHQRIMMINYMDILKER KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGGGLITPDAQKGGFFSQCWKFGELSOPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPPIDTPLKEENEGFVKVTDAPPNKESISKHHEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMMKDLSGYKGSSTPTKGEBNKAPDRITESL FFELSSAGGGLIGDVDFGADLLGMGREVENLI LENTQLLETKNALNIVKNDLAKVDELTCEK DVLQGELAVKQAKLKLEEKNRELEELERKA RAEAEDARQKAKDDDSDIPTAQRKRFTRVE MARVLMERNQYKERKIMELQEAVRWTFEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTFSVKRRSSTLSQLP GOKSKAFDPLSEETEASLASRREQKREQVRQ VKAHVQKEDGRVQAFGSULDQEKYQCVTROM QGENKMRNLPVPYLIPLEEKDTSMKLWGA VGVALSGGKTRDGGSVVGASVYKDVAGLD TEGSKQRSASQSSLDVLDQELKEQQKELKNQ GENSKMRNLPVPYLIPLEENDTSMKLWGA VGVALSGGKTRDGGSVVGASVYKDVAGLD TEGSKQRSASQSSLDVLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAAVQPGILLDS FTVCNSHVLCIASVPGAEETDYPAGEDLSESG QVDKASLCGSMTINSSAETDSLLGGTTVVGC SAEGVTGAATSPSTNGASPVMDKPPEMBAEN SEVDENVPTJAEELATEATEGNAGSAEDTVOIS QTGVYTEHVFTIPPLGVQPEDLSPVYQSSND SDAYKDQSVLFNEQUREAQKNSSLLPT MVLGQANGCLYVHSSVAQWRKCLHSIKLKD SLISIVHVKGGVLVALADGTLAHFRGYDRQ DLSNYILLDLGRPHIBISRCMTVVHDKVWCG YRNKIYVVQPKAAKIEKSFDAAHPRKESYPRQ I ABVGGRGWVSILDSTLRLYHAHTVQHLQ		1	1	1		1	LAI DEGVENVEGI DI SPKEIJERVTRGEOPPER
QIRITTRKFNRENSNILDNILSRMEQYANDL EELVEERTQATLEEKKRAEAALLYQILPHSVAE QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE STPMQVVTLINDLYTCFDAVIDNFDVYKVET IGDAYMVVSGLPVRNGRLHACEVARMALAL LDAVRSFRIRHRPQEQLRLRIGHTGPVCAGV VGLKMPRYCLFGDTVASRMESNGEALIKI HLSSUETKAVLIEEFGGFELERGDVEMKGKG KVRTYWLJGERGSSTVASSMEGALIKI HLSSUETKAVLIEEFGGFELERGDVEMKGKG KVRTYWLJGERGSSTYROFELIKYDEEVVKELP LVVAVLIADISVFAQDQEHQVELELLRDDNE QLITQYEREKALRKHAEEKFIEFEDSQEQEKK MSERVSGLAGSIYREFERLIVRYDEEVVKELP LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQYEREKALRKHAEKFIEFEDSQEQEKK DLOTRVESLESGYTRLGLKAKNYADQISILEE REAELKKENALHQRITEMINYMEHLERT KLHQLSGSDQLESTAHSRIKKEPISISGIFPLP AGDGLTPDAQKGGETPGSQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTOTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEKSESVQAIESTFELL DMMCKLSGYKGSSTYTKGIENKAPDRNTESL FFELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNVKNDLLAWDGLTCKK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEADARGKKADDDDSDIPTAQRRCTTRV MASVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMGEKKRSSIWQFFSSTSSTSTIK KSEPPVNILKYNAPTSVKRSSSTSTIK KSEPPVNILKYNAPTSVKRSSSTSTIK KSEPPVNILKYNAPTSVKRSSSTSTIK KSEPPVNILKYNAPTSVKRSSSTSTIK KSEPPVNILKYNAPTSVKRSSSTSTIK KSEPPVNILKYNAPTSVKRSSSTSTIK GGMSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYLRRLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASYYKDVAGLD TGSKGRSASQSSLDFULDQELKEQQKELKNQ ELSSLVWICTSTHSATKVLIDAVQPGNILDS FTVCNSHVLCLASVPGAETDYPAGEDLESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTJEELSTEATEATGNAGSAEDTVVDIS QTOVYTEHVTIDPLGVOIPEDLSPVYQSSND SDAYKDQISVLPRGQUKELGNIKLESDLADKSLLPT MWLGAQNGCLYVHSSVAOWRKCLHSIKLKD SLISIVHVKGTVLVALADGTLAIFHRGVDCQW DLSNYILLDLGRPHIBISICMTVVHDKVWCG YRNKIYVVQPKAAKIEKSFDAAPRKESQYRQ LANVIGUGWYSILLDSILLALHTHATTYOHLQ	į.						DOLAL OCHI EEL GLI MORCWAEDPOERPPFO
EELVEERTQAXLEEKRRAEALLYQILPHISVAE  QLKRGETYQAEAFDSVTALSAE STPMQVVTLLADLYTCFDAVUDRDVYKVET IGDAYMVVSGLPKRORGHACEVARMALAL LDAVRSFRIRHRPQEQLRLRIGHTGPVCAGV VGLKMPRYCLFGDTVNTLASRRENGEALKI HLSSEITKAVLEEFGGFELELRGDVEMKOKO KVRTYWLLGERGSSTRG  DAPGREPVRLPTMELEDGVVYQEEPGGSGAV MSERVSGLAGSIYREFERLIVRYDEEVVKELP LVVAVLENLDSVFAODQEHQVELELLRDDNE QLTTQYEREKALRKHAEEKFEPEDSQEGEKK DLQTRVESLESGTRQLELKAKNYADQISILEE REAELKKEYNALHQRITEMIENTYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGGGLLTPDAQKGGFTSEGWKFGELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTOTLPKEENEGVTADAPNKESISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMMKDLSGYKGSSTPTKGIENKAFDRNTESL FFELSSAGSGLIGDVDTAGPKRTESKH VQVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMMKDLSGYKGSSTPTKGIENKAFDRNTESL FFELSSAGSGLIGDVDFGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFSRLFSSSSNTIK KYEPPVNLKVYNAPTSHVTSVKKRSSTLSQLP GOKSKAFDPLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLDCKYRQVTNG QGENKMRNLPVPYTSVKKRSSTLSQLP GOKSKAFDPLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLDCKYRQVTNG QGENKMRNLPVPYTSVEKRSSTLSGLP GOKSKAFDPLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLDCKYRQVTNG QGENKMRNLPVPYTSVEKRSSTLSGLP GOKSKAFDPLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLDCKIKNG GOGNKMRNLPVPYTSVAKRSSTLSGLP GOKSKAFDPLSEETEASLASRREQKREQYRQ VKAHVGKEDGRVQAFGWSLDCKIKNG GOGNKMRNLPVPYTDELGVYNGVTNAG SAEGVTGAATSPSTNGASPWANDKPPEMBAEN SEVDENVTTAEEXTEATEONAGSAEDTVODS GOTOVTTEHVTTDPLGVQPEDLSPVYQSSND SDAYKDQUSVLPREGOLVREAQKNSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SLSIVHVKGGVLVALADGTLALHPHATVQHLQ DLSNYTHLDLGRPHIBISRCMTVVHDKVWCG YRNKIYVVQPKAAKIEKSFDAHPRKESQVCA 1 a WYGGGWVVSILDLALHATVQHLQ	ĺ	ţ		1		1	OTHER DESIGNATION LINES OF ANNI.
QUKRGETVQAAFDSVITYSDINGITALSAE STPMQVVTLINDLYTCFDAVIDNPDYKVET IGDAYMVVSG, PVRNGRLHAGEVARMALAL LDAVRSFRIRHPQEGOLRLRIGHITGPVCAGV VGLKMPRYCLFGDTVNTASRMESNGEALKI HLSSETKAVLEFGGFBLELRGDVEMKOKG KVRTYWLLGERGSSTRG  DAPGRIPPVRLPTMELEDGVVQEEPGGSGAV MSERVSGLAGSIVREFERLIVRYDEEVVKELIP LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQYEREKALRKHAEEKFIEFEDSQEGKK DLQTTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHORHTEMIHNYMEHLERT KLHQLSGSDQLESTHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETTGSQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHEV QVAQETRNVSTGSAENEKSEVQAIESTFEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNVKDLIAKVDELTCEK DVLQGELEAVKQAKLKLEKNRELEEELRKA RABAEDARQKAKDDDDSDIPTAQRKFTRVE MARVLMENNQYKERLMELQBAVRWTEMIR ASRENPAMQEKKRSSIWQFSRLFSSSSNTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASREQKREQVRQ VKAHVQKEDGRVAGWSPGKVRQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVSLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKORSASSSLDKLDQELKEQOKELKNQ EELSSLVWICTSTHSATKVLIDAVQPGNILDS FTVCNSHVLCLGSVPGASPTFNGDSSVYAGDLD SPTVCNSHVLCLGSVPGASPTFNGASSPVMCKPPEMEAEN SEVDENNPTAEEAVTATERDNAGSAEDTVDIS QTGYTTEHVFTDPLGNUPPDLSPVYQSSND SDAYKDQISVLPREQDLVREAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSRLKD SILSIVHVKGIVLVALADGTLAIFHRGVDCQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCO YRNKIYYVQPKAMKEKSFDAHPRKESQVRQ LSNYHLLDLGRPHHSIRCMTVVHDKVWCO YRNKIYYVQPKAMKEKSFDAHPRKESQVRQ	)		1			1	CIRCLERATINE ISSNEED TO BELLEVILLE TO THE VICE OF THE PROPERTY
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MSERVSGLAGSIYREFERLIVKYDEEVVKELIP LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQYEREKALRKHAEEKFIEFEDSQEQEKK DLOTRVESLESOTTROLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKPQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAAENEKKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGERNKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSIWOFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGTTVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATTEATGNAGSAEDTVADIS QTGYTEHVFTDPLGWQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVABSAQAENTAHRKESDAPRKELSHKLKD SILSVHVKGGVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHISIRCMTVVHDKVWCG YRNKTYVVQPKAMKIEKSFDAJFRKESQVRQ LAWVGDGSTLRLYHAHTTYQHLQ	ŀ		1				KVRTYWLLGERGSSIRG
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KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLITPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQEELEAVKQAKLKLEEKRELEELRKA RAEAEDARQKAKDDDDSDITAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWGFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGRILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDL VREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRCLHSIKLKD SILSTVHVKGIVLVALADGTLAIFHRGVDQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ	ſ						OFTIGIER PROPERTY AND
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QVAQETRNVSTGSAENEEKSEVQAIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAK VDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKFTRVE MARVLMERNQYKERLMELQEAVR WTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLK YNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGYNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTIDPLGNVQPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAOKGGETPGSEQWKFQELSQPR
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FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEA.TEGNAGSAEDTVDIS QTGVYTEHVFTDPLGIVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHISIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV
LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDSDIPTAQRKFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGIVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDGRPHHSIRCMTVVDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV OVAOETRNVSTGSAENEEKSEVQAIIESTPEL
DVLQGELEAVKQAKLKLEEKNRELEELRKA RAEAEDARQKAKDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVJDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ L AWVGDGVWYSIRLDSTLRLYHAHTTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL
DVLQGELEAVKQAKLKLEEKNRELEELRKA RAEAEDARQKAKDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVJDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ L AWVGDGVWYSIRLDSTLRLYHAHTTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FFELSSAGSGLIGDVDEGADLLGMGREVENLI
MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGNQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LFNTOLLETKNALNIVKNDLIAKVDELTCEK
MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGNQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK
ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLK YNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEE\ATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAFAEDAROKAKDDDDSDIPTAORKRFTRVE
KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCLASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEE\ATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVI MERNOYKERLMELOEAVRWTEMIR
GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEE\ATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMOEKKRSSIWOFFSRLFSSSSNTTK
VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNILKYNAPTSHVIPSVKKRSSTLSQLP
QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVVDIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIKKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSNTTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ
VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VX AHVOKEDGRVOAFGWSLPQKYKQVTNG
TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTV\DIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG
EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEE\ATEATEGNAGSAEDTV\DIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA
FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKORSASOSSLDKLDOELKEQQKELKNQ
QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEE\ATEATEGNAGSAEDTV\DIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ
SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEE\ATEATEGNAGSAEDTV\DIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG
SEVDENVPTAEE\ATEGNAGSAEDTVDIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYVLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG
QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYVLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG
SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN
MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SFYDENYPTAEEVATEATEGNAGSAEDTVDIS
SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSNTTIK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS
DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDSIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRVETMIR ASRENPAMQEKKRSSIWQFFSRLFSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGIVQIPEDLSPVYQSSND SDAYKDOISVLPNEODLVREEAQKMSSLLPT
YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWVSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIKKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS GDAYKDQISVLPNEQDLVREEAQKMSSLLPT AVVI GAONGCLYVHSSVAOWRKCLHSIKLKD
1 AWVGDGVWYSIRLDSTLRLYHAHTYQHLQ							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHILERT KLHQLSGSDQLESTAHSRIKKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWGFFSRLFSSSSNTTK KPEPPVNILKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPYYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SII SIVHVKGIVLVALADGTLAIFHRGVDGQW
DVDIEPYVSKMLGTGKLGFSFVRITALMVSC							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLGVQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DI SNYHLLDLGRPHHSIRCMTVVHDKVWCG
DVDIEPYVSKMLGTGKLGFSFVRITALMVSC							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIVVVOPKAMKIEKSFDAHPRKESQVRQ
							DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKELKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEATEATEGNAGSAEDTVDIS QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ

			LCEA	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide		l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, 3=30 inc,
dence		l	!	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			Ì	peptide	1	/-possible nucleotide deletion, \-possible
	ľ		1		1	nucleotide insertion
			<b></b>	sequence	<del></del>	NRLWVGTGNGVIISIPLTETVILHQGRLLGLR
				ļ		ANKTSGVPGNRPGSVIRVYGDENSDKVTPGT
	1	1	1		1	ANK ISO VPOINT OF OPLICIED ANK EEVA VPGOV
	1	Ì	ì	ļ		FIPYCSMAHAQLCFHGHRDAVKFFVAVPGQV
		}	)	]	ļ	ISPQSSSSGTDLTGDKGRGHLHRSLVVRRP
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	1		1			REPEILWYKECRTKTWRPSIVFKRDTLLIREV
		1		1	1	REDDIGNYTCELKYGGFVVRRTTELTVTAPL
		1			1	TDKPPKLLYPMESKLTIQETQLGDSANLTCRA
			1			FFGYSGDVSPLIYWMKGEKFIEDLDENRVWE
		1	}		1	SDINKILKEHLGEQEVSISLIVDSVEEGDLGNYS
	l		1			SDI/KILKEHLGEGEVSISLIVDSVEEGDEGITTS
		1	1			CYVENGNGRRHASVLLHKRELMYTVELAGG
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İ	1	1	1			OMROKHYYRSYEYDVPPTGTLPLTSIGNQHI
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					1.004	NSARGGVGVRGARAMATVQEKAAALNLSAL
806	2156	A	6614	3	1584	HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT
		-		1		HSPAHRPPOPSVAQAFTGATTVWSSIMVEQT
ļ		- 1	1			QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
}		1	1			IQNKYFGDVDIPRAKVVRVCQALMDYKVFE
		1	- 1			AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD
	1	1	l	ļ	ŀ	SOLGKENKLYSPARYADALFKSSDIRSASLED
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1	į.		J	j		ROSTMVNSSNYLDRGILKAYSDSQEDEWLSA
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ł		1				AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE
1	Ì	1	1	1	1	LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV
,		1		1		NGKTEIALEATOLLLKLLDFQNREEFRRLLYF
1			1			MAVAANPSEFKLOKESDNRMVVKRIFSKAIV
}						DNKNLSKGKTDLLVLFL\MDHQKDVFKIPGT
					1	L\HKIVS\VK\LMAIQNGRDPNRDAGYIYCQRI
		1		1		LUMIVO V KUNTALQUOI I VI I VTI DEDCVI CA
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1		-			1	KEKKK\LLGQFYKCHPDIFIEHFGD
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807	2157	Α	6615	4170	207.	POILLLALLTLGLAAQHQDKVPCKM/VKML
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1		Ì	1		1	LSGNQLRSILASPLGFYTALRHLDLSTNEISFL
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						THTT SLAENSLTRLTRHTFRDMPALEQLDLHS
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						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVI MDIEDGAFEGLPRLTHLNLSRNSLTCISD
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLOOLRVLDLSCNSIEAFQTAS\QPQAEFQLT
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WI.DLRENKLLHFPDLAALPRLIYLNLSNNLIR
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR I PTGPPODSKGIHAPSEGWSALPLS\APSGNAS
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSOLLNLDLSYNEIELIPDSFLEHLTSLCFL
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSOLLNLDLSYNEIELIPDSFLEHLTSLCFL
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NI.SRNCLRTFEARRLGSLPCLMLLDLSHNALE
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE TI FI GARALG\SLRTLLLOGNALRDLPPYTFA
						LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NI.SRNCLRTFEARRLGSLPCLMLLDLSHNALE

SEQ ID No. of nucleotide sequence						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucle ontice ontice of sequence   ISSN   ISS	SEQ ID	SEQ ID	Met	SEQ	Predicted		D-Acrartic Acid F=Glutamic Acid.
nucleotide seq- uence    VISN   09496   1041   1058		NO: of	hod	ID NO:			D=Aspartic Acid, D=Glutainie Vicing
Sequence		nentide		in	nucleotide		F=Phenylalanine, G=Glycille, 11-1113tidatic,
09/496		1 * *			location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
### 1944   September   Septemb							M=Methionine, N=Asparagine, P=Proline,
uence side of peptide sequence peptide sequence peptide sequence of peptide sequence	seq-	uence					O=Glutamine, R=Arginine, S=Serine,
Peptide	uence	1	1	914			T-Threening V=Valine W=Tryptophan
Peptide		]	1	į	amino acid		1=110coninc, v=vanna, v=15proposas
Incledide insection   Incledide insection   IDLISS/PGLEVATGALGGLEASLEVLALQGN   IDLISS/PGLEVATGALGGLEASLEVLALQGN   IDLISS/PGLEVATGALGGLEASLEVLALQGN   IGLMVLQVDLPCFICLKRINLARNRI.SHLPAW   TQAVISLEVLDLRNNSSSLPGAMAGGLETSILR   RLYLQGNPLSCCORGWLAQLHQGRVDVDA   TQDLICRESSQEEVSISHPREDCEEGGLKN   NLIIILTHLVSABLITTLAACCCVARQKFNQQ   YKA   TQDLICRESSQEEVSISHPEPOCEGGIKN   NLIIILTHLVSABLITTLAACCCVARQKFNQQ   YKA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   AGNORALITA   TOTALITA   TOTALITA   AGNORALITA   TOTALITA   TOTALITA   AGNORALITA   TOTALITA   TOTALITA   AGNORALITA   TOTALI		<b>h</b>	Į.		residue of	sequence	Y=1 yrosine, X=Unknown, '-stop codon,
		L	Į.	1	nentide	1	/=possible nucleotide deletion, \=possible
LDIJSSNFGLEVATGALGGILFASLEVIALQON   GLMM/QDIPFICKRRINAENRISENLAW   TQAVSLEVIDLERNISFSILPGSAMGGLETSLE   RLYLQONPLSCCONGWIAAQLHQGRVDVDA   TQDLICRESSQEEVSLSHVPFEDCEKGGLKN   NLIILTEVSALLTTLAACCCVRRQKFNQQ   YKA   KALSOVIYINTHLEREAAEVALLERNEEG   AKHENNTEKKIPGGGSDASPEAGSGGGV   ALKERGLVSACGIVONGIGSGIFVSKGVLEN   AGSVGLALIWVTGFITVVGALCYAELGVNI   PRSGDYFYVDDIGGGLAGELR WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGELR WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGELR WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGELR WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDDIGGLAGER WAVLVTYFITVAGALCYAELGVNI   PRSGDYFYVDIGGNO   PRSGDYFT   PRSGDO   PRSGDT   PRSGDT   PRSGDYFT   PRSGDO   PRSGDT   PRSGDYFT   PRSGDO   PRSGDT   PRSGDO   PRSGD   PRSGD   PRSGD   PRSGDYFT   PRSGD   PRSG	i		}	İ		İ	nucleotide insertion
GLMV.QVDI.PCRICLRRIN.JAENRLSHLPAW   TQAVSLEVIDLRNNSFSLIPGSAMGGLETSLR   RLYLQGRPLSCCGNGWLAAQLHQGRVDVDW   TQDLICRSSQEEVSLSHVPEDCEKGGLKN   NLIILTFILVSAILLTILAGCCVRRQKFNQQ   YAA   SECTION   NLIILTFILVSAILLTILAGCCVRRQKFNQQ   YAA   RHRNNTEKHPGGESDASPEAGSGGGGV   ARKREIGLVSACGIIVGNIGSGIFVSPKGVLEW   ARKRINTEKKHPGGESDASPEAGSGGGGV   ALKREIGLVSACGIIVGNIGSGIFVSPKGVLEW   ARKRINTEKKHPGGESDASPEAGSGGGGV   ALKREIGLVSACGIIVGNIGSGIFVSPKGVLEW   AGSVGLALIVWIVGFITVGALCYAELGVNI   PRSGGDYFYYKDIBGGLAGFLRLWIAVLVTY   TQAVALLTISNYLQFPTCPFPSGLRLLA   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLL   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVNCSSVRWATRVQDIFTAGKLC   ALLILLITWVGTAGVRWATRVGTAGVR	l	<u> </u>	<b>↓</b>	<b></b>	sequence	<del> </del>	LDLSSNPGLEVATGALGGLEASLEVLALQGN
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VLIDCVGYGLLIATLMWFISNKYLVKRQSRD	ļ		-				AT LENG CUSTICEGEVI DMGFFETIKLLLWV
## STOPPENGYAFDVHLNAFYPLLVILHFIQLFFIN ## HVILTDTFIGYLVGNTLWLVAVGYYIYVTFL GYSVGLLFFSALPPLKNTVILLYPFAPLILLYG LSLALGWNFTHTLCSFYKYRVK  ## SPASGHCRLNGAAVAMFGCLVAGRLVQTAA QQVAEDKFVFDLPDYESINHVVVFMLGTIPFP EGMGGSVYFSYPDSNGMPVWQLLGFVTNGK PSAIFKISGLKSGEGSQHPFGAMNIVRTFSVAQ IGISVELLDSMAQQTPVGNAAVSSVDSFTQFT QKMLDNFYNFASSFAVSQVPDDTQ/RPSEMF IPANVVLK WYENFQRRTSTEPSLLENIIWIKIN F ## LEGSLNTERAKYYLTITMPHFTVTKVEDPEEG AAASISQEPSLADIKARIQDSDEPDLSQNSITG EHSQLLDDGHKKARNAYLNNSNYEEGDEYF DKNLALFEEEMDTRFKVSSLLNRMANYTNLT QGAKEHEEAENITEGKKKPTKTPQMGTFMG VYLPCLQNIFGVILFLRLTWVVGTAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSY FMISRALGPEFGGAVGLCFYLGTTFAAAMYIL GAIEIFLVYIVPRAAIFHSDDALKESAAMLNN MRVYGTAFLVLMYLVVFIGVRYVNKFASLFL ACVIVSILAIYAGAIKSSFAPPHEPVCMLGNRT LSSRHIDVCSKTKEINNMTVPSKL WGFFCNSS QFFNATCDEYFVHNVTSIQGIPGLASGITTEN LWSNYLPKGEIEKPSAKSSDVLGSLNHEYVL VDITTSFTILLVGIFFPSVTGIMAGSNRSGDLKD AQKSIPIGTILAILITTSFYYLSNVVLFGACIEGD VI RDKFGDAYKGNLVVGTLSWPSPWVIVIGS	1	1				1	APPRIATE AMERICAN AME
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A spartic Acid. F=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ĺ	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
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			]	1		RLLLSFNYIRTVTASSFPFLEQLQLLELGSQYT
1						PLTIDKEAFRNLPNLRILDLGSSKIYFLHPDAF
1	1					QGLFHLFELRLYFCGLSDAVLKDGYFRNLKA
	1		1	1	1	LTRLDLSKNQIRSLYLHPSFGKLNSLKSIDFSS
		1			1	NOW MODIFFI PRI OCETT CEECI A AXICI VED
						NOIFLYCEHELEPLQGKTLSFFSLAANSLYSK
						NQIFLVCEHELEPLQGKTLSFFSLAANSLYSK VSVDWGKCMNPFRNMVLEILDVSGNGWTV
						NOIFLYCEHELEPLQGKTLSFFSLAANSLYSK

	-50.10	1 1 1 1 1	CTO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in		corresponding	i=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	İ	ļ	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	l		amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
		Ì		peptide		nucleotide insertion
	1	1		sequence		RVFETLKDLKVLNLAYNKINKIADEAFYGLD
						NLQVLNLSYNLLGELYSSNFYGLPKVAYIDL
		1		1		NLOVENEST NEEDELTS SAFT OF ROMAN TOTAL
		1				QKNHIAIIQDQTFKFLEKLQTLDLRDNALTTIH
		1				FIPSIPDIFLSGNKLVTLPKINLTANLIHLSENR
		1	1			LENLDILYFLLRVPHLQILILNQNRFSSCSGDQ
		ł				TPSENPSLEQLFLGENMLQLAWETELCWDVF
	1	1				EGLSHLQVLYLNHNYLNSLPPGVFSHLTALR
	1	1				GLSLNSNRLTVLSHNDLPANLEILDISRNQLL
			ļ			APNPDVFVSLSVLDITHNKFICECELSTFINWL
}	-	1				NHTNVTIAGPPADIYCVYPDSLSGVSLFSLSTE
,			1	1	1	GCDEEEVLKSLKFSLFIVCTVTLTLFLMTILTV
	i		ļ	ì	<b> </b>	TKERGECEICYKTAORLVFKDHPQGTEPDMY
1	1	1		1	1	KYDAYLCFSSKDFTWVQNALLKHLDTQYSD
1		1				ONRENI CFEERDFVPGENRP\ANIQDAIWNSR
·		1		1	}	KIVCLVSRHFLRDGWCLEAFSYAQGRCLSDL
		1		1		NSALIMVVVGSLSQYQLMKHQSIRGFVQKQQ
	1	İ	1			YLRWPEDLQDVGWFLHKLSQQILKKEKEKK
	İ					KDNNIPLQTVATIS
İ	1			<u> </u>		RDRAGVRPAGKQHAAAAFYDVGGDRPWDS
816	2166	A	6646	1	3811	GNTQLPPRNPVKANAMFGAGDEDDTDFLSPS
1		1				GGARLASLFGLDQAAAGHGNEFFQYTAPKQP
ľ		ļ				KKGQGTAATGNQATPKTAPATMSTPTILVAT
	1	,				KKGQGTAATGNQATEKTAFATIGGTTTEVTT
	1					AVHAYRYTNGQYVKQGKFGAAVLGNHTTR
İ						EYRILLYISQQQPVTVARIHVNFELMVRPNNY
			1 .			STFYDDQRQNWSIMFESEKAAVEFNKQVCIA
		1	i			KCNSTSSLDAVLSQDLIVADGPAVEVGDSLE
		ł	1			VAYTGWLFQNHVLGQVFDSTANKDKLLRLK
}	ļ				1	LGSGKVIKGWEDGMLGMKKGGKRLLIVPPA
1			i			CAVGSEGVIGWTQATDSILVFEVEVRRVKIA
			1	1		KDSGSDGHSVSSRDSAAPSPIPGADNLSADPV
		1				VSPPTSIPFKSGEPALRTKSNSLSEQLAINTSPD
						AVKAKLISRMAKMGQPMLPILPPQLDSNDSEI
ì	İ	ĺ	1	1		EDVNTLQGGGQPVVTPSVQPSLQPAHPALPQ
			1			MTSQAPQPSVTGLQAPSAALMQVSSLDSHSA
1	ļ		ļ			VSGNAQSFQPYAGMQAYAYPQASAVTSQLQ
	İ					PVRPLYPAPLSOPPHFQGSGDMASFLMTEAR
]		.		1		OHNTEIRMAVSKVADKMDHLMTKVEELQKH
	-		1			SAGNSMI IPSMSVTMETSMIMSNIQRIIQENER
		1			1	LKOEILEKSNRIEEONDKISELIERNQRY VEQS
1	1			1		NI MMEKRNNSLOTATENTOARVLHAEQEKA
						KVTEELAAATAOVSHLQLKMTAHQKKETEL
1	ł	1				OMOLTES LIKET DLL RGOLTK VOAKLSELQET
				1	· ·	SEGAOSKEKSEKONRKOLELKVTSLEEELTDL
						RVEKESLEKNLSERKKKSAQERSQAEEEIDEI
						RKSYQEELDKLRQLLKKTRVSTDQAAAEQLS
				1		LVQAELQTQWEAKCEHLLASAKDEHLQQYQ
		-		-		EVCAQRDAYQQKLVQLQEKSVCFA\CLALQA
1						QITALTKQNEQHIKELEKNKSQMSGVEAAAS
		-		1	1	DPSEKVKKIMNQVFQSLRREFELEESYNGRTI
		1		1	1	DESERVANIANA ALCO I MODE DE LE COCE EL CONTROL DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPANIA DEL COM
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[			1	1		EKAEERPRRPSQEQSASASSGQPQAPLNRERP
1				-		ESPMVPSEQVVEEAVPLPPQALTTSQDGHRR
				1		KGDSEAEALSEIKDGSLPPELSCIPSHRVLGPP
					)	TSIPPEPLGPVSMDSECEESLAASPMAAK\PDN
1				1		PSGK\VCVREVAPDGPLQESSTRLSLTS\DPEE
1	1			1	1 .	GDPLALGPESPGEPQPPQLKKDDVTSSTGPHK
1				1		FLSSTEAGSTVAGAALRPSHHSQRSSLSGDEE
						DELFKGATLKALRPKAQPEEEDEDEVSMKGR
		1			1	PPPTPLFGDDDDDDDDDDWLG
ſ	1	1	1	1		THE STATE OF THE S
817	2167	A	6649	63	1073	FFRSSSDNGSPIRQYE/HSTPAHQGPVMGLEG

SEQ ID NO: of muck- peptide peptide peptide in succious peptide custom peptide custom peptide custom in succious peptide custom peptide custom peptide custom in succious peptide custom per							Amino acid sequence (A=Alanine C=Cysteine,
NO. of old USSN operation of Periodic of P	SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Aramic C-Cystome,
incerce coulde sequence where the corresponding sequence where the control of the		NO: of	hod	ID NO:		1 ***	D=Asparulc Acid, E=Glucine H=Histidine
### Corresponding of the provided with the provided sequence   1914   19	nucl-	peptide	]	1			I I I I I I I I I I I I I I I I I I I
sequence 914 914 914 914 914 914 914 914 914 914				USSN			1=1501eucine, N-Lysine, L-Leatine,
uence   914   ng to first amuno acid residue of peptide e   peptide		, -	i	09/496	correspondi		M=Memionine, N=Asparagine, r=rionine,
amino acid residued sequence peptide sequence peptide sequence seq	•	i .		914	ng to first		Q=Glutamine, R=Arginine, 5-3ct life,
## pepide squence   pepide   puccesside insertion   puccesside   pucce			1		amino acid		T=Threonine, V=Valine, W=Tryptopilari,
818 2168 A 6660 357 1890 A 6661 65 2686 SIGNICLAEASMORTHLUNGTHAND ALEXE THE ACTION AND ACTION AND ALEXE		1			residue of	sequence	Y=Tyrosine, X=Unknown, Y=Stop codon,
SAGANSOLRIV VOKITOAGKSATONSLIGRK VPHSGTAAKSITKKCEKSSSWKETELVVVD TEGIPTEVPNABTSKEIRCULTSPGPHALLL VPHGRYTEEBHKAFREIKMFGFRARSFMIL FTRKDDLGDTN-HDYLREAPPEDIQDLMDIFG DEYCALNKATGAGEAGRAGLGLIGRVV RENKEGCYTNRMYGRAEELGKOTOAMGEL HIVELEBERARIRES-KEIRKLEUKVE VEGERR KKOMEKKLAGCAHYAVROQRARTEVESKD GIBELIMTAL OLASPILLALFAED APSGWTRVVITLDPGSLESSPPSLLDPGMP GISARGLSEGROLAVITRALALKSTLDA VIHEFTIDBLUDTIL-CSWCBALDGIKPPQLA THALLOMPGGEGYVTRYSSVWP.ILLALKSTLD GISARGLSEGROLAVITRALALKSTLDA THALLOMPGGEGYVTRYSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTER VERNENGEGYTRYSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSSVWP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGEGYTRSTVP.ILLALKSTLD RENGERGER VERNENGER VERNENGER RENGERGER VERNENGER VERNENGER VERNENGER RENGER VERNENGER VERNENGER VERNENGER VERNENGER RENGER VERNE			1	1	peptide		/=possible nucleotide deletion, \=possible
VPHSGTAAKSITKKCEKRSSSWKETELVVVO					sequence		nucleotide insertion
1		<del> </del>	<del>                                     </del>	<del> </del>			KS/ARNSQLRIVLVGKTGAGKSATGNSILGKK
VVPLGRYTEEHHATTEKILKMFGERARSHD				1			VFHSGTAAKSITKKCEKRSSSWKETELVVVD
BTTKKDDLGDTNLHDYLREAPEDIQDLMDIYG   DRYCALNNKATGAREQAQRAQLGLIGRIVG   RENKEGCYTNRMYQRAEEIQKQTQAMQE   RRVELEREKARIREEYEKIRKLEDKYEQEKR   KKQMEKKLAEQEAHYAVRQQRARTEVESKD   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBLIMTALQIASHLIRIFABU   GILBRITINI   GILBRIT   G			i				TPGIFDTEVPNAETSKEIIRCILLTSPGPHALLL
BRYCALINKATGARGAGAQRAQLIGILIQMY				1		Ì	VVPLGRYTEEEHKATEKILKMFGERARSFMIL
RENKEGCYTNRMYQRAEEEIQKQTQAMQEL   HRVELEREKARRESYEEKIKLEDKYQQKR   KKQMEKKLAEQEAHYAVRQQRAMTEVESKD   GILELIMTALQIASFILLALGAAD     818   2168   A   6660   357   1890   APSGSWTRVVLTLDPGSLRSRSPRSLLDPGMP   GISARGLSHEERKQLAWALVALVASLLDA   YIIEFPITDALWDTLPCSWQRALDGLRPPQLA   TMLLGMPGGGVVVRYRSWTLALVASSLDA   YIIEFPITDALWDTLPCSWQRALDGLRPPQLA   TMLLGMPGGGVVVRYRSWTLALAKSTA   CALAFTRMPGFQTPSEFLENPSQSSRLTAPFR   KHVPPKQHERRLGELVKKLSDFTGLHPGC   RRGLRFGHLSFRMALGIGLGMYKSIEGDQRL   VERAQRLDQELLQALEKEEKSNPQVVGTSPR   HSPHHVVRWVDPTALCEELLTLENPCQGRA   RLLLTGLHACGDLSVALLRHPSCCPEVALA   SVGCCYMKLSDPFGYLPSQWAGILPGYLPG   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLQKAGPGLRTHCY   YRLREGACHALEFYAERLJFTTCHALFYAERLAGACHALAGPN   YRLREGACHALEFYAERLJFTTCHALFYAERLAGACHALAGPN   YRLREGACHACHACHACHACHACHACHACHACHACHACHACHACHA		1		ļ			IFTRKDDLGDTNLHDYLREAPEDIQDLMDIFG
## HRVELEREKARIREEYFEKIRKLEDKYGEKR KKQMEKKLAGCAHTYAVOGRARTEVESKO GILELIMTALQIASFILLRI-FAED  ## A 6660 357 1890 APSGSWTRV/ILDPGSLRSSPRSILDPGMP GISARGI-SHEGRKQL-AVALTRVLALYRSILDA YIIEFFIDAL WDTIP-CSWQBASRSPRSILDPGMP GISARGI-SHEGRKQL-AVALTRVLALYRSILDA YIIEFFIDAL WDTIP-CSWQBASRILDFFOLD HILLGAMFGGEVVRYRSVWPLILLALKSTA CALAFTRMGFQTPSEFLENSQSSRLTAFFR KHYMPKKQHEIRRIGELVKKLSDFT/GLIFFOC RRGLRPGHLSRFMALGI-GLMVKSIEGDQRL VERAQRLDGELQ-LALEKEKENPQVVGTSFR HSPHHVVRWVDPTALCELLIPLENPCQGRA RILLTGHACGDL-SVALLFSPEVGGPRVHEIKIE YVGRGLORVGLD-QL-BLALALQAHL-AG-VIEL- RAALETVIRRARPELRRPGVGGPRVHEIKIE YVQRGLORVGLD-PLO-BLALALQAHL-AG-VIEL- RAALETVIRRARPELRRPGVGGRVHEIKIE YVQRGLORVGLD-PLO-BLALALQAHL-AG-VIEL- RAALETVIRRARPELRPGVGGRVHEIKIE YVQRGLORVGLD-PSPLS-SPRN-LV-VT-KM-LG GSAECQDGSDESQETCL-SVTCK-SODFS-COGR NNCPIP-WRCDG-QVDCCMSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDECLOSSDE ASCPVLTCGPASFCCNSCIPQL-WACNDDPD CEDGSDEWPORCRGL-YYFQDDSSPC-SAFEH CLSGCGHSSWRCDGGPPCKGNSDEENCAW TCRPDEFQCSDGNCHGSRQCDREYDCKMS DEVGCVNTLCEGPNIFEK-GSCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGPNIFEK-GSCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCC-LCPD-GN-GN-FRAFK KGGLNGVIDIS-VITEN-NU-WG-RT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LLAENLIS-FEDMVJ-PHI-LT-OPR-GV-NWCERT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LLAENLIS-FEDMVJ-PHI-LT-OPR-GR-VNC-ERT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LLAENLIS-FEDMVJ-PHI-LT-OPR-GR-VNC-ERT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LAENDMRSCLT-GE-AA-VATOETSTVLKVS STAWT-OHT-THE VT-T-	l		)		1		DRYCALNNKATGAEQEAQRAQLLGLIQRVV
## HRVELEREKARIREEYFEKIRKLEDKYGEKR KKQMEKKLAGCAHTYAVOGRARTEVESKO GILELIMTALQIASFILLRI-FAED  ## A 6660 357 1890 APSGSWTRV/ILDPGSLRSSPRSILDPGMP GISARGI-SHEGRKQL-AVALTRVLALYRSILDA YIIEFFIDAL WDTIP-CSWQBASRSPRSILDPGMP GISARGI-SHEGRKQL-AVALTRVLALYRSILDA YIIEFFIDAL WDTIP-CSWQBASRILDFFOLD HILLGAMFGGEVVRYRSVWPLILLALKSTA CALAFTRMGFQTPSEFLENSQSSRLTAFFR KHYMPKKQHEIRRIGELVKKLSDFT/GLIFFOC RRGLRPGHLSRFMALGI-GLMVKSIEGDQRL VERAQRLDGELQ-LALEKEKENPQVVGTSFR HSPHHVVRWVDPTALCELLIPLENPCQGRA RILLTGHACGDL-SVALLFSPEVGGPRVHEIKIE YVGRGLORVGLD-QL-BLALALQAHL-AG-VIEL- RAALETVIRRARPELRRPGVGGPRVHEIKIE YVQRGLORVGLD-PLO-BLALALQAHL-AG-VIEL- RAALETVIRRARPELRRPGVGGRVHEIKIE YVQRGLORVGLD-PLO-BLALALQAHL-AG-VIEL- RAALETVIRRARPELRPGVGGRVHEIKIE YVQRGLORVGLD-PSPLS-SPRN-LV-VT-KM-LG GSAECQDGSDESQETCL-SVTCK-SODFS-COGR NNCPIP-WRCDG-QVDCCMSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDEQGCP-PKTC SQDEFRCHDGKCISRQFVCDSSDECLOSSDE ASCPVLTCGPASFCCNSCIPQL-WACNDDPD CEDGSDEWPORCRGL-YYFQDDSSPC-SAFEH CLSGCGHSSWRCDGGPPCKGNSDEENCAW TCRPDEFQCSDGNCHGSRQCDREYDCKMS DEVGCVNTLCEGPNIFEK-GSCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGPNIFEK-GSCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCCL-CPD-GPC-NACNT-LCEGNIFEK-KSGCCTID-BVC NMARDCRDWSDEPIKE-GGTNECLDNNGGCS HVCNDLKIGPCC-LCPD-GN-GN-FRAFK KGGLNGVIDIS-VITEN-NU-WG-RT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LLAENLIS-FEDMVJ-PHI-LT-OPR-GV-NWCERT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LLAENLIS-FEDMVJ-PHI-LT-OPR-GR-VNC-ERT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LLAENLIS-FEDMVJ-PHI-LT-OPR-GR-VNC-ERT TLSNGGC-VICL-PAPOIN-PHIS-FKT-CA-CPD-GM LAENDMRSCLT-GE-AA-VATOETSTVLKVS STAWT-OHT-THE VT-T-			1			1	RENKEGCYTNRMYQRAEEEIQKQTQAMQEL
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VNRCIPQFWRCDGQVDCDNGSDEQGCPFKTC SQDEFRCHDGKCISRQFVCDSDRDCLDGSDE ASCPVLTCGPASFQCNSSTCIPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH CLSGECIHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMII CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRI YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCIPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\(\text{L}\text{AVACTOTTYVLKVS}\) STAVKTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\(\text{RGNEKKPSSVRALSIVL}\) PIVLLVFLCLGVFLLWKNWRLKNINSINFDN VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHIILISKAEDYRSYRFFKLTVITEYLLLF				1			AAGTA VODRCERVE QCQDGRC OTTEN VOD
SQDEFRCHDGKCISRQFVCDSDRDCLDGSDE ASCPVLTCGPASFQCNSSTCIPQL WACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH CLSGECHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCHGSRQCDREYDCKDMS DEVGCVVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEGFQLDPH TKACKAVQSLAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWIDINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARNDMRSCLTEGGEAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSNFDNB VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGELCGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFFKLTVITEYLLLF							GSAECQDGSDESQETCESVTCKSGDF3CGCPPKTC
ASCPVLTCGPASFQCNSSTCEPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH CLSGECHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSLAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERI TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARIDMRSCLTEGGEAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNI VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSFTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFFKLTVITTEYLLLF	ĺ		1	1			VNKCIPQFWKCDGQVDCDNGSDEQGCTRTG
CEDGSDE WPQRCRGLYVFQGDSSPCSAFEH CLSGECHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERI TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGN\EKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNI VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHIILISKAEDYRSYRFPKLTVITEYLLLF							SQUEFKCHDGACISKQFYCDSDADCEDGSDE
CLSGECIHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARUDMRSCLTEGEAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGIRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNI VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHIILISKAEDYRSYRFFKLTVITEYLLLF		1		İ	1		ASCPVLTCGPASPCCNSSTCTQLWACDIDED
TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NILAENILSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARNDMRSCLTEGEAAVATQETSTVRLKVS STAVRTQHTITTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGNÆKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNI VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFFKLTVITEYLLLF			j	}		1	CEDGSDEWPURCROLI VIQUESSI CEALIMIT
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NMARDCRDWSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NILAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\(\text{LAR}\)DMRSCLTEG\(\t	1		İ		ļ		TCRPDEFQCSDGNCIHOSKQCDRETDCRDMS
HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARDMRSCLTEGEAAVATQETSTVRLKVS STAVRTQHTITRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG/RGN/EKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNI VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTV FGYLHILLISKAEDYRSYRFFKLTVITEYLLLF	1			1			DEVOCANA ILCERLARACIONECI DANIGGOS
CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NILLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNF VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTV\ FGYLHIILISKAEDYRSYRFFKLTVITEYLLLF	Ì	1			1		NWAKDCKD & SDELIKE COLINECT DITTE
TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWIDIINEAIFSANRLTGSDV NLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALSIVL PIV\LVFLCLGVFLLWKNWRLKNINSINFDNH VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF							HACUDING AFCICANGUAGE CECT DER
TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\GRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNH VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF					1		CODPDICSOLLANDERDIRANDED VALLED SEL
CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNH VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF							TKACKAVGSIAYLFFINKHEVKNIYILDKSEI
WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALSIVL PIV\LVFLCLGVFLLWKNWRLKNINSINFDNI VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF		1	1		1		L2PILLY AND TEASURE ASSET ASSE
ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWIDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNF VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTV FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF			-				CSTQLDRAHGVSSYDTVISKDIQAPDOLAVD
KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARIDMRSCLTEGIEAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGIRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNF VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF	1		İ				WIHSNIYWTDSVLGTVSVADTKGVKKKTLFR
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PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\(LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSCLTEG\(\text{LARVDMRSLRTEG\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSLK\(\text{LARVDMRSG\(\text{LARVDMRSG\(\text{LARVDMRSG\(\text{LARVDMRSG\(\text{LARVDMRSG\(\text{LARVDMRS\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDMR\(\text{LARVDM			1			ſ	KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL
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NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\(\text{EAAVATQETSTVRLKVS}\) STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\(\text{RGN\(\text{EKKPSSVRALSIVL}\) PIV\LVFLCLGVFLL\(\text{WKNWRLKNINSINFDNF}\) VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSFTSL\(\text{WGLLFLSAA}\) LSL\(\text{WPTSGEICGPGIDIRNDYQQLKRLENCTV}\) FGYLHILLSK\(\text{AEDYRSYRFPKLTVITEYLLLF}\)		1			ļ		PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV
TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALS\VL PIV\LLVFLCLGV\FLL\WKNW\RLK\NINSI\NFDN\FV\QK\TTEDEV\HICH\NQDG\YS\YPSRQ\MVSLED DVA  820 2170 A 6666 17 4146 ERGISSQI\KG\MKS\GSGGG\S\FTSL\WGLL\FL\SAA LSL\WPTS\GEI\CGPGIDI\RD\YQ\QL\KRL\ENCTV\F\GY\HILL\S\KAED\YRS\Y\F\F\KL\TV\TTE\LL\F							NI LAENI LSPEDMVLFHNLTOPRGVNWCERT
LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RG\MEKKPSSVRALS\VL PIV\LLVFLCLGVFLL\WK\NWRLK\NI\NS\NFD\MIV VYQKTTEDEVHICH\NQDGYS\YPSRQ\MVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKG\MKS\GSGGG\SPTSL\WGLLFL\SAA LSL\WPTS\GEI\CGPGIDI\R\ND\YQQL\KRL\E\NCTV\ F\GYL\HILL\SK\AED\YR\Y\RF\KLT\VIT\EY\LL\F							TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM
STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\RGN\EKKPSSVRALSIVL PIV\LVFLCLGVFLL\WKNWRLK\NINSINFDN\H VYQKTTEDEVHICH\NQDGYSYPSRQMVSLED DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSL\WGLLFLSAA LSL\WPTSGEICGPGIDIR\nDYQQL\KRL\E\NCTV\ FGYL\HILLISK\AEDYRSYR\FPKLT\VITEYLLLF	ļ						LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS
VTMSHQALGDVAG\RGN\EKKPSSVRALS\VL PI\substitute VFLCLGVFLL\WKN\WRLKN\INS\INFDN\F VYQKTTEDE\SHICH\NQDG\YS\SYP\SRQ\M\SLED\D\VA\BY\T\T\T\T\T\T\T\T\T\T\T\T\T\T\T\T\T\T\				1		1	STAVRTOHTTTRPVPDTSRLPGATPGLTTVEI
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820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF	1						DVA
LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF				1	12	4146	FRGISSOIKGMKSGSGGGSPTSLWGLLFLSAA
FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF	820	2170	A	6666	17	4140	I SLWPTSGEICGPGIDIRNDYQQLKRLENCTVI
RVAGLESLGDLFPNLTVIRGWKLFYNYALVIF			-				FGYLHILLISKAEDYRSYRFPKLTVITEYLLLF
KYNODODO	1					1	RVAGLESLGDLFPNLTVIRGWKLFYNYALVIF
<u> </u>		<u> </u>					

		<del></del> _	1.000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in			I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	i		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	:		ì	amino acid	of peptide	I=I hreonine, V=Valine, w-Tryptophian,
	ļ		ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	1	ł	peptide	1	/=possible nucleotide deletion, \=possible
	}		}	sequence		nucleotide insertion
	L	<del> </del>	<del> </del>	sequence	<del> </del>	EMTNLKDIGLYNLRNITRG\AIRIEKNADLCYL
	1		1			STVDWSLILDAVSNNYIVGNKPPKECGDLCP
	1		1			GTMEEKPMCEKTTINNEYNYRCWTTNRCQK
	1	1	1			MCPSTCGKRACTENNECCHPECLGSCSAPDN
	Ļ	1		ļ.		DTACVACRHYYYAGVCVPACPPNTYRFEGW
	ļ	į .				DIACVACRITTIAGVCVFACITITIAGV
		ł	İ	1		RCVDRDFCANILSAESSDSEGFVIHDGECMQE
					İ	CPSGFIRNGSQSMYCIPCEGPCPKVCEEEKKT
]	1	1	l			KTIDSVTSAQMLQGCTIFKGNLLINIRRGNNLA
}	1	1	1		1	SELENFMGLIEVVTGYVKIRHSHALVSLSFLK
Ì	1	}		1		NI RLILGEEOLEGNYSFYVLDNQNLQQLWD
			1	1		WDHRNLTIKAGKMYFAFNPKLCVSEIYRMEE
1	1		1	1		VTGTKGRQSKGDINTRNNGERASCESDVLHF
1	1		1			TSTITSKNRIIITWHRYRPPDYRDLISFTVYYK
	1			1		EAPFKNVTEYDGQDACGSNSWNMVDVDLPP
	1	1	1	}		NKDVEPGILLHGLKPWTQYAVYVKAVTLTM
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ļ				ļ		VENDHIRGAKSEILYIRTNASVPSIPLDVLSAS
1	j	j	}	1	ŀ	NSSSQLIVKWNPPSLPNGNLSYYIVRWQRQP
						QDGYLYRHNYCSKDKIPIRKYADGTIDIEEVT
	1				1	ENPKTEVCGGEKGPCCACPKTEAEKQAEKEE
i	1					AEYRKVFENFLHNSIFVPRPERKRRDVMQVA
<b>!</b>	ļ		i	1		NTTMSSRSRNTTAADTYNITDPEELETEYPFF
}	1		ļ	1		ESRVDNKERTVISNLRPFTLYRIDIHSCNHEAE
1	ł	1	1			KLGCSASNFVFARTMPAEGADDIPGPVTWEP
i	1					RPENSIFLKWPEPENPNGLILMYEIKYGSQVE
Į.	1	1	Ì	İ		DQRECVSRQEYRKYGGAKLNRLNPGNYTARI
1			Į.	1		QATSLSGNGSWTDPVFFYVQAKRYENFIHLII
	1	1	1			QATSESGNGSWIDPVFFIVQARRIENTIEM
	j	-	1		1	ALPVAVLLIVGGLVIMLYVFHRKRNNSRLGN
		1				GVLYASVNPEYFSAADVYVPDEWEVAREKIT
			1			MSRELGQGSFGMVYEGVAKGVVKDEPETRV
ľ		1	1	į.	1	AIKTVNEAASMRERIEFLNEASVMKEFNCHH
	j					VVRLLGVVSQGQPTLVIMELMTRGDLKSYLR
				1	İ	SURPEMENNPVLAPPSLSKMIQMAGEIADGM
	İ	j	j	]		AYLNANKFVHRDLAARNCMVAEDFTVKIGD
			Į.	1		FGMTRDIYETDYYRKGGKGLLPVRWMSPESL
1	1		1	1		KDGVFTTYSDVWSFGVVLWEIATLAEQPYQ
						GLSNEQVLRFV\MEGGLLDKPDNCPDMLFEL
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						ASSSSLPLPDRHSGHKAENGPGPGVLVLRASF
		1	1	}	1	DERQPYAHMNGGRKNERALPLPQSSTC
931	2171	A	6691	106	825	GRVLFRGCGVGHKGQVLMGTFILAQDWLSE
821	2171	1 ^	0071	100		SNHVFCVSSMLRLOKRLASSVLRCGKKKVW
		)		1	1	LDPNETNEIANANSROQIRKLIKDGLIIRKPVT
		1		i		VHSRARCRKNTLARRKGRHMGIGKRKGTAN
1	1			1	1	ARMPEK VTWMRRMRILRRLLRRYRES/KRYR
	]			1		ESKKIDRHMYHSLYLKVKGNVFKNKRILMEH
	1			1		ESTAINMENT TOUT THE ADDITION OF THE STAIN OF
				1		IHKLKADKARKKLLADQAEARRSKTKEARK
		i		1		RREERLQAKKEEIKTLSKEEETKK
922	2172	A	6715	772	21	DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI
822	21/2	^	0/15	1		SGAKSSSS/RFTDSKRYEK\DFQ\SCFGLHETR\
	1	Ì		1	1	SGDI\CNA\CVLL\LKRWKKLPAGSKK\NWNH
1		1			1	VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST
i	1					QISKLQKEFKR\HNSDAHSTTS\SASP\AQSPLF
	1	-				TVNQFRWTGSDTGVGFPGSNRNHPVFSFLDL
i			1		1	TYWKRQKICCGNYKGRFGEVLIDTHLFKPCC
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				İ		SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM
000	2153	ļ	6727	13	4063	SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM PYLATLOLDSSLLIPPKYOTPPAAAOGQATPG
823	2173	A	6727	3	4063	SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA
823	2173	A	6727	3	4063	SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA
823	2173	A	6727	3	4063	SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM PYLATLOLDSSLLIPPKYOTPPAAAOGQATPG

	VO		072	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ì	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last allillo	Q=Glutamine, R=Arginine, S=Serine,
цепсе			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
4000		İ	İ	amino acid	of peptide	T=I hreonine, V=Vaime, w=Itypiopilai,
		ľ	<u> </u>	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	ļ	}	peptide		/=possible nucleotide deletion, \=possible
		i	i	sequence		nucleotide insertion
		↓	<del> </del>	sequence	<del>}</del>	SSQPSQDGQESNVPSVGSLADPDYLNTPQMN
	1		l .		]	TPVTLNSAAPASNSGAGVLPSPATPRFSVPTP
						RTPRTPRTPRGGGTASGQGSVKYDSTDQGSP
	1					ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLIL
	1	1				SDSVMNIFKDRNFDSCCICACNMNIKGADVG
	1	1	1		-	SDSVMNIFKDRNFDSCCICACHVIIVIRGIDA V
	1	ļ	ļ	Ì		LYIPDSSNEDQYRCTCGFSAIMNRKLGYNSGL
	l				ì	FLEDELDIFGKNSDIGQAAERRLM\MCQSTFL
	1	1	1	ĺ		POVEGTKKPOEPPISLLLLLQNQHTQPFASLN
	!		1		İ	FI DVISSNNROTLPCVSWSYDRVQADNNDY
	1		1		ļ	WTECFNALEQGRQYVDNPTGGKVDEALVRS
	1		1	1	1	ATVHSWPHSNVLDISMLSSQDVVRMLLSLQP
	1		1	i	1	THE OF A TOP
	1		1	1		FLQDAIQKKRTGRTWENIQHVQGPLTWQQFH
	1		1	1	1	KMAGRGTYGSEESPEPLPIPTLLVGYDKDFLT
ĺ	1	1				ISPFSLPFWERLLLDPYGGHRDVAYIVVCPEN
	1	}		1	1	EALLEGAKTFFRDLSAVYEMCRLGQHKPICK
1		1		i	1	VLRDGIMRVGKTVAQKLTDELVSEWFNQPW
1	ł	1	1	İ		SGEENDNHSRLKLYAQVCRHHLAPYLATLQL
						DSSLLIPPKYOTPPAAAQGQATPGNAGPLAPN
1	İ		1			GSAAPPAGSAFNPTSNSSSTNPAASSSASGSSV
	1					PPVSSSASAPGISQISTTSSSGFSGSVGGQNPST
1			1	1	1	GGISADRTQGNIGCGGDTDPGQSSSQPSQDG
]	}	}	1	i	1	GGISADKIQUNIGCOODIDI QQDDQI DQD
i	1		1	1		QESVTERERIGIPTEPDSADSHAHPPAVVIYM
Į.			1			VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD
1		ł	l l			NLPEHMRNSFILQIVPCQYMLQTMKDEQVFY
Į.		İ				IQYLKSMAFSVYCQCRRPLPTQIHIKSLTGFGP
1	1	1	ļ	}		AASIEMTLKNPERPSPIQLYSPPFILAPIKDKQI
	1		1		[	ELGETFGEASQKYNVLFVGYCLSHDQRWLL
		1	ł		1	ASCTDLHGELLETCVVNIALPNRSRRSKVSAR
	1		1			KIGLQKLWEWCIGIVQMTSLPWRVVIGRLGR
1	1			1		LGHGELKDWSILLGECSLQTISKKLKDVCRM
}	]		1	ļ		LGHGELKDWSILLOECSEQTISIACEN VMPDAV
1	l.	1	1	1		CGISAADSPSILSACLVAMEPQGSFVVMPDAV
į	1	İ	1	1		TMGSVFGRSTALNMQSSQLNTPQDASCTHIL
İ		1		1		VFPTSSTIQVAPANYPNEDGFSPNNDDMFVDL
ł	1	Ì	Í	ĺ		PFPDDMDNDIGILMTGNLHSSPNSSPVPSPGSP
1		1				SGIGVGSHFOHSRSOGERLLSREAPEELKQQP
1			1			LALGYFVSTAKAENLPQWFWSSCPQAQN\QC
						PLEIK ASI HHHISVAOTDELLPARNSQRVPHP
1	1	1	Į.			LDSKTTSDVLRFVLEQYNALSWLTCNPATQD
1	ļ	1	1	1	1	RTSCLPVHFVVLTQLYNAIMNIL
ļ						VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR
824	2174	A	6732	2440	365	VERULUKKKI PROGRAM I CORRECCOCOG
024	-117	1		}		RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG
I				1		GGGGGTIKRPGITGPTAATSPSGEPGNAASAP
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	Į	1			1	GLAAREGNVKVLRKLLKKGRSVDVADNKG
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1					!	KTFEGFCALHLAASQGHWKIVQILLEAGADP
		-				KITEUTCALILAASQUI WALYQUELAGADI
	1	-				NATTLEETTPLFLAVENGQIDVLRLLLQHGAN
			-		1	VNGSHSMCGWNSLHQASFQENAEIIKLLLRK
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						I SSGADPDLYCNEDSWOLPIHAAAQMGHIKI
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLIPLTNRACDTGLNKVSPVYSAVFGGHE
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLIPLTNRACDTGLNKVSPVYSAVFGGHE
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCI FII LRNGYSPDAOACLVFGFSSPVCMAFQ
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCFFFGIVNILLKYGAOINELHLAYCLKYEK
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA KYKEWIPHILVAGFDPLILLCNSWIDSVSIDT
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA KYKEWLPHLLVAGFDPLILLCNSWIDSVSIDT LIETI FETNWKTI APAVERMLSARASNAWIL
						LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA KYKEWIPHILVAGFDPLILLCNSWIDSVSIDT

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	İ	in	nucleotide	location	F=Phenylalanine, G=Glychie, H=Hausine
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
ł .	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	acrice.	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ļ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		į	1	peptide		/=possible nucleotide deletion, \=possible
	1	1	1		ļ	nucleotide insertion
l				sequence	<del> </del>	QLPLPRSLHNYLLYEDVLRMYEVPELAAIQD
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1					1262	RIMGLFDRGVQMLLTTVGAFAAFSLMTIAVG
825	2175	Α	6735	277	1252	TDYWLYSRGVCKTKSVSENETSKKNEEVMT
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		ļ .	1			ASEFYKTRHNIILSAGIFFVSAGLSNIIGIIVYIS
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				1		ASAITRIPSYRYRYQRRSRSSSRSTEPSHSRDA
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						EFYGPEKSLQPIWPYNKKDSDRNEQLSQWDS
						PMRVKLSIWKPYVRTLLIELLPWALLINESKW
1		i	1	[		DLWLFEGEKIVLQVPAGKIIIPPNFQEAFQIGIY
						WANTNTVHKSVAIKLVHNLTSPKWKDGGNG
	-					EVVTLDEEAFVDTEIRLGAFPGHQKLCQFCIS
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						CNPHSGKEYFRVPDSATFSICPGGEQPAMKSS
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						DNIFLCVAPGAGPLPGEEPVAALFELYCVEIC
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				1		HISKGTLTSITNLATSLARNMDRLSLDEEHYN
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						AGIVDQPMQNFQKTSEAQASAGHKAKGVISG
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SEQ ID No. of Mot No. of No. o							
NO. of No	CEO ID	SEO ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
sociode sequence venore position of the properties of the person of the	,						D=Aspartic Acid, E=Glutamic Acid,
eetide seg- uence  914  914  914  914  914  914  914  91		1		1	nucleotide		F=Phenylalanine, G=Glycine, H=Histidine,
sequence  914 914 914 914 914 914 914 914 915 915 915 916 915 916 916 916 917 917 917 917 917 917 917 917 917 917	1			USSN	location		J=Isoleucine, K=Lysine, L=Leucine,
uenice    Page   Peptide			Ì	09/496			M=Methionine, N=Asparagilie, r-1 foline,
residue of peptide sequence     V=Tyrosine, X=Unknown, **Stop coton, /-possible nucleotide detion, *pos			1	914			Q=Glutamine, K=Argillile, S=Scribe,
## Appssible nucleotide deletion, impossible nucleotide insertion nucleotide insertion uncleotide insertion uncleotide insertion of CISCUPKERIGEAAELVSQTGYGILHGA GLSCUPKERIGEAGUA (CISCUPKER) CONTROL ADDAMSHIVKYVW KMLQSLGRFEVHMALDVIV.KGSGGEHEGG LLITSEVLFVSVSSEDTUQAPFVTEIDCAQD SKQNNLLTVQLKQFRVACDVEVDGVRERLSE QQYNRLDVITIKTSCHLAPSCSSMOPICFVWA AEPPSTVKTVHYLDPIHFAQVFLSKTTMVK NKALRKGFP  ### A 6748 2 1662 ** PVGAPRRGSPFGSFGNFGHOGPCHPKFRTK NKALRKGFP LDSGSLTSLDSSVFCSFGGEGEPLALGDCTTVN VGSRFVLSQGALSCFPHTRLGKLAVVAVSY REPGALAAVSPSLELCDDANSVDNEVFEDRS SQAFRYVLHYNETGLALSSLLDS LDSGSLTSLDSSVFCSFGGEGEPLALGDCTTVN VGSRFVLSQGALSCFPHTRLGKLAVVAVSY REPGALAAVSPSLELCDDANSVDNEVFEDRS SQAFRYVLHYNETGLALSSLGE QYWGIDELSIDSCCRDRYFRRKEISETLDFKK DTEDQSSQHESEQDFSQGCPTVRQKLWILL EKPGSSTAARFQVISIHVAGQLALSSLQE QYWGIDELSIDSCCRDRYFRRKEISETLDFKK DTEDQSSQHESEQDFSQGCPTVRQKLWILL EKPGSSTAARFQVISIHVAGQLALSSLQE SVLDLQLELEYVCISVFTGFFVLTRLCVRD RCRFLKKYPNIDLLALBFYTILLVESLSGSQT TOFLERNVAGHCGGCLRLARLAWRAKAWA WATTSMT TYGYCDIRPDTTTGKVAFMCLISGILVLALPY ANNORSACYFTLKLEAAVQRAFALCLGEPVFV ANNORSACYFTLKEAAVQRAFALCLGEPVFV ANNORSACYFTLKEAAVQRAFALCLGEPVFV ANNORSACYFTLKEAAVQRAFALKLTK NIADTSYSTVARDVYARSIMEMILSLKGRER ASTRESSGCDFWT ASSGFGCSMHSSNKVASSPSGNTQSSPSKOK EWMVRPTTVMSPSGNFQLDSSFSNGCKGGG SASQSPSCDSKSGGTTFNALFFGCODFGTN DDSDLECKSADHTRSCTFNALFFGCODFGTN DDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSADHTRSCTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSDLECKSTFNALFFGCODFGTN NDSD							V=Tamesine V=Unknown *=Ston coden
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ASCVSPTLWRPQAAATGLEMPSSGRALLDSP LDSGSLTSLDSSVFCSGGGEPEPLALGDCTTVN VGGSRFVLSQQALSCFPHTRLGKLAVVVASY RRRGALAAVPSPELCDDANPUSYFDRS SQAFRYVLHYYRTGRLHVMEQLCALSFLQEI QYWGIDELISDSCCRDRYPRRELSETLDFKK DTEDQESQHESEQDFSQGPCPTVRQKLWNIL EKFGSSTAARIFQVISIIFYQVSIINMALMSALL SWLDLQLLELEVVCISWFTGEFVLRFLCVRD RCFFLRKVPNIDLLALIFYTITLVESLSGSQT TQELENVGAHCPGCLRLLARIAMLKAWGR HSTGLRSLGMTTQCVEEVGLLLFLSVGISIF STVEYFAGSIBPDTTFTSVCAWWATTSMT TVQYGDIRPDTTTGKIVAFMCLSGILVALAPI AINDRFSACFYFLKLKEAAVRQREALKKLTK NAIADSYISVNLRDVYARSMEMRLKGRER ASTRSSGGDDFWF GTHPASSGFVDLPFAAVSAATREELGEPVFFV TASSGFQSMHSSNFKVRSSFSSGNTOSSPKSKQ EVMYRPTVMSPSGNPQLDSKFSNQGKGGS ASGSGPSCDSKSGGHTPKALFGPGGSMGLK NGAGNGAKGKGKRRSTSISASFDQRDPGTPN DDSDIKECNSADHIKSDDSQHTPHSMTPSNAT APRSSTPPHGGTTATEPTPAGKTAKVVYVFS TEMANKAAEAVIKGQVETIVSFHIQNISNK TERSTAPLNTIGSLARINDFRCTQPPPAPAN DQNSSGNTRLQPTPPBAFARAAPPRFLDRE SPGVENKLIPSVGSASSTLPCTGGPPSTFN NRAYTPVSQGSNSSADPKAPPPPVSGEPPT LGENPOLSOGGLHERRSLGVTRQFCPGOHR DVFFSDEMVPFSNMSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQCSLQ DMMVHQHGPRGVKGBPPPTQWTPSEGWTA GGTEPFSDCINMPHSLPPRGMAPHENMPGSQ MRLPGAFGMINSEMGEPNYPPASRFGLSGV SWPDDVYKIPDGRNFFPQQUISSGFGREFP NPQGLSEEMFQQQLAEKGLGTPGMAMEGIR PSMEMINSEMGGPNYPPASRFGLSGV SWPDDVYKIPDGRNFFPQQGISSGFGREFP NPQGLSEMFQQQLAEKGLGTPGMAMEGIR PSMEMINSMEMGENPYPPYNPASRFGLSGV SWPDDVYKIPDGRNFFPQQGISSGFGREFP NPQGLSEMFQQQLAEKGLGTPGMAMEGIR PSMEMINSMEMGENPYNPASRFGLSGV SWPDDVYKIPDGRNFFPQQGISSGFGREFP NPQGLSEMFQQQLAEKGLGTPGMAMEGIR PSMEMNRMFGSGRIMEPNNPIFFRPVGG SWPDDVYKIPDGRNFFPQQGISSGFGREFP NPQGLSEMFGQQAEKGLGTPGMAMEGIR PSMEMNRMFGSGRIMEPNNPIFFRGHPQGC ULFYSGEFFOQOLAEKGLGTPGMAMEGIR PSMEMNRMFGSGRIMEPNNPIFFRFGWPGG SWPDDVKLPDGRNFFPQQGLSEFGFGPQOHR RCGLFFFTMSQGFGSNSGLRNLEFPGIPQQC ULFYSGEFFTLANSQGFGREFP NPQGLSEMFGAAAASQVHIRSSFJAAPSFGNTSS PEPPLSSGPFPLKSFTMHQVQ SPMLGSPSGNLKSPQTPSSLAGAPLAACASSIKSSPJAAPSFGNTSS PEPPLSGGPFRHKSFTMHQVQ SPMLGSPSGNLKSPQTPSSLAGAMALONYESG GPPPPTLASOGAASASVHIKSSFSPAAPSGWTSS GPPPPTASOGAASSVIPGSLSFSPAAFSGWTSS GPPPPTASOGAASSVIPGSLSFSPAAFSGWTSS GPPPPTASOGAASSVIPGSLSFSPAAFSGWTSS GPPPPTASOGAASSAFAHLTMSFAMLONYESG			<del>  .                                     </del>	(749	12	1662	FVGAPRRGNPFGSPGNPGRHQGPCHRPRGTK
LDSGSLTSLDSSVFCSEGEGEPLAIGDCF1VN VGGSRFVLSQQALSCPHTRL GKLAVVVASY RRFGALAAVFSPLELCDDANPVDMSFFDRS SQAFRYVHYRTGRLHVMEQLCALSFLQEI QYWGDELSIDSCCCDRYFRRKELSTLDFKK DTEDQESQHESEQDFSQGFTVRQKLWNIL EKFGSSTAARIFGVISIIFVGVSIBMALMSAEL SWLDLQLLEILEYVCISWFTGFFVLFLCVRD RCRFLRKVPNIDLLAILFFTVILLVESLSGSQT TQELENVGAHCFGCLRLLALRAMLKAWGR HSTGLRSLGMTTIQCYEVELLLFLSVGISIB STVEYFAEQSIPDTTFTSVPCAWWANTTSMT TVGYGDIRPDTTTGKURGLLLALFLSVGISIB STVEYFAEQSIPDTTFTSVPCAWWANTTSMT TVGYGVDIRPDTTTGKURGLLLALFLSVGISIB STVEYFAEQSIPDTTFTSVPCAWWANTTSMT TVGYGVDIRPDTTTGKURGLLSGLVLALFI AINDRFSACYFTLKLKEAAVRGREALKKLTK NIAIDSYSIVNLRDVYARSMMLRLKGRER ASTRSSGGDPWF  828 2178 A 6786 5672 1360 GTHFASSGFVPLFFAAVSAATREELGEPVFV TASSGFQSMHSSNPRVRSSPSGNTQSSPKSKQ EVMVRPTVVMSPSGNPQLDSKFSNGHCOSS ASQSQSPSDCDSKSGGHTFKALFGPGGSMGLK NGAGNGAKGKGRERSISADSFDQRDGTPN DDSDLECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGQTTATEPTPAQKTPAVVYVFS TEMANKAAEAVLKGQVETIVSFHIQNISNNK TERSTAPLNTQISALRNDPKPLFQQPPAPANQ DQNSSQNTRLOFSVGSPASTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADFKAPPPPPYSGCEPT LGENPDGLSQGQLEHERSLQTLLDQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGF QAMMAGSSGLGKGGFGRFSPPYSGFPT LGENPDGLSQGQLEHERSLQTLLDQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGF QAMMAGSSGLGKGGFGRFPPYNGAPFFGQGFG QAMMAGSSGLGKGGFFRSLGTLDHDHMTT EGIAWLKLQCFFYEEKRRFEQVVVQCSLQ DMMVHQHGPRGVVRGPPPYQMTPSEGWAP GGTEPTSDGINMPHSLPPFGGMAEGIR PSMEMNRMPGSGSULGKPFPRPVGAFFGPGGF NPGGLSEEMFQQLAEKRRFEQVVVGCSLQ DMMVHQHGPRGVVRGPPPYQMTPSEGWAP GGTEPTSDGINMPHSLPPFGGRGEFFP NPGGLSEEMFQQLAEKRRFEQVVXGSLG SWPDDVPKIPDGRNFPPQGGFSGFGREFFP NPGGLSEEMFQQLAEKRRFEQVVYGCSLQ DMMVHQHGPRGVVRGPPPYQMTPSEGWAP GGTEPTSDGINMPSLPPFGGREFFPQGFGFEF NPGGLSEEMFQQLAEKRFEGMYPSGM KGDVNLNVNMGSNSQMIPQKMREGGNPFPRIPVEGF PSPFGGDMLPSQGSMLFACAGFEEE MLLRPGGGSMLFARPSPTSPLYRBFTHUGVQ SPMLGSPSGNLKSPGIPPQLAGMAEGR PSMEMNRMPGSSGNLRALREPIGPDQ RTNSRLSHMPLLHNFSSNPTSLNTAPPVQRG LGRKPLDISVAGSQSVHYSSFPTYTMPFETIL SGRSSPPULASSAGNAVFFESTPTTMPFETIL GREPPFTSDGTRKSPSTPTTMPFETTL	827	2177	A	0/48	1 2	1002	ASGVSPTLWRPOAAATGLEMPSSGRALLDSP
VGGSRFVLSQOALSCFPHTRLGKLAVVASY RRRGALAAVPSPLELCDDANPVDNEYFFDRS SQAFRYVLHYYRTGRI.HVMEQLCASFLQEI QYWGIDELSIDGCCRDRYPRKELSETLDFKK DTEDQESQHESEQDFSQGPCPTVRQKLWNIL EKPGSSTAARIFGVISIIFVGVSIINMALMSAEL SWLDLQLLELBYVCISWFTGEFVLRFLCVRD RCRFLRKVPNIDLLAILPFVITLLVSLOSIQT TQELENVGAHCPGCLILLFLAURMI.KA WGR HSTGLRSLGMTITQCYEEVGLLLIFLSVGISIF STVEYFAEGSPDTTFTSVACAWWATTISMT TVGYGDIRPDTTTGKIVAFMCLSGISLUV.LLPI AIINDFSACYFTLKLKEAAVROREALKKL.TK NIATDSYJSVNLRDVYARSIMEMLRLKGRER ASTRSSGGDDFY TASSGFOSMISSNPKVRSSPSGNTCSSPKSKG ASTRSSGGDFYLPFAAVSAATREELGEPVPFV TASSGFOSMISSNPKVRSSPSGNTCSSPKSKG GTHPASSGFVPLPFAAVSAATREELGEPVPFV TASSGFOSMISSNPKVRSSPSGNTCSSPKSKG NGAGNAKKGKRERESISDFORDROFGTPN DDSDIECNSADHIKSQDSQHTPISMTPSNAT APRSSTPPHGQTTATEPTRAQKTPAKVYNAYA APRSSTPPHGQTTATEPTRAQKTPAKVYNAYA TERSTAFLNTQISALRNDPKPLPGOPPAFANO DONSSQNTRLQFPTPFAARAAPPREPLDRE SFGVENKLIPSVGSSPASSTPLPPDGTGFNSTPN NRAVTPVSQSNSSSADPKAPPPPPVSGCPPT LGENPDGLSGEOLEHRERSLOTLRDIGMLFP DEKEFTGAQSGGPQONPGVLJGPOKKPEGP QAMMAGSGLGKGPPRTDVGAPFPOGHR DVFFSDEMVPSPMNSQSSTIGPDLDHMTT EQIAVLKLQGEFYEEKRRFEQVVVQCSLQ DMMVHQHGPRGVVRGPPPYGMTSEGMAP GGTEPFSDESINMPHSLPPFGGFSCPGREFF NPGGLSEMFQQQLAEKQLGLPPGMAMEGIR PSMENNRMPGSGRHMEFGNNPFTSEUWAP GGTEPFSDESINMPHSLPFRGMAPHPNMPGSQ MRLPGFAGMINSEME GPNVPNASRFGLSGV SWPDDVPKLIPDGRNFPPPQGGFSCPGREFF NPGGLSEMFQQQLAEKQLGLPPGMAMEGIR PSMENNRMPGSGRHMEFGNNPFTSEUWAP GGTEPFSGESMMPHSLPFFGRAPPSGMAMEGIR PSMENNRMPGSGRHMEFGNNPFTFRUYEGP LSPSRGDFFRGJPPCMGFGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREGGREFF NPGGLSEMFQQQLAEKQLGLPPGMAMEGIR PSMENNRMPGSGRMMPGKMREGGNSGLRLEPIGPDQ YGMGPRPLPLNSGOPGSNSGLRLEPIGPDQ RTNSRLSHMPLPLNPSSNFTSLNTAPPYQGG LGRKPLDISVAGSQVHSSPLPPSGGMTS GPSPPTASGAGASPFULKSFSTPTTMPEYGL GGSPPPTASGAGASPFULKSFSTPTTMPEFTL			1		Ì		LDSGSLTSLDSSVFCSEGEGEPLALGDCFTVN
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QYWGIDELSIDSCCRDRYFRERLSETLUMIL DEDOCOMES OPECOPTYOR (LIWIL) EKPOSSTAARIFOVISIIF VOG SIIIMALMSAEL SWLDLQLLEILEYVCISWFTGEFVLRELCVRD RCRELRKVPNIDLLAILPFYITLLVESLSGISQT TQELVENVGAHCPGCLRILLRALRMI KAA WGR HSTGLRSIG, GMTTQCYEVGLLLLELSVGISBF STVEYFAEQSIPDTIFTSVPCAWWATTSMT TVGYGDBPDTTTGKTVAFMCILSGILVLALPI AINDRFSACYFTLKLKEAAVRQREALKKLTK NIATDSYISVNLRDVYARSIBEMLRLKGRER ASTRSSGDDEWF ASTRSSGODDEWF TASSGFOSMHSSINFKVRSSPSGNTOSSPKSKQ EVMVRPPTVMSPSGNPQLDSKRSKQGOGS ASQSOPSPCDSKSGGHTPKALPGPGGSMGLK NOAGNGAKGKGRERSISADSFOQRDPGTPN DDSDIKECNSADHKSQDSQHTPKALPGPGGSMGLK NOAGNGAKGKGKRERSISADSFOQRDPGTPN DDSDIKECNSADHKSQDSQHTPKALPGPGGSMGLK TERSTAPLNTQISALRADPKPLPQOPPAPANQ DOMSSONTRLQPTPPPAPKPAPPRPLDRE SPGVENKLIPSVGSPASTLPPDGTGFONSTPN NRAVTIVSQGSNSSSADPKAPPPPVSSGEPTI LGENPDGLSQEQLEHERESUCJTLRDIQRMLFP DEKEPTGAQSGGPQONGGVLDGPÇKKPEGPI QAMMAQSOSLGKGFGPRTDVAPFSFOQHLDHMTP EQIAWLKLQQEFYEEKRRPEQVVVQQCSLQ DMMYHQHGPRQVVRGPPPYQMTPSGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNNYPPSSWFGLSGW SWPDDVKRIPDGRNFPQGGTSGFGGREFF NPQGLSEEMFQQLAEKGLGLPPGMAMEGR PSMEMNRMFSGSRHMEPGGNPIPFPYGFO LSPSRGDPFRGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPGKREAGAGPE MKLRPGGSDMLTAQQKMVPLPFGEHFQQE YGMGPRFLPMSQOPGSNSGLNLREPIGPQG YGMGPRFLPMSQOPGSNSGLNLREPIGPQG RTSNELSHMPPLLINPSSNFTSLNTAPPPVQG LGRKPLDISVAGSQVHSPGINPLKSFTMHQVQ SPMLGSPSGNLKSPJTPSQLAGMLAGPAAAA SKSPPVLGSAAASPVHLKSPSLAASPSGWTSS PEPPLQSRGPPPNIKKSPLASSIFSLYTMPPESTI	1			1			RRPGALAAVPSPLELCDDANPVDNEYFFDRS
DTEDQESQHESQOPFSQGPCPTYRQKLWML EKPOSSTAARIFQVISIIFVOSIINMALMSAEL SWLDLQLLEILEYVCISWFTGEFVLRFLCVRD RCRFLRKVPNIDLLAILPFYITLLVESLSGSQT TQELENVGAHCPGCLRLLRALVRMLKAWGR HSTGLRSLGMTTTQCYEVGLLLLFLSVGISIF STVEYFAEQSIPDITTISVPCAWWAMTISMT TVGYGDIRPDTTTGKIVAFMCILSGILVLALPI AINDRFSACYFTLKLKEAAVROREALKKI.TK NATDSYISVNLRDVYARSIMEMLRLKGRER ASTRSSGGDDFWF  TASSGFQSMHSSNPKVASSASGRTQSSPKSKQ EVMVRPPTVMSPSGPTQSSFTQSSPKSKQ EVMVRPPTVMSPSGPTQLDSKFSNQGKOGGS ASQSQPSPCDSKSGGHTPKALPGPGGSMGLK NGAGNGAKGKGKRERSISADSFQRDGTTPN DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGGTTATEPTPAGKTFAKVVYYFS TEMANKAAEAVLGQVETIVSFHQNISNNK TERSTAPLNTQISALRNDPFPLPQOFPAPANQ DQNSSQNTRLQVTPTPLPAAPKPAPPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADPKAPPPPVSGEPPT LGENPPGLSQEGLEHRESLQTLRDIQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPTTDVGAPFPPOGHR DVPSSPDEMVPPSNNSQSGTGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVGFPFYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVKRDPGRNFPPQGFFGGRGERFP NPGGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMINGSGSGMHEPGNNPIPFRYEGE LSPSRGDPPKGIPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MKLRPGGSDMLFAQQKMVPLPFGEHPQQE YGMGPRFFLPMSQOPGSNSGINALEPIGPQQE RTNSILS.SHMPPLLTNPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHISPGINNLEPIGPQTS SILSHMPPLLTNPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHISPGINALEPIGPQTS SILSHMPPLLTNPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINALEPIGPQTS SILSHMPPLLTNPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINALESPIGPTS PEPPLQSGGPPPNIKKSPLTARSPGAMLGOVESS BEPPLQSGGPPPNIKKSPLTARSPGAMLGOVESS BEPPLQSGGPPPNIKKSPLTARSPGAMLGOVESS BEPPLQSGGPPPNIKKSPLTSTPTTMPPETIL	1					1	SQAFRYVLHYYRTGRLHVMEQLCALSFLQEI
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TVGYGDIRPDTTIGKIVAFMCILSGILVLALPI AINDRFSACYTILKLEAAVRQREALKKLTK NIATDSYISVNLRDVYARSIMEMLRLKGRER ASTRSSGCDDFWF TGHPASSGVPVLPPAAVSAATREELGEPVPFV TASSGFQSMHISSNPKVRSSPSGNTOSSPKSKQ EVMVRPPTVMSPSGNPQLDSKFSNQGKQGGS ASQSQPSPCDSKSGGHTPKALPGPGGSMGLK NGAGNGAKGKGKRERSISADSFDQRDGTDFN DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGQTTATEPTPAQKTPAKVVVVFS TEMANKAAEAVLKGQVETIVSFHIQNISNNK TERSTAPLNTQISALRNDPKPLPQOPPAPANQ DONSSQNTRLQPTPPTAPAPKPAAPPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADPKAPPPPVSSGEPPT LGENPDGLSQGQLEHRERSLQTLRDIQRMLFP DEKEPTGAQSGGPQONPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPCGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAVLKLQCEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPSDGINMPHSLPPRGMAPHENMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGJEPFGMAMEGR PSMEMNRMIPGSQRHMEPGNNPIFPRDVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPGKMEAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE TYGMGPRFPLPMSQQPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLFLINPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHSFGINPLKSPTMHQVQ SPMLGSPSGNLKSPOTIPGSLGGMLAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS FPEPLQSFGIPPNIKAPLTMASPAMLGNVESG				-			HSTGLKSLGMTTQCTEEVGLEELESVOOR
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DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS TEMANKAAEAVLKGQVETIVSFHIQNISNNK TERSTAPLNTQISALRNDPKPLPQOPPAPANQ DQNSSQNTRLQPTPPIPAPARKPAAPPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTFN NRAVTPVSQGSNSSSADPKAPPPPVSSGEPPT LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGFGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPQGIFSGPGRGFFP NPQGLSEEMFQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MILKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLFLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGNPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPASPFGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPIL				ļ			ASOSOPSPCDSKSGGHTPKALPGPGGSMGLK
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TEMANKAAEAVLKGQVETTVSFHIQNISNNK TERSTAPLNTQISALRNDPKPLPQQPPAPANQ DQNSSQNTRLQPTPPIPAPAPKPAAPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADPKAPPPPVSSGEPPT LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQLAWLKLQQEFYEEKRRPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPQGIFSGPGRERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRFFLPMSQQPGSNSGLRNLREPIGPDQ RTNSRL SHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSFSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSSLPSSTIPYTMPPEPTL		}					DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT
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DQNSSQNTRLQPTPPPAAAPKPAAPPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPT LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVFFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQLAWLKLQQEFYEEKRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPQQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQQPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPSSTPYTMPPEPTL							TEMANKAAEAVLKGQVETIVSFHIQNISNIK
SPGVENKLIPSVGSPASSTPLPPDGTGFNSTPN NRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPT LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEPTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPASPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL							TERSTAPLNTQISALRNDPRPLPQQPPAPANQ
NRAVTPVSQGSNSSSADPKAPPPPVSSGEPPI LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGFI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQLAWLKLQQEFYEEKRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSIPPTSLPAPSPGWTSS PEPPLQSPGIPPNIKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEFTL				1			DONSSON IKLOP I PRI PROGREDI STEN
LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEFTGAQSGEPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVFFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQLAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQQPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL			)	}	į	1	SPGVENKLIPS VUSPASSTELT DUTCH NOTE.
DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEFFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTIMIQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSSLPSSTPYTMPPEPTL	[				Ì		NRAV IPV SQUSINSSSADI RATTITI VODESTI
QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG'SLPSSTPYTMPPEPTL	1		1	Ì			DEVERTGA OSGGPOONPGVI.DGPOKKPEGPI
DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQCCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL	Į.		ł				OAMMA OSOSI GK GPGPRTDVGAPFGPOGHR
EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL					1		DVPESPDEMVPPSMNSOSGTIGPDHLDHMTP
DMMVHQHGPRGVVRGPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDVPKIPDGRNFPPGQGIFSGPGRERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL					1		FOIAWI KLOOEFYEEKRRKPEOVVVQQCSLQ
GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL							DMMVHOHGPRGVVRGPPPPYQMTPSEGWAP
MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL	}			1	1		GGTEPESDGINMPHSLPPRGMAPHPNMPGSQ
SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL	1		,				MRLPGFAGMINSEMEGPNVPNPASRPGLSGV
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PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL							NPOGI SEEMFOOOLAEKOLGLPPGMAMEGIR
LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL							PSMEMNRMIPGSORHMEPGNNPIFPRIPVEGP
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MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL		)					V CDVNI NVNMGSNSOMIPOKMREAGAGPEE
YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPGSLPSSTPYTMPPEPTL							MI KI RPGGSDMLPAOOKMVPLPFGEHPQQE
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LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL			İ				RTVSRLSHMPPLPLNPSSNPTSLNTAPPVQRG
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residue of peptide sequence   Y=Tyrosine, X=Unknown, *=Stop or /=possible nucleotide deletion, \text{ possible nucleotide insertion}   NTVASSDDDSPPARSPNLPSMNN QNPRISGPNPVVPMPTLSPMGMT   MPSPNAVGPNIPPHGVPMGPGLM GSQEPPMVPQGRMGFPQGFPVV   HNGPSGQQGSFPGGMGFPGEGP  SSADAALCKPGGPGGPDSFTVLC   DPDLQEVIRPGATGIPEFDLSRIIP YFPRGEVPGRKQPQGPGPGFSHN APRMGLALPGMGGPGPVOTPDL GHNPMRPPAFLQQGMMGPHHR   MPGQPTLMSNPAAAVGMIPGKL   HPGPVGSPGMMSMQGMMGPMGPVGPGPGFGGGGGGGGGGGGGGGGGGGGGGGGG	han.
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829 2179 A 6797 433 3 ASFFNFSICICKIILEVGPPVGHPASSRWGV 830 2180 A 6800 3 1911 KTVASSDDDSPPARSPNLPSMMNN QNPRISGPNPVVPMPHGPMNNN GSQEPPVPNGRGFGGRGR ASTCPPSPGGGGRAGRAGAGPAMELRARGWWLLA ARGDPASKSRSCGEVRQIYGAK AEISGEHLRICPQGYTCCTSEME ELETALRDSSRVLQAMLATQLR LNDSERTLQATFPGAFGELYTQI SEIL IV VYRGANI HILETLAEFW	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
RTVASSDIDISPPARSPNLPSMINN QNPRISGPNPVVPMPTLSPMGMT MPSPNAVGPNIPPHGVPMGPGLN GSQEPPMVPQGRMGFPQGFPPVG HNGPSGGQGSFPGGMGFPGEGPI SSADAALCKPGGPGGPDSFTVLC DPDLQEVIRPGATGIPEFDLSRIP YFPRGEVPGRKQPQGPGPGFSIN APRMGLALPGMGGPGPVGTPDI GHNPMRPPAFLQQGMMGPHIR MPGQPTLMSNPAAAVGMIPGKL HPGPVGSPGMMSMQGMMGPV GPGGR/GSRSPRSLQCAPGGGRR ASTCPPSPGGSGADRFGPSPPPS AAASSTSSGASCPPVPASSRWGV GEREPRDRPSERPRLV  B30 2180 A 6800 3 1911 DPERAFGPRTPRAPRRRRRLLL DREPRAPGPWLCPSRAGTAQDP VAGGAAGPAMELRARGWWLLA ARGDPASKSRSCGEVRQIYGAK AEISGEHLRICPQGYTCCTSEME ELETALRDSSRVLQAMLATQLR UNDSERTLQATFPGAFGELYTQI SSELPL VYRGANI HILEETLAEFW	O ADC) ACIDIT
MPSPNAVGPNIPHGVPMGPGLM GSQEPPMVPQGRMGFPQGFPPVC HNGPSGQGSFPGGMGFPQGFPPVC HNGPSGQGSFPGGMGFPQGFPVC BSADAALCKPGGPGPDSTVLC DPDLQEVIRPGATGIPEFDLSRIIP YFPRGEVPGRKQPQGPGPGFSHN APRMGLALPGMGGPGPVGTPDL GHNPMRPPAFLQQGMMGPHIR MPGQPTLMSNPAAAVGMIPGKL HPGPVGSPGMMMSMQGMMGP ASFFNFSICICKIILEVGPPVGHPA GPGGR/GSRSPRSLQCAPGGGRR ASTCPPSPGGSGADRFGPSPPPS AAASSTSSGASCPPVPASSRWGV GEREPRDRPSERPRLV  B30 2180 A 6800 3 1911 LPERAFGPRTPRAPRRRRRLLL DREPRAPGPWLCPSRAGTAQDP VAGGAAGPAMELRARGWWLLA ARGDPASKSRSCGEVRQIYGAK AEISGEHLRICPQGYTCCTSEME ELETALRDSSRVLQAMLATQLR LNDSERTLQATFPGAFGELYTQI SEI BLVVRGANIHLEETLAEFW	ON STIENT
GSQEPPMVPQGRMGFPQGFPPVCHNGPSGQQSFPGGMGFFGGGPISSADAALCKPGGPGGPDSFTVLCDPDLQEVIRPGATGIPEFDLSRIPYFPRGEVPGRKQPQGPGPGFSHMAPRMGLALPGMGGPGPVGTPDLIGHNPMRPPAFLQQGMMGPHIRMMPGQPTLMSNPAAAVGMIPGKLHPGPVGSPGMMSMQGMMGPHIRMMPGQPTLMSNPAAAVGMIPGKLHPGPVGSPGMMSMQGMMGPWGPGPGPGSPGGGGGGGGGGGGGGGGGGGGGGGGG	QPLSH3NQ
HNGPSGQGSFPGGMGFPGEGPI SSADAALCKPGGPGPDSFTVLC DPDLQEVIRPGATGIPEFDLSRIIP YFPRGEVPGRKQPQGPGPGFSHA APRMGLALPGMGGPGPVGTPDII GHNPMRPPAFLQQGMMGPHIRI MPGQPTLMSNPAAAVGMIPGKL HPGPVGSPGMMSMQGMMGPH ASFFNFSICICKIILEVGPPVGHPA GPGGR/GSRSPRSLQCAPGGGRR ASTCPPSPGGSGADRFGPSPPPS AAASSTSSGASCPPVPASSRWGV GEREPRDRPSERPRLV  830 2180 A 6800 3 1911 LPERAFGPRTPRAPRRRRRLLL DREPRAPGPWLCPSRAGTAQDP VAGGAAGPAMELRARGWWLLA ARGDPASKSRSCGEVRQIYGAK AEISGEHLRICPQGYTCCTSEME ELETALRDSSRVLQAMLATQLR LNDSERTLQATFPGAFGELYTQU SEI PL VYRGANI HLEETLAEFW	ASHNPIMGH
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B36 2186 A 6862 315 11 PPRSRPSCWRKKVGPGRPWWGGTGPPGQG RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI			[	1	1		CNSARNVPDDILOLLEEERWAFVMVSLFHGE
GGDYDGAGKYRKKTTCKAPWRTSSRMSS     836   2186   A   6862   315   11   PPRSRPSCWRKKVGPGRPWWWGGTGPPGQG     RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL     PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT     GPGSGRPPP   VLRGQRGPAGGLAEERRGRNEWRIHDVTT     APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC     NEDGLTALHQCCIDNFEEIVKLLLSHGANVN     AKDNELWTPLHAAATCGHINLVKILVQYGA     DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY     QGITQEKINEMRVAPEQQMIADIHCMIAAGQ     DLDWIDAQGATLLHIAGANGYLRAAELLLDH     GVRVDVKDWDGWEPLHAAAFWGQMQMAE     LLVSHGANLNARTSMDEMPIDLCEEEFKVL     LLELKHKHDVIMKSQLRHKSSLSRRTSHRQA     S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI			[	İ			LIOWOPIRPMCSTVADHFDHIKAV\IGSKFIGI
836 2186 A 6862 315 11 PPRSRPSCWRKKVGPGRPWWWGGTGPPGQG RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI			1	1		1	GGDYDGAGKYRKKTTCKAPWRTSSRMSS
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PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELK'HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI	836	2186	A	0862	212	111	RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL
837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELKYHKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI			1		1	1	PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT
837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK'HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI	1		1.	1	1	1	GPGSGRPPP
APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELKYHKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI					<del></del>	1615	VI RGORGPAGGLAEERRRGRNEWRIHDVTT
NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELKYHKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNLYRKEYE/GEEAI	837	2187	A	6863	12	1012	APEPGLVORRSRLLIVSOVRYFLKNKVSPDLC
AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI							NEDGI TAL HOCCIDNEEEIVKLLISHGANVN
DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI						1	AKDNEL WTPLHAAATCGHINLVKILVOYGA
QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI							DI LAVINSDGNMPYDI CEDEPTI.DVIETCMAY
DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI							OCITOEKINEMR VA PEOOMIA DIHOMIA AGO
GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI		1		1	1		DI DWIDA OGATI I HIA GANGVI RA AFILLI DH
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S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI							TEANUMUMINAVI SMITEMI IDECEEPEL KAT
LWQRSA\AEDQRTSTYNGDIRET\RTDQENKD					1	1 .	CCVCVVVDDTOPVCTCDNI \VDKEVF/CFF 41
LWQKSAVAEDQKTSTTWDDKETWTDQENAD			1		1		1 MOBS VYEDOBLELANGUBEL/BLDUENKU
					<u> </u>		LW QKOM WED QK 131 1 HODINET KTD QENKD

	_				D V and and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	****	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location		M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	Ì	ĺ	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	)		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ì	ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
		Ì	l .	peptide	,	nucleotide insertion
	ļ	1		sequence	<u> </u>	PNPRLEK\PVLLSEFPTKIPRGELDMPVENGLR
	1				1	APVSAYQYALANGDVWKVHEVPDYSMAYG
			1		Į.	APVSAYQYALANGDVWKVALVIDISHITI
	1					NPGVADATPPWSSYKEQSPQTLLELKRQRAA
		ì	ł			AKLLSHPFLSTHLGSSMARTGESSSEGKAPLI
		1				GGRTSPYSSNGTSVYYTVTSGDPPLLKFKAPI
	1	1	ţ			EEMEEKVHGCCRIS
838	2188	A	6865	6291	739	AGPLEPRVQGAMALQLWALTLLGLLGAGAS
636	2166	1		1	(	LRPRKLDFFRSEKELNHLAVDEASGVVYLGA
		1	1			VNALYQLDAKLQLEQQVATGPVLDNKKCTP
İ	1	l l	1		1	PIEASQCHEAEMTDNVNQLLLVDPPRKRLVE
		ļ	1	ļ		CGQLLKGI\CALRALSNISLRLFYEDGSGEKSF
	Ì	}	l			VASNDEGVATVGLVSSTGPGGDRVLFVGKG
		1	ł	}	ì	NGPHDNGIIVSTRLLDRTDSREAFEAYTDHAT
ļ		1				YKAGYLSTNTQQFVAAFEDGPYVFFVFNQQD
l		1				KHPARNRTLLARMCREDPNYYSYLEMDLQC
İ						RDPDIHAAAFGTCLAASVAAPGSGRVLYAVF
		ł	}			SRDSRSSGGPGAGLCLFPLDEVHAKMEANRN
İ						ACYTGTREARDIFYKPFHGDIQCGGHAPGSSK
1	1	1	1			SFPCGSEHLPYPLGSRDGLRGTAVLQRGGLN
1	į	1				LTAVTVAAENNHTVAFLGTSDGRILKVYLTP
					1	DGTSSEYDSILVEINKRVKRDLVLSGDLGSLY
	ŀ		1		1	AMTQDKVFRLPVQECLSYPTCTQCRDSQDPY
1	i				Ì	CGWCVVEGRCTRKAECPRAEEASHWLWSRS
Ì		-	-	1		KSCVAVTSAQPQNMSRRAQGEVQLTVSPLPA
ļ						LSEEDELLCLFGESPPHPARVEGEAVICNSPSS
		1	- }			IPVTPPGQDHVAVTIQLLLRRGNIFLTSYQYPF
1		1			1	YDCRQAMSLEENLPCISCVSNRWTCQWDLR YHECREASPNPEDGIVRAHMEDSCPQFLGPSP
ł		- 1			1	AHECKE AS AN LEGGAN LOTAK GSSI HAGSD
	Ì	1	1			LVIPMNHETDVNFQGKNLDTVKGSSLHVGSD LLKFMEPVTMQESGTFAFRTPKLSHDANETL
	ſ			1		LLKFMEPVIMQESGIFAFKIFKLSHDANETE
1	1					PLHLYVKSYGKNIDSKLHVTLYDCSFGRSDC SLCRAANPDYRCAWCGGQSRCVYEALCNTT
1	1	1	1	}		SECPPPVITRIQPETGPLGGGIRITILGSNLGVQ
	1	1	Ì	Ì		AGDIQRISVAGRNCSFQPERYSVSTRIVCVIEA
		ļ	Ì	1		AGDIQRISVAGRICSFQFER 13V51R1VCVDF
İ			ŀ			KPLSVEPQQGPQAGGTTLTIHGTHLDTGSQED
		ļ				VRVTLNGVPCKVTKFGAQLQCVTGPQATRG
1	1	]	1	į.		QMLLEVSYGGSPVPNPGIFFTYRENPVLRAFE
]		1			}	PLRSFASGGRSINVTGQGFSLIQRFAMVVIAEP
1						LQSWQPPREAESLQPMTVVGTDYVFHNDTK
			1		Į.	VVFLSPAVPEEPEAYNLTVLIEMDGHRALLRT
		1		1	1	EAGAFEYVPDPTFENFTGGVKKQVNKLIRAR
ļ	Į					GTNLNKAMTLQEAEAFVGAERCTMKTLTET
				}	1	DLYCEPPEVQPPPKRRQKRDTTHNLPEFIVKF
1		1			1	GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM
				i	1	VVVIAVSVYCYWRKSQQAEREYEKIKSQLEG
1		- 1		{		LEESVRDRCKKEFTDLMIEMEDQTNDVHEAG
	1			1		LEESVKUKUKKET I DUNIENEDŲ TRO TIEAU
				1		IPVLDYKTYTDRVFFLPSKDGDKDVMITGKL
	1					DIPEPRRPVVEQALYQFSNLLNSKSFLINFIHT
						L'ENQPEFSARAKVYFASLLTVALHGKLEYYT
ļ		-			1	DIMHTLFLELLEQYVVAKNPKLMLRRSETVV
						ERMLSNWMSICLYQYLKDSAGEPLYKLFKAI
	1	1		l		KHQVEKGPVDAVQKKAKYTLNDTGLLGDD
		1				VEYAPLTVSVIVQDEGVDAIPVKVLNCDTISQ
	1	- 1	ŀ	l		VKEKIDQVYRGQPCSCWPRPDSVVLEWRPG
	i					
1			İ			STAQILSDLDLTSQREGRWKRVNTLMHYNVR
						DGATLE SKVGVSOOPEDSOODLPGERHALL
						DGATLILSKVGVSQQPEDSQQDLPGERHALL FFFNRVWHLVRPTDEVDEGKSKRGSVKEKE
						DGATLE SKVGVSOOPEDSOODLPGERHALL

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D-Accordic Acid F=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine K=I.vsine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
•			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uence	1		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown,stop codon,
	1	1	1	peptide	-	/=possible nucleotide deletion, \=possible
	4		1	sequence	1	nucleotide insertion
	<u> </u>		<b></b>	Sequence	<del> </del>	HIWKTNSLPLRFWVNILKNPHFIFDVHVHEVV
	ļ	}	ł		1	DASI SVIAOTEMDACTRTEHKLSRUSPSNALL
	1	l l	1	J	1	VAKEISTVKKMVEDYYKGIROMVQVSDQDM
		[	1	ŀ		NITHI AFISRAHTDSLNTLVALHQLYQYTQKY
			i			YDEINALEEDPAAQKMQLAFRLQQIAAALE
	ļ	Ì	1	1		NKVTDL RARRLALQCHVCVCALTPGEQSGRRLPGQT
	2189	A	6872	1	1485	RARRLALQCHVCVCALTTGEQSGIGGET Q2
839	2107	Α	00,2	1		WLMFSCFCFSLQDNSFSSTTVTECDEDPVSLH
		1	1		ļ	EDQTDCSSLRDENNKENYPDAGALVEEHAPP
	1	1	]	ļ		SWEPQQQNVEATVLVDSVLRPSMGNFKSRKP
	1	1	ĺ	ł		VSIEW AFSGRSHGESOETEHVVSSQSECQVKA
	1		1			GTDAHESPONNAFKCOET\VRL\QPRIDQRIAI
		1				CDKDAFFTR\ODLNEEEAAQVHGVKDPAPAS
		}		1	1	TOSVI ANDGTDSADPSPVHKDGONEADSAPE
[		1	1	1	1	DLHSVGTSRLLL/YHITDGDNPTAVRHGCSL/F
				1	1	SGQSQRFNLDPESAPSPPSTQQFMMPRSSSRC
	ŀ	ì	}			SCGDGKEPQTITQLTKHIQSLKRKIRKFEEKFE
1	1	ì	1	1		QEKKYRPSHGDKTSNPEVLKWMNDLAKGRK
l .	1			İ		QEKKYRPSHODKISNPEVERWINIDE BEOLET
	1	1	1	{		QLKELKLKLSEEQGSAPKGPPRNLLCEQPTVP
	1			}	Ĭ	RENGKPEAAGPEPSSSGEETPDAALTCLKERR
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ł	l		_ <del> </del> _	<del></del>	2054	FEDEVESFIRI FAMSLADLTKTNIDEHFFGVAL
840	2190	A	6873	2	2034	ENINDRSAACKRSPGTGDFSRNSNASNKSVDY
1	1	1	1			SPSOCSCGSLSSOYDYSEDFLCDCSEKAINKN
1	1	-	1	}		YLKQPVVKEKEKKKYNVSKISQSKGQKEISV
1	1		í	1		EKKHTWNASLFNSQIHMIAQRRDAMAHRILS
			1		,	ARLHKIKGLKNELADMHHKLEAILTENQFLK
1		1				QLQLRHLKAIGKYENSQNNLPQIMAKHQNEV
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1	1	ı				KNLRQLLRKSQEKERTLSRKLRETDSQLLKT
		1	i			KDILQALQKLSEDKNLAEREELTHKLSITTK
1	İ	1	ł	1		MDANDKKIQSLEKQLRLNCRAFSRQLAIETR
1	ì	,	1			KTLAAQTATKTLQVEVKHLQQKLKEKDREL
(	l l	l l	<b>\</b>	]		ETKNIVSHRILKNLHDTEDYPKVSSIKSVQAD
Į.	1	l	-			DVII PETSMRHOGTOKSDVPPL/TIKGKKAIG
	ì	-	1			MIDHKEKSTEINHEIPHCVNKLPKQEDSKKKI
	1	)	1			EDI SGEEKHLEVOILLENTGRUKDKKEDUEK
		1	ļ			VAUGUTEOFI PPKIIEVIHPERESNUEDVLVK
1		1		ļ	[	EKFKRSMQRNGVDDT\LGKGTAPYTKGPLRQ
1		1	1	İ		RRHYSFTEATENLHHGLPASGGPANAGNMR
1		1				KKHA2LIEWIEURUGELVOOLVILIOURG
1	1	1		1	1	YSHSTGKHLSNREEMELEHS\DSGYEPSFGKS
1			- 1			SRIKVKDTTFRDKKSSLMEELFGSGYVLKTD
			1			
				1		OSSPGVAKGSEEPLOSKESHPLPPSQASTSHA
						QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA EGDSKVTVVNSIKPSSPTEGKRKIII
					2967	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPARGTRAASGWOPPTYHSGRAFSARYPRP
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPARGTRAASGWOPPTYHSGRAFSARYPRP
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SPRGYSSHHGPSWRKKYSLVNRPPGPSDPPA
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA SPRAYRPI HGARGGOPPVPOOHVLERQVQLS
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDORPREGEGEPPRGOLOPSRPTRARG
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLYCOKEPGKPRMVKSVGSVGDSP
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPROAREASLVVTCRTNKF
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF RKNNYKWVAASSKSPRVARRALSPRVAAEN
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF RKNNYKWVAASSKSPRVARRALSPRVAAEN VCKASAGMANKVEKPQLIADPEPKPRKPATS
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF RKNNYKWVAASSKSPRVARRALSPRVAAEN VCKASAGMANKVEKPQLIADPEPKPRATS SKPGSAPSKYKWKASSPSASSSSSFRWQSEAG
841	2191	A	6874	3	2867	QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII  SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF RKNNYKWVAASSKSPRVARRALSPRVAAEN VCKASAGMANKVEKPQLIADPEPKPRKPATS

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Icoleucine K=Lysine, L=Leucine,
otide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O-Glutamine R=Arginine, S=Serine,
uence	1	}	914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \=possible
	{		1	sequence		nucleotide insertion  KGLVQVTKHRLCRLPPSRAHLPTKEASSLHA
	<del> </del>					VRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLS
			· [	1		LPSWRARRLSLSRSLVLNRLRPVASGGGKAQ
	1					DGSPWWRSKGYRCIGGVLYKVSANKLSK1SG
	}	1		1	[	OPSDAGSRPLLRTGRLDPAGSCSKSLASKAVQ
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				Ì		CERCPYTHDPEKVAVCTRFVRGICKKIDGIC
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í	ł	ļ				LCKLPSFISLQSSPSPGAQPRVRAPRAPLTKDS
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842	2192	Α	6898	506	2071	PNIKEKVINVDDDGNELGSGIMELTDTELILTT
				Ţ		DEPOSVKWHYLCLRRYGYDSNLFSFESGRRC
				ļ		OTGOGTEAEKCARAEELFNMLOEIMQNNSIN
1			1			VVEEPVVERNNHQTELEVPRTPRTPTTPGFAA
}	-	Ì		İ	[	QNLPNGYPRYPSFGDASSHPSSRHPSVGSARL
			1			PSVGEESTHPLLVAEEQVHTYVNTTGVQEER KNRTSVHVPLEARVSNAESSTPKEEPSSIEDR
		1				DPQILLEPEGVKFVLGPTPVQKQLMEKEKLE
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						NTENVTVPASAHKIEYSRRRDCTPTVFNFDIR
		Į.				RPSLEHRQLNYIQVDLEGGSDSDNPQTPKTPT
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	ļ	1				PRDDGTSR\KTRHNST\DLPL AGRPGTTHASGKMAYQSLRLEYLQIPPVSRA
843	2193	A	6919	2	663	VTTACVI TTAAVOLELIIPFULYFNPELIFAAF
1		1			ļ	OUND ITNE FEGPVGFNFLFNMIFLYRYCKM
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	1					WTHIFFLGRCISQSTWWNKNSENTIYFESYF
844	2194	-	6928	902	366	HRLCMPIQGACGERME/FSLLLPGLECNGVIL AHCNLRLPGSSNSPASASQVAGITGVCHHAR
844	2194	1		l l		LIFVFSVETGFLHAGQAGLELLTSGDPPASAS
1		}		1		QSAGITGKSQHTRPGYEFIIPYSAAQEDALKA
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1					İ	VDKKWDSNVIETFDIARLTVNADVGYYSWK
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK
						HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVI
1						YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK
	1					MYKACLKYPEWKQKHL\PHFKPWL\HPEQSP LPSLALS\ELSVQHADS\LENIDESAV\AESREE
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		1			[	PGAGRALGAAAAPALSPLHPPGTWWHRARP
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SEQ ID SEQ III D NO. of nucleotide peptide coulded sequence unner the peptide sequence unner the period of peptide sequence unner the period of peptide sequence unner the period of peptide sequence unner the period of peptide sequence period of peptide sequence unner the period of peptide sequence period of peptide sequence unner the period of peptide sequence period of				050	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO. of NO. of the mucle oxide	SEQ ID	SEQ ID	Met	SEQ			D=Aspartic Acid, E=Glutamic Acid,
nucre outde sequence peptide control of the property of the pr	1		nod				F=Phenylalanine, G=Glycine, H=Histidine,
contect   corresponding to first at mino acid residue of peptide residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide sequence   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide   corresponding to first at mino acid residue of peptide	nucl-			1			I=Isoleucine, K=Lysine, L=Leucine,
### Before the control of the contro	eotide						M=Methionine, N=Asparagine, P=Proline,
### Particle of peptide residue of peptide sequence peptide sequence peptide sequence peptide sequence per per per per per per per per per pe	seq-	uence	i				O=Glutamine, R=Arginine, S=Serine,
Page   Page	uence			914	, .		T=Threonine, V=Valine, W=Tryptophan,
Peptide   Pept	}		1				Y=Tyrosine, X=Unknown, *=Stop codon,
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ELTILGETQEEDELIPRKDYSELJDYS VIEWLETMONKKGRRYEAVKWMVYPA CTGLVGLPVDFFVRLFTQLKFGVVOTGY QKGCLALSLELLGPNLTFVELSELJGSL AGSGITBGKCYLYARQVPGLVRIPTUTU GYLLTVAAMLILGLGSPMIBSGSVVGA FQSISLRKIQPNFPYFRSDRYGKDKDRF AAAGVAAAFGAPIGGTLFSLEGSSFW TWKVIPCSMSAFITILNFTRSGIQFGSW PGLLNFGEFKCSDSDFKCHLWTAMDL VMGVIGGILGATIFNCLKKLAKYRMRI KPKLVRVLESLLVSLVTTVVVFVASM RQMSSSQIGDISSPQLVCTEDVNSSIKTI NDTYNDMATLFFNPGESALQLFHQDG TLALFFVLYFLLACWTVGISGHPYSGIFVP GAAFGRLVANVLKSYIGLGHNYSGTTA AFLGGVVRMTISLTVLLESTNETTYGLE LMVGKWTGDFFNKGNVDIHVGLRGVP ETEVENDKLSTABDIMEPTLTVYPHTR SLRTTVHHAFPVVTENRGNEEPKMC NNIKFKKSSLITRAGEGRASSMKSYF RNMCDEHLASEPPAKEDLLQOMLESTNETTYGLE LMVGKWTGDFFNKGNVDIHVGLRGVP ETEVENDKLSTABDIMEPTLTVYPHTR SLRTTVHHAFPVVTENRGNEEPKMC NNIKFKKSSLITRAGEGRASSMKSYF RNMCDEHLASEPPAKEDLLQOMLESTNETTYGLE LMVGKWTGDFFNKGNVDIHVGLRGVP ETEVENDKLSTABDIMEPTLTVYPHTR SLRTTVHHAFPVVTENRGNEEPKMC NNIKFKKSSLITRAGEGRASSMKSYF RNMCDEHLASEPPAKEDLLQOMLESTNETTYGLE LMVGKWTGDFFNKGNVDIHVGLRGVP ETEVENDKLSTABDHITVYPHT SLRTTVHHAFPVVTENRGNEEPKMC NNIKFKKSSLITRAGEGRASSMKSYF RNMCDEHLASEPRALTVYPHTV SLRTTVHHAFPVVTENRGNEEPKMLV NNIKFKVSSLITRAGEGRASSMKSPHRYVTVPV TVSNTTHVGQVFNLFTMGLRHLPVVN NVGIITRHLTYFELOALLANG NNIKFKSSLITRAGEGRASSMKSPHRYVTVPV CLICKRSMSVSKEVNLRRHYOTHMSH MFRANDELLDTLDHTNTTQLAFTR NFDVSEELLDTVPMTGTKSGNLEFSKF MFRANDELHELKKGLRKYLLGISDT QKQVFANPSTQKSPVQPVEDLAGNU NFTENSKLVAVSATGTTPMVDANNG KSRNATFCKGAELKSICCHHPESLOCA DHVMDVVXSVNWINGSRGNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKALSKGLNHSEFTT DSQYGSLLYYTELKWLSKGLNHSEFTT DSQYGSLLYYTELKWLSKALSKGLNHSEFTT DSQYGSLLYYTELKWLSKALSKGLNHSEFT DSQYGSLLYYTELKWLSKALSKGLNHSEFT DSQYGSLLYYTELKWLSKALSKGLNHSEFT DSQYGSLLYYTELKWLSKALSKGLNHSEFT DSQYGSLLYYTELKYTLLKYTH NFTAMATATATATATATATATATATATATATATATATATAT			<u> </u>	L		2672	RRKMAGCRGSLCCCCRWCCCCGERETRTPE
### VILEVLETMDNKKGRRYEAVKUMVOTSV CTGLVGLEVDFFVRLETGLKFGVVQTSV CTGLVGLEVDFFVRLETGLKFGVVQTSV QKGCLALSLLELLGFNLTTVFLESLLGSVGA GFUSTLRVGFNFYFRESDFQLVRETGLWGVLYAR GVLTTVAAMLINGLGSPMIHSGSVGA FQSISLRKIQFNFYFRESDFQKDKRDF AAAGVAAAFGAPIGGTLFSLEEGSSFW TWKVLFCSMSATIFILNFFRSGIQFGSW PGLLNFGEFKCSDSDKCKGLWTAMDLG VMGVIGGLLGATTNCLNKRLAVYRMAN KPKLVRVLESLLVSLTVTVVFVASMV RQMSSSQIGNDSFQLQVTEDVNSSIKI NDTYNDMATLFPNQESALQLFHQDG TLALFFVLYFLLACWTYGISVPSGLFV GAAFGRLVAVVLKSYIGLGHYSGTFAI AFLGGVRMTISLTVILESTNEITYGL LMVGKWTGGFFNGGIVGHYSGTFAI AFLGGVRRMTISLTVILESTNEITYGL LMVGKWTGGFFNGGIVGHYSGTFAI AFLGGVRRMTISLTVILESTNEITYGL LMVGKWTGGFFNGGIVGHYSGTFAI AFLGGVRRMTISLTVILESTNEITYGL LMVGKWTGGFFNGGIVGLGFFYGFAI AFLGGVRRMSSSAGPRLSVSAG NNIKFKKSSLTFAGEGRKRSQSMSSY RNMCDEFILASEFAKEDLLQOMLERR PNLYPDQSFSDWTMGEFRPLTFHFGLI LVTLLVRGVCYSESQSSAGPRLSVSAG YRPYPDHEIDLDTLLNFRMTUDVTTPM TVSPNTHVSQVFNLFRTMGLRHLPVY TVSPNTHVSQVFNLFRTMGLRHLPVY TVSPNTHVSQVFNLFRTMGLRHLPVY TVSPNTHVSQVFNLFRTMGLRHLPVY SWRRILEAGFIKFTVIRHPUDLELSNG VGKRKIDQEGRVFQEKWERAYFFVCH CICKESMSVSKEYNLRHPQTHSKY MERMBDEKLHELKKGLRKYLLGSLSSA VGKRKIDQEGRVFQEKWERAYFFVCH CICKESMSVSKEYNLRHPQTHSKY MERMBDEKLHELKKGLRKYLLGSLAGNU EKRISTVA YSIADDEITDINTTIQLAFI NFDVSEELLDTVPMTGTKSQNEIFSRV NFCNNSKLVSVASTGTPHVDANNOI KSRVATFCKGAELKSICGHPBSLOAD DHYMDVVKSVNWICSGRMHSEFTT DSQYGSLLYYTELKWLSRGLVILKFTSL WSRGLVLAKSGLVLKFTSEL WSRGLVLAKSGLVLKFTSL WSRGLVLAKSGLVLKFTSL WSRGLVLAKSGLVLKFTSL WSRGLVLKSVSSCHAPSLFCAU WSTHLTRNAHPFTLKLVSNRESDGL KAELKTEFQKRLSDFKLYRSELLTL WSRGLVLKSVSSCHAPSLFCAU WSTHLTRNAHPFTIKLVSRNESDGL KAELKTEFQKRLSDFKLYRSELLTL WSRGLVLKSVSSCHAPSLFCAU WSTHLTRNAHPFTIKLVSNRESDGL KAELKTEFQKRLSDFKLYRSELLTL WSRGLVLKSVSSCHAPSLFCAU WSTHLTRNAHPFTIKLVSRNESDGL KAELKTEFQKRLSDFKLYRSELLTL KSTHLTRNAHPFTIKLVSRNESDGL CFNANTKTPIQGLSEYTRINQCPKEA  B48 2199 A 6999 963 5 LDFLCHRDMGDNTSITEFILLGSLDSK MYFLSHLAVVDUAYACNTVFRKLVL AXPISEAGRAMOTFLEFSTAVTECLLVL AXPISEAGRAMOTFLEFSTAVTECLLVL AXPISEAGRAMOTFLEFSTAVTECLLVL AXPISEAGRAMOTFLEFSTAVTECLLVL AXPISEAGRAMOTFLEFSTAVTECLLVL AXPISEAGRAMOTFLEFSTAVTECLLVL	846	2196	A	6944	42	2072	FLTILGETOEEEDEILPRKDYESLDYDRCINDP
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FQSISLRKIQFNPYFRSDRYGKLOKRDF AAAGVAAFGAPIGTISLEEGSSFW TWKVLFCSMSATFILNFFRSGIQFGSW PGLLNFGEFKCSDSKKCLWTAMDLG VMGVIGGLGATNCLNKRLAKYRMRI KPKLVRVLESILVSLVTIVVVYVASMV RQMSSSSQIGNDSFQLQVTEDVNSSIKT NDTYNDMATLFFNPQESAILQLFHQDG TILALFFYLYFILLACWTYGISVPSGIFVPY GAAFGRLVANVLKSYIGLGHIYSGTFAI AFLGGVVRMTISLTVILESTINETTYGLE LMVGKWTGDFFNKGNYDIHVGLRGVP ETEVEMDKLRASDIMEPNLTYVYPHTR SILRTTVHHAPPVVTENRGNEKEFMKG NNIKFKKSSILTRAGEQRKRSQSMKSYR RNMCDEHJASEPTAEKEDLLQQMLERR PNLYPDQSPSEDWTMEERFRPLTFHGLI LVTILVRGVCYSEQSSASOPPLSYAE PRYPDTHDLDLTILNPRMIVDVTPYM TVSSNTHYSQVFNLFRTMGLRHLPVN TVSSNTHYSQVFNLFRTMGLRHLPVN TVSSNTHINTYELQARIACHTYPL TVSSNTHYSQVFNLFRTMGLRHLPVN TVSSNTHINTYELQARIACHTYPL SSKERIGLEAOFICHTURDLFGLELSNG VKRKINQEGRVFQEKWERAYFFVEW CLICKRSMSVSKEYNLRRHYQTHSKI- MERMDEKLHELKKGLRKYLLGLSDT OKOVPANPSPTQKSPVQPVERWERAYFFVEW CLICKRSMSVSKEYNLRRHYQTHSKI- MERMDEKLHELKKGLRKYLLGLSDT OKOVPANPSPTQKSPVQPVERWERAYFFVEW CLICKRSMSVSKEYNLRRHYQTHSKI- MERMDEKLHELKKGLRKYLLGLSDT OKOVPANPSPTQKSPVQPVERMERFRYD NFCINWSKLVSVASTGKLGRSVULGLSDT OKOVPANPSPTQKSPVQPVERMEFTT DSQYGSLLYTTEIK WLSRGLVLKFFFE DSFMSRGKPLPQLSSIDWRDLAFLY HINALNISLQGHSQUTOMYDLIRAFL- WETHLTRINLAHFPTLKLVSRNESDGI KIAELKTEFQKRLSPKLYESELLTPSS DSVHEELQMEVIDLQCNTVLKTKYDK FYKYL WGSYPKYKHHCAKILSMFGST LSFIMKLSKTKYCSQLKDSQWDSVLH- WETHLTRINLAKFTPLLASRNESDGI KIAELKTEFQKRLSPKLYESELLTPSS DSVHEELQMEVIDLQCNTVLKTKYDK FYKYL WGSYPKYKHHCAKILSMFGST LSFIMKLSKTKYCSQLKDSQWDSVLH- LSFILKSKTKYCSQLKDSQWDSVLH- LSFILKSKTKYCSQLKDSQWDSVLH- ASAPVQCLLLMAATTSTEELLIGFVGF LLFGLFRSTFYTHLLGFFUGFLICAFT ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLAKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAATTSTOPLALKFTFL ASAPVQCLLLMAAT	•	1	1			1	GVILTVAAMLLI\GLGSPMIHSGSVVGAGLPQ
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TWKVLFCSMSATFTLNFFRSGIQFGSWC PGGLLNFGEFKCSDSDK-LIN-TAMDLG VMGVIGGLLGATFNCLNKRLAKYRMR KPKLVRVLESLLVSLVTTVVVPVASMVV RQMSSSSQIGNDSFQLQVTEDVNSSIKTI NDTYNDMATLFFNPQESALLQLFHQDG TLALFFVLYFLLACVTYGISVPSGLFVP GAAFGRLVANVLKSYIGLGHIYSGTFAI AFLGGVYRMTISLTVLLESTNEITYGLF LMVGKWTGDFFRKGNYDHVGLRGVP ETEVEMKKLRASDIMEPNLTVVPPHRT SURTITVHHAFPVYTENRRNEKEFMKG NNIKFKKSSILTRAGEQRKRSQSMKSYF RNMCDEHLASEFPAEREDLLQQMLERR PNLYPOQSPSEDWTMEERFRPLTTHGLI LVTLLVRGVCYSESQSSASQFPLSYAER PYRYPDHDLDLTLNPRMIDVVTPVM TVSSNTHVSQVFNLFTRIMGLRHLPVN VGITTRINTYELQARLRQHYQTI NTNSSSVTNSAAGVEDLNIQVTVPDM LSSIERIKQLREQVNLDLFSKRFGEAIGVY VPYRKITFNPGCVVIDGMPGGVYKAP SSMRRILAAEFIKTVIRPLFGLELSNG VGKRKIDQEGRVFQEKWRAYFFVEW CLICKRSMSVSKEYNLRRYTVIRPLFGLELSNG VGKRKIDQEGRVFQEKWRAYFFVEW CLICKRSMSVSKEYNLRRYTJCHLSGLSTD OKQVFANPSPTQKSPVQPVEDLAGNLV EKIRSFVAYSIAIDEITDINNTTQLAFTER NFDVSEELLDTVPMTGTKSGNEFSRVI NFCINWSKLVSVASTGIDINNTTQLAFTER NFDVSEELLDTVPMTGTKSGNEFSRVI NFCINWSKLVSVASTGIDINNTTQLAFTER NFDVSEELLDTVPMTGTKSGNEFSRVI NFCINWSKLVSVASTGIDINNTTQLAFTER DSFMSRGKPLPQLSSIDWRBLAFLY HINALNISLQGHSQIVTQMYDLRAFL-L WETH TRNNLAHFPTLKLVSRNESDGI KIAELKTEFQKRLSPKLVSSELLTSNS DSVHEELQMEVIDLQCNTVLKTKYDK FYKYLWGSYPKYKHHCAKILSMFGST LFSIMKLSKTKYCSQLKDSQWDSVLH HINALNISLKTKYCSQLKDSQWDSVLH HISMLSKTKYCSQLKDSQWDSVLH LSELSKLKSKTKYCSQLKDSQWDSVLH LSFIKLSKTKYCSQLKDSQWDSVLH LSFIKLSKTKYCSQLKDSQWDSVLH LSFIKLSKTKYCSQLKDSQWDSVLH LSFIKLSKTKYCSQLKDSQWDSVLH LSFIKLSKTKYCSQLKDSQWDSVLH ASAPVQCLLLMAATSPQGLAKPHSGT CFNANTKIPIQRLESYTRTNIQCPKEA ASAPVQCLLLMAATSPPGLAKPHSGT CFNANTKIPIQRLESYTRTNIQCPKEA ASAPVQCLLLMAATSPPGLAKPHSGT CFNANTKIPIQRLESYTRTNIQCPKEA ASAPVQCLLLMAATSPPGLAKPHSGT LLFGLFFLFTFATUELLGFPVGFLL AXPPGFAGRMMOTFLFSTFATVERLLY AXPSGFAGRMMOTFLFSTFATVERLLY AXPSGFAGRMMOTFLFSTFATVERLLY AXPSGFAGRMMOTFLFSTFATVERLLY AXPSGFAGRMMOTFLFSTFATVERLLY AXPSGFAGRMMOTFLFSTFATVERLLY			}	}			AAAGVAAAFGAPIGGTLFSLEEGSSFWNQGL
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RQMSSSQIGNDSFQLQVTEDVNSSIKTI NDTYNDMAILFPNQESALQLFHQDG TILALFFVLYFLLACWTYGISVPSGLFVP GAAFGRLVANVLKSYIGLHTYSGTFAI AFLGGVVRMTISLTVILLESTNNEITYGLF LMVGKWTGDFFNKGIVYDHVGLRGVP ETEVEMDKLRASDMEPPLITYVPYPHTR SILRTTVHHAFPVVTENRGNEEFMKGI NNIKFKKSSILTRAGEQRRSQSMKSYP RNMCDEHIASEPAEKEDLLQQMLERR PNLYPDOSPSEDWTMEERFRPLITHGLL LVTLLVRGVCYSESQSSASQPRLSYAEN YPRYPDIHDLDLTLLNPRMIVDVTPYM TVSPNTHVSQVFNLFRTMGLRHLPVVN INGITTRHNITYPCLQARLRQHYQTI NTNSSSVTNSAAGVEDLNIVQVTVEDN SSMRRILEAAEFIKFTVIRPLFGLELSNG VGKRKIDQEGRVFQEKWERAYFTVEVV CLICKRSMSVSKEYNLRRHYQNTHSKH MERMGDEKLHELKKGLRKYLIGLBDT QKQVFANPSPTQKSPVQPVEDLAGNLV EKIRSFVAYSIAIDEITDINNTIQLAFTEN NFDVSEELLDTVPMTGTKSGNEIFSRVI NFCNWSKLVSVASTGTPPMVDANNGI KSRVATFCKGAELKSICCHPESLCAQ DHVMDVVVKSVNWICSGLNHSEFTT DSQYGSLLYYTEIKWLSRGLVLKRFFE DSFMSSRGKPLQLSSIDWRDLAFLVT HLNALNISLQGHSQIVTQMYDLIRAFLL WETHLTRNLAHFPTLKLVSRNESDGI KIAELKTEFGKRLSDFKLYSESLTLSSS DSVHEELQMEVIDLQCNTVLKTKFDE DSFMSRGKPLYSHHICAFLVL WETHLTRNLAHFPTLKLVSRNESDGI KIAELKTEFGKRLSDFKLYSESLTLFSSI DSVHEELQMEVIDLQCNTVLKTKFDFL FYKYLWGSYRKHHCAKILSMFGST LFSIMKLSKTKYCSQLKDSQWDSVLH FYKYLWGSYRKHHCAKILSMFGST LFSIMKLSKTKYCSQLKDSQWDSVLH FYKYLWGSYRKHHCAKILSMFGST LFSIMKLSKTKYCSQLKDSQWDSVLH SAPPVQCLLLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLUMAATFSPQGLAKPHSGI CFNANTKIPIGRLESTTATVFCLUL'			1		1	J	KPKI VRVLESLLVSLVTTVVVFVASMVLGEC
NDTYNDMATLFFPQESLAQUFYGISVPSGLFVP TLALFPVLYFLLACWTYGISVPSGLFVP GAAFGRLVANVLKSYIGLGHIYSGTFAT AFLGGVVRMTISLTVILESTNEITYGLF LMVGKWTGGFFRKGINYDIHVGLRGVP, ETEVEMDKLRASDIMEPRLTVYYPHTR SURTTVHHAFPVVTENGREKEFMKG NNIKFKKSSULTRAGEQRKRSQSMKSYF RNMCDEHLASEPAEKEDLLQQMLERR PNLYPDQSPSEDVMEERRPLTHGLL LVTLLVRGVCYSESQSSASQPRLSYAER YPRYPDIHDLDLTLLNPRMIVDVTPYM TVSPNTHVSQVFNLFRTMGLRFLPVVN IVGIITRHNLTYEFLQARLRQHYQTI NTNSSSVTINSAGVEDLNIVQVTVPDN LSSIEKIKQLREQVNDLFSRKFGEAIGVI VPYRKITFNIPGCVVIDGMPPGVVYRAP SSMRRILEAAEFIKFTVIRPLPGLELSNG VGKRKDDGGRVFQEKWERAYFFVEVV CLICKRSMSVSKEYNLRRHYQTINSKE MERMBDEKLHELKKGLRRYLLGLSDT QKQVFANPSPTQKSPVQVEDLAGNLV EKIRSFVAYSLAIDEITDINNTTQLAFFR NFDVSEELLDTVPMTGTKSGNEFSRVI NFCNWSKLVSVASTGTPMVDANNOI KSRVATFCKGAELKSICCHHPESLCAQ) DHVMDVVVKSVNWICSRGLNHSEFTTI DSQYGSLLYYTEIKWLSRGLVLKRFFE DSFMSSRGKPLPQLSSIDWIRDLAFLVI HINALNISLQGHSQIVTQMYDLIRAFLL WETHLTRINLAHPFTLKLVSRNESDGI KIAELKTEFQKRLSDFKLYESELTLFSS DSVHEELQMEVIDLQCONTVLKTKYDK FYR YLWGSYSFYKHHCAKUSMFGST LFSIMKLSKTKYCSQLKDSQWDSVLH  848 2198 A 6985 3 289 SVQYLPGRPTTHASTDAPLMLKFTPL ASAPVQCLLLMAATFSPQGLAKPHSGI CFNANTKIPIQRLESYTRITNIQCPKEA ASPPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIQRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIQRLESYTRITNIQCPKEA ASPPVGLESTARTVTLEILLIUGTGTLGLISLDSR MYFFLSHLAVVDIAYACNTVPRMLV9 AXPISFAGRMWDTLFSTFAVTFLCLLL'			1		}		ROMSSSSOIGNDSFQLQVTEDVNSSIKTFFCP
TILALFFVLYELLACWTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP GAAFGRIAMAVLKTYGISVPSGLFVP LMVGKWTGDFFNKGNYDITYGISTNEITYGIP ETEVEMOKLRASDIMEPNLTVYPHTR SILRTTVHHAFPVYTENRGEKEFMKG NNIKFKKSSILTRAGEGYRRSGSMKSYP RNMCDEHIASEPAEKEDLLQQMLERR PPLYPOSPSSEDWTMEERRFLTHGIL LVTLLVKGVCYSESQSSASQPRLSYAE YPRYPDHDLDLTLLNPRMVDVTPYM TVSPNTHVSQVFNLFTMOMPDVVTPDN LSEEKIKQLREQNIDLFSKRFGEAIGVI VPYRKITFNPGCVVIDGMPPGVVFAP SSMRRILEAAEFIKFTVIRPLPGLELSNG VGKRKIDQEGRVFQEKWERAYFPVEVC CLICKRSMSVSKEYNLRRHYQITHSK MERMEDEKLHELKKGLRKYLLGLSDT QKQVFANPSPTQKSPVQPVEDLAGNLV EKIRSFVAYSIAIDEITDINNTTQLAFFR NFDVSEELLDTVPMTGTKSGNEIFSRVI NFCINWSKLVSVASTGTFPMVDANNGI KSRVATFCKGAELKSICGIHPESLCAQ DHVMDVVVKSVNWICSRGLNHSEFTI DSQYGSLLYTEIKWLSSGLVIKRFFE DSFMSSRGKPLQLSSIDWRDLAFLVT HINALNISLQGHSQIVTJGMYDLIRAFLL WETHLTRNLAHPPTLKLVSRSDGI KIAELKTEFQKRLSDFKLYSSELTLFSSI DSVHEELQMEVIDLQCNTVLKTKTYDL WETHLTRNLAHPPTLKLVSRSDGI KIAELKTEFQKRLSDFKLYSSELTLFSSI DSVHEELQMEVIDLQCNTVLKTKTYDL ASAPVQCLLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESYTRITNIQCPKEA ASAPVQCLLMAATFSPQGLAKPHSGI CFNANTKIPIGRLESTFAVTFECLLL  B49 2199 A 6999 963 5 LDFLCHRDMGDNITSITEFLLGEPVGF LLFGLFSLFVYTLLGNGTLGLISLDSS MYFFLSHLAVVDIAYACNTVPRMLVA AXPISFAGRMMGTFTSFTAVTECLLL					1	1	NDTYNDMATLFFNPQESAILQLFHQDGTFSP
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AFLGGVRMTISLTVLIESTNEITYGLE LMVGKWTGDFFNKGINDIHVGLRGVP ETEVEMDKLRASDIMEPNLTYVYPHTR SILRITVHHAFPVVTENRGNEKEFMKG NNIKFKKSSLI TRAGEQRKRSQSMKSYP RNMCDEHIASEEPAEKEDLLQQMLERR PNLYPDQSPSEDWTMEERFRLIFHGLI LVTLLVRGVCYSESQSSASQPRLSYAEB YPRYPDHDLDLTLLNPRMIVDVTPYM TVSPNTHVSQVFNLFRTMGLRHLPVVN IVGITTRHNLTYEFLQARLRQHYQTI  847 2197 A 6951 3 1994 NTNSSSVTNSAAGVEDLNIVQVTVPDN LSSIEKIKQLREQVNDLFSRKFGEAIGVI VPYRKITENPGCVVIDGMPPGVVFKAP SSMRRILEAAEFIKFTVIRFLPGLELSNG VGKRKDQEGRVFOEKWERAYFFVEV CLICKRSMSVSKEYNLRRHYQTNHSKF MERMRDEKLHELKKGLRKYLLGLSDT QKQVFANPSPTQKSPVOPVEDLAGNLV EKIRSFVAYSIAIDEITDINNTTQLAFFR NFDVSEELLDTVPMTGTKSGNEIFSRVI NFCNWSKLVSVASTGTPPMVDANNGI KSRVATFCKGAELKSICCIHFESLCAQ DHVMDVVKSVNWICSRGLNHSEFIT DSQYGSLLYYTEIKWLSSGLVLKRFFE DSFMSSRGKPLPQLSSIDWIRDLAFLVT HLNALNISLQGHSQIVTOMYDLRAFLX WETHLTRNILAHFPTLKLVSRNESDGI KIAELKTEFQKRLSDFKLYESELTLFSSI DSVHEELQMEVIDLQCNTVLKTKYDK FYKYLWGSYPKYKHCAKILSMFGST LFSIMKLSKTKYCSQLKDSQWDSVLHI SSAPVQCLLLMAATFSPQGLAKPHSGT CFNAINTKPIQRLESYTRITNIQCFKEA  848 2198 A 6985 3 289 SVQYLPGRPTRTHASTDAPLMKFTFLI ASAPVQCLLLMAATFSPQGLAKPHSGT CFNAINTKPIQRLESYTRITNIQCFKEA LDFLCHRDMGDINTSTIEFLLLGFPVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLVGG LLFGLFSLFYVFTLLGNGTILLGFLSLDSR MYFFLSHLAVVDLAYACNTVYRMLV							GAAFGRLVANVLKSYIGLGHIYSGTFALIGAA
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KIAELKTEFQKRLSDFKLYESELTLFSSI   DSVHEFLQMEVIDLQCNTVLKTKYDK   FYKYLWGSYPKYKHHCAKILSMFGST   LFSIMKLSKTKYCSQLKDSQWDSVLHI   SVQYLPGRPTRTHASTDAPLMLKFTPL   ASAPVQCLLLMAATFSPQGLAKPHSGT   CFNAINTKIPIQRLESYTRITNIQCPKEA   CFNAINTKIPIQRLESYTRITNIQCPKEA   LDFLCHRDMGDNITSITEFLLLGFPVGF   LLFGLFSLFYVFTLLGNGTILGLISLDSF   MYFFLSHLVAVVDIAYACNTVPRMLVI   AKPISFAGRMMOTFLFSTFAVTECLLL'						1	WETHI TRINI AHEPTI KLUSRNESDGI NYI
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VSYMCILCALQIQSKEVQKKALCTOL			1			_!	V21WCITCYIFAIA3VE AAVAVI G1G121PG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	p <b>e</b> ptide	1	in USSN	nucleotide location	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Scrine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
	<del></del>	<del>                                     </del>	<del> </del>	5544555	<del> </del>	GLFYGTAIIMYVGPRYGNPKEQKKYLLLFHS
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		1			1	LAALSADLCFLALGPAW\CLRFS/GACGVQVA
					]	CGAAWTLALLLTVPSAIYRRLHQEHFPARLQ
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		1				VHKLPCRDDDGVTAKDLSKQLHSSVRTGNLE
						TCLRLLSLGAQANFFHPEKGTTPLHVAAKAG
		1	1			QTLQAELLVVYGADPGSPDVNGRTPIDYARQ
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						HKNGHYIIPQMADSLDLSELAKAAKKKLQAL
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						REIHKLQAENLQLRQPPGPVPTPPLPSERAEH
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				1		LSRHGSGADSDYENTQSGDPLLGLEGKRFLE
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		1	1	,		EQVTKNIQELLRAAQEFKHDSFVPCSEKIHLA
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852	2202	A	7016	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLL
W2	2202	' *		1		TVKGLLKPSFSPRNYKALSEVQGWKQRMAA
1		1	1		}	KELARONMDLGFKLLKKLAFYNPGRNIFLSP
					ļ	LSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP
1	1	1	1			EKDLHEGFHYIIHELTQKTQDLKLSIGNTLFID
1	1		1			QRLQPQRKFLEDAKNFYSAETILTNFQNLEM
		1			1	AQKQINDFI/ESKTHGKINNLIENIDPGTVMLL
1	İ	1	1			ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS
		ĺ		i		VKVPMMFRSGIYQVGYDDKLSCTILEIPYQK
					1	NITAIFILPDEGKLKHLEKGLQVDTFSRWKTL
	[				1	LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVS
1			1		1	KIFEEHGDLTKIAPHRSLKVGEAVNKAELKM
			1			DERGTEGAAGTGAQTLPMETPLVVKIDKPYL
			1			LLIYSEKIPSVLFLGKIVNPIGK
853	2203	A	7017	1	3293	MTHACNPSTLGGQGRRITRSHGRRRSSRGPV
						ARHVAAGAGHENKHGGSRRFPAGVAPRRAM
		1	1	1	1	ANVSKKVSWSGRDRDDEEAAPLLRRTARPG
						GGTPLLNGAGPGAARQSPRSALFRVGHMSSV
		1				ELDDELLEP\DMDPPHPFPKEIPHNEKLLSLKY
				1	į.	LEST DADVICENOTET EEEDDINIALAERTAEIKR
1				i		ESLDYDNSENQLFLEEERRINHTAFRTVEIKR
						WVICALIGILTGLVACFIDIVVENLAGLKYRVI KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV

NO: of NO: of hod ID NO: beginning nucleotide D	amino acid sequence (A=Alanine C=Cysteine,
NO. 01 NO. 01 NO.	=Aspartic Acid, E=Glutamic Acid,
	=Phenylalanine, G=Glycine, H=Histidine,
nucl-   popular   Im   Indetestina	= Phenylalanine, O-Otychic, 11-Thistianic,
eotide seq- USSN location corresponding I=	=Isoleucine, K=Lysine, L=Leucine,
seq uence 09/496 correspondi to last amino M	M=Methionine, N=Asparagine, P=Proline,
yence 914 ne to first acid residue Q	=Glutamine, R=Arginine, S=Serine,
amino acid of peptide T	=Threonine, V=Valine, W=Tryptophan,
residue of sequence Y	(=Tyrosine, X=Unknown, *=Stop codon,
lesidae ez	=possible nucleotide deletion, \=possible
i popular	nucleotide insertion
sequence n	VGSVIVAFIEPVAAGSGIPQIKCFLNGVKIPH
	A02AIAVIELAWOOMI OMICCI VACKECDVI
	VVRLKTLVIKVSGVILSVVGGLAVGKEGPMI
]	HSGSVIAAGISQGRSTSLKRDFKIFEYFRRDTE
K	(RDFVSAGAAAGVSAAFGAPVGGVLFSLEEG
	ASFWNQFLTWRIFFASMISTFTLNFVLSIYHG
	MWDLSSPGLINFGRFDSEKMAYTIHEIPVFI
	AMGVVGGVLGAVFNALNYWLTMFRIRYIHR
	PCLQVIEAVLVAAVTATVAFVLIYSSRDCQPL
	QGGSMSYPLQLFCADGEYNSMAAAFFNTPEK
	SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT
	SVVSLEHDFFGSTNFLIEGETEVITERENT
	YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG
	AAIWADPGKYALMGAAAQLGGIVRMTLSLT
	VIMMEATSNVTYGFPIMLVLMTAKIVGDVFIE
	GLYDMHIQLQSVPFLHWEAPVTSHSLTAREV
	MSTPVTCLRRREKVGVIVDVLSDTASNHNGF
	PVVEHADDTQPARLQGLILRSQLIVLLKHKVF
	VERSNLGLVQRRLRLKDFRDAYPRFPPIQSIH
	VSQDERECTMDLSEFMNPSPYTVPQEASLPR
	VFKLFRALGLRHLVVVDNRNQVVGLVTRKD
	LARYRLGKRGLEELSLAQTGPKAQATAEGRV
	AGAAQQPCQLRAVTLEDLGLLLAGGLASPEP
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	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ
	QEEQGREVACGALQKNQEDSSRRVDLEVAR
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2004	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP
854 2204 A 7037 139 2604	WLLWVVAATGTLVLLAADAQGQKVFTNTW
	AVRIPGGPAVANSVARKHGFLNLGQIFGDYY
	HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL
	EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG
	EQQVARRIARDVIQETDIRIQQWIESO
	VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI
	EKNHPDLAGNYDPGASFDVNDQDPDPQPRY
	TOMNDNRHGTRCAGEVAAVANNGVCGVGV
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	AYNARIGGVRMLDGEVTDAVEARSLGLNPN
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	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATOFGNVPWYSEACSSTLA
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATOFGNVPWYSEACSSTLA
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNONEKOIVTTDLRQKCTESHTGTSAS
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTIDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYQGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYQYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPOVLDTHYSTENDVETIRASVCAPCHAS
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYQYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPOVLDTHYSTENDVETIRASVCAPCHAS
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	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYQYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS OSSRESPPQQPPRLPPEVEAGQRLRAGLLPS
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SFEDEGRGERTAFIKDQSAL
	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL ORPASOLLAPFAAEALPGAPRAAMAQHFSLA
855 2205 A 7058 3 1441	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF
855 2205 A 7058 3 1441	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF
855 2205 A 7058 3 1441	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SSEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL
855 2205 A 7058 3 1441	HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
icl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
tide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
:q-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence		}	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ĺ		ļ	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	1 1	/=possible nucleotide deletion, \=possible
			1	sequence	1	nucleotide insertion
		<del> </del>	<del> </del>	3cquoit-		YFDLPGALLCARVVDYLTKLNNGQKTFDFW
		}		}	}	KDIVAAIQHNYKMSAFKENCGIYFPEIKRDPG
		1	l			RYLHSRPESVKKWLRQLKNAGKILLLITSSHS
		1	}	1		DYCRLLCA\YILGNDFTDLFDIVITNALKPGFF
						SHLPSQRPFRTLENDEEQEALPSLDKPGWYSQ
		1				GNAVHLYELLKKMTGKPEPKVVYFGDSMHS
		1				DIFPARHYSNWETVLILEELRGDEGTRSQRPE
	1	1	ł		1	ESEPLEKKGKYEGPKAKPLNTSSKKWGSFF\I
		ļ	Ì			DSVLGLENTEDSLVYTWSCKRISTYSTIAIPSI
	1	ł	1	1		EAIAELPLDYKFTRFSSSNSKTAGYYPNPPLV
						LSSDETLISK
356	2206	A	7082	396	1635	SSPSVFEFEHAVQPVFTMEFLKTCVLRRNACT AVCFWRSKVVQKPSVRRISTTSPRSTVMPAW
20	2200	1.,	1			VIDKYGKNEVLRFTQNMMMPIHYPNEVIVK
		-	İ			VHAASVNPIDVNMRSGYGATALNMKRDPLH
			1	1		VHAASVNPIDVNMRSGTGATTELITEREDVKYFK
	1	1	t			PGDEVWAAVPPWKQGTLSEFVVVSGNEVSH
	1	}	1		1	KPKSLTHTQAASLPYVALTAWSAINKVGGLN
		İ				DKNCTGKRVLILGASGGVGTFAIQVMKAWD
		- 1				AHVTAVCSQDASELVRKLGADDVIDYKSGSV
		1	}			EEQLKSLKPFDFILDNVGGSTETWAPDFLKK
	1			ļ.	ł	WSGATYVTLVTPFLLNMDRLGIADGMLQTG
		}	}	ļ	1	VTVGSKALKHFWKGVHYRWAFFMASGPCL
			1	1		DDIAELVDAGKIRPV\IEQTFPFSKVPEAFLKV
		-			1	EDGUADGKTVINVV
					2417	I DDDKMTPOSLLOTTLFLLSLLFLVQGAHGK
857	2207	Α	7088	320	2417	- LOUDEDER CORNOTHRSSLHYKP LYDLAGU
			ì			NORE AT TVHAPFPA AHPASKSFPDPKULT FIF
		- 1				L VVIDE LA GRI HI LYGKRDFLLSDKASSLLC
			}	ł		OHOREST AOGPPLLATSVISWWSPUNISLES
			1	l	İ	ACETECEUSPPHTGAHNASVUMCELKRULQL
	1			1		LSQFLKHPQKASRRPSAAPASQQLQSLESKL
	1	ł				SVRFMGDMGSFEEDRINATVWKLQPTAGLQ
			ļ			DLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKG
	1	}	1 .			RSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
	1		ſ			KVLGIVVQNTKVANLTEPVVLTFQHQLQPKI
	Ì	1	- [	1		VTLQCVFWVEDPTLSSPGHWSSAGCETVRR
				1		TOTSCFCNHLTYFAVLMVSSVEVDAVHKHY LSLLSYVGCVVSALACLVTIAAYLCSRVPLP
					)	RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEP
	ł	1				RRKPRDYTIKVHMILLLAVFLLDTSI ELEGI ALTGSEAGCRASAIFLHFSLLTCLSWMGLEG
		1				YNLYRLVVEVFGTYVPGYLLKLSAMGWGF
		- 1		1		FLVTLVALVDVDNYGPIILAVHRTPEGVIYP
				1	ļ	MCWIRDSLVSYITNLGLFSLVFLFNMAMLA
	i			{		MCWIRDSLYSTITNEOLISE TEATH
		Ì	-	1		WAI TERSEASCITEOL VVI.YLESIII SEQUELLE
	1	1		ļ		WYWSMRLQARGGPSPLKSNSDSARLPISSG
		1			1	TSSSRI
	1	1				DACAVESSOTNIWERGMCDDKKGHRCPS*(
858	2208	A	7091	185	415	QPQHFHVAFHTEAEGAMFYFRLHVIHRVM
333			Ì	1		QQQLFPSTLFSWLLE
ļ	]		Ì			FFFWRQSLALLPRLECSGATGAHCNLHFPGS
859	2209	A	7136	3	302	DCPTSAS*IAGITGACYHAWLLFVFLAETGF
0.59	1200			1		HVGQGGLELLTSSDPSGSASQSAGITGVSHC
				1		
	Ì	1				ALSTETRTPDMRRLLLVTSLVVVLLWEAGA
860	2210	A	7156	23	591	PAPKVPIKMQVKHWPSEQDPEKAWGARVV
1 000	2210	'`				PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGI
Į.	1			1	1	I DOUBLING IN VALUE ACCULATION TO THE WORK OF ACCU
		1			1	GPILPGTKAWMETEDTLGRVLSPEPDHDSL'

SEQ III   NO: of nucleotide corresponding nucleotide corresponding sequence   Sequence						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
No. of   N			Met	SEQ	Predicted		D=A spartic Acid. E=Glutamic Acid,
		1	hod	J i			F=Phenylalanine, G=Glycine, H=Histidine,
Sect			i			corresponding	I=Isoleucine K=Lysine L=Laucine,
Second   S	t ∫ s	seq-				to last amino	M=Methionine, N=Asparagine, P=Proline,
	\u	uence			correspondi		O=Glutamine, R=Arginine, S=Serine,
Part   Part	:	i	}	914			T=Threonine, V=Valine, W=Tryptophan,
Popsible nucleotide deletion, V-possible nucleotide n			l	ļ	***************************************		V=Tyrosine X=Unknown, *=Stop codon,
Sequence	,					sequence	/=possible nucleotide deletion, \=possible
	1		1	1			avolectide insertion
DHITYIPQ*GSRGHICPRPYPRICPS   CPS	1				sequence	ļ	LIDDREED OF FREI WYMPNHOVLLGPEEDQ
CPS						1	DHIYHPQ*GSRGHHCPRPVPRPRLLGLGPSLP
2211   A   7161   1220   1003   NVVCTIAF*EKKMGF*ISLSCL LTITIRIMFHCTYLFASVCLSL LTITIRIMFHCTYLFASVCLSL SSAMILQ   LKYYHIIMGIYKTGKKVIL*K KSAMILQ   LKYYHIIMGIYKTGKKVIL*K KSAMILQ   LKYYHIIMGIYKTGKKVIL*K KSAMILQ   LKYYHIIMGIYKTGKKVIL*K KSAMILQ   LKYYHIIMGIYKTGKKVIL*K   KYNIOKLSSINJYYHQNIVSFSCLPATGPT*GLVLV   RGQHEHKRMRAP*SCRVTWN   CKENYQSPEKECDYNILANS   CKENYQSPEKECDYNILANS   CKENYQSPEKECDYNILANS   CKENYQSPEKECDYNILANS   LYNYQOTATLAALEGTATYM KYNADATTYN KYNAD	1		ŀ		J	}	,
LTTTTRIMFHCTYLFASVCLSL	1		í		L		DRIVETAE*EVEMGE*I SLSCLVLLEVLELDCI
		2211	A	7161	1220	1003	NYVCTIAL ERRIVOL ESCUED VIEW INTLLSPNCL
2212   A   7211   665   847	1			1	1		
Main	1		1	1		1	KSAMILQ .
R63	<del></del> +	2212	A	7211	665	847	LKYYHIIMGIYKIGAKVIL KSSINSING SVA
2213   A   7212   724   7257		2212	1				YKNIQKLSFSNYVIHQNIVISSDWOIDI
LVWDSPSCLPATOPT**OLVTVN		2213	Α	7212	924	1273	HGSSCALGDLAPG*LPSGP*LSSPA*RL*ING
CIKPNYQSPRECDYNILANDA	1	2213	1 1	/			LVWDSPSCLPATGPT*GLVLVLGGPDCT*WA
864   2214   A   7214   845   1619   SDKGGKADRKNHHAFFL	1		}	]		1	RGQHEHKRMRAP*SCRVIVNLAKKKNIDQ
PPKVPVDADHIVQGQDPGRAF   No.   PPKVPVDADHIVQGQDPGRAF   No.   No.   PPKVPVDADHIVQGQDPGRAF   No.   PROBLEM   No.   PROBLEM   No.   PROBLEM   PROBLE			1			1	CIKPNYQSPPKECDYNILANSVA
DPKVPVDADHVQGQDPGRA/    KVSKDPLAPDEVGDTDEGHD    HGHDQEEVAYEERACEGGKF    DEALREAMFKVAKYAGGTNI    PISFAVFPNEDGSLQKKLKVW    PAPSDKSVKIEEREGITYYSM    YVAQATRIRAALEGTATYRC    MKPYGRNEIPILLKT    RRLGAVAHAYTSSTLGGRGG    LANMAKPRLY    B66   2216   A   7257   641   1310   TCTYKYLMGWIRGRRSRHSV    DLKKSDFSTRWQKQRCPVVF    FCCILAVAMGIRFIIMVAIWS/    QIPLTESYCGFCPKNWICYKN    WYESQASCMSQNASLLKVY;   KSYHWMGLVHIPTNGSWQW    IEMQKGDCALYASSFKGYLE    QRTV    R68   2218   A   7298   3   272   PDTVIGGRGSGGKEFGRWYI    R69   2219   A   7332   1223   332   PRRDAEDRESCLNPAFFIGI    R69   2219   A   7332   1223   332   PRRDAEDRESCLNPAFFIGI    R70   2220   A   7382   216   1018   EHQRLTERTQFLDESRKNP    AGOGRGREGAESGSREGG   FWSPSORRGCGGRRAPPS    KRYGGFMKKDGENKRD   KRYGGFMKKDGENKRD   AGOGRGREGAESGSREGG   FWSPSORRGCGGRRAPPS    KGLQLLISLLAFICEEVVSQ   VSCSAFLLSLILIVYCTPFY    FYITLGTGCVFLLASIIFVSTI    GFIASFMFLLDFITIMLYEKR		2214	<del> </del>	7214	845	1619	SDKGGKKADRKNHLRHAFPLLPHRVRERLH
KVSKDPLAPDEVGDTDGHD		2214	A	1214	L C+0	1	DPKVPVDADHVOGODPGRAAHDIHGEDVIE
Hohdoevayeera/CegraceGord   Deal Reampkvakyaggtnn   Deal Reampkvakyaggtnn   Deal Reampkvakyaggtnn   Desal Reampkvakyaggtnn   Desal Reampkvakyaggtnn   Desal Reampkvakyaggtnn   Desal Reampkvakyaggtnn   Desal Reampkvakyaggtnn   Desal Reampkvakyaggtne   Desal Reampkvakyagg			1				KVSKDPI APDEVGDTDEGHDRHGHREVGQK
DEALRAMPKVAKYAGGTINT    PISFAVFPNEDGSLQKKLKVW    PAPSDKSVKIEEREGITVYSM    YVAQATRIRAALEGTATYRC    MKPYGRNEIWLLKT    RRIGAVAHAYTSSTLGGRGG    LANMAKPRLY    LANMAKPRLY    LANMAKPRLY    LANMAKPRLY    CTYKYLMGWIRGRRSRHSV    LANMAKPRLY    CTYKYLMGWIRGRRSRHSV    LANMAKPRLY    CTYKYLMGWIRGRRSRHSV    LANMAKPRLY    CTYKYLMGWIRGRRSRHSV    LANMAKPRLY    FCCFIAVAMGIRFILMYAIWS,   QPITIESYCGPCPKNWICYK,   WYESQASCMSQNASLLKYY;   KSYHWMGLVHIPTNGSWW    IIEMOKGDCALYASSFKGYIE    QRTV    ORTV    MFFGQTLWLMNANARFCSIFT    MFFGQTLWLMNANARFCSIFT    MFFGQTLWLMNANARFCSIFT    MFFGQTLWLMNANARFCSIFT    KGSCPAGGSRMVSESD*EGR    KGSCPAGGSRMKRJGFMKMDAE    KRYGGFMKKNDAE    KRYGGFMKKNDAE    KELLETGDNERSHHQDGSI    KRYGGFMKKNDAE    KELLETGDNERSHHQDGSI    KRYGGFMKKNDAE    KELLETGDNERSHHQDGSI    KRYGGFMKKNDAE    KGLLELGLEVOKOW   KGLLETGDNERSHHQDGSI    KRYGGFMKRNGGFMKF    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KGLLETGDNERSHHQDGSI    KRYGGFMKRYGGFMKKNDAE    KGLLETGDNERSHHQDGSI    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KGLLETGNERSHHQDGSI    KRYGGFMKRYGGFMKKNDAE    KRYGGFMKRYGGFMKKNDAE    KGLLETGNERSHHQDGSI    KRYGGPMKRYGGFMKKNDAE    KGLLETGNERSHHQDGSI    KGSCPAGGSGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	l		1	İ	1	l .	HGHDOFEVAYEERACEGGKFATVEVIDKPV
PISFAVFPNEDGSLQKKLKVW   PAPSDKSVKIEEREGITVYSM   YVAQATRIRAALEGTATYRC   MKPYGRRNEIWLLKT   RRLGAVAHAYTSSTLGGRGG   LANMAKPRLY   RRLGAVAHAYTSSTLGGRGG   LANMAKPRLY   LANMAKPRLY   TCTYKYLMGWIRGRRSHISV   DLKKSDFSTRWQKQRCPVVF   FCCFLAVAMGIRFIIMVAIWS, QIPLTESYCGPCPKNWICYKN   WYESQASCMSQNASLLKVY, KSYHWMGLVHIPTNOS WQW   IEMQKGDCALYASSFKGYIE   QRTV   QRTV   WTENGAMORASLLKVY, WYESQASCMSQNASCHAPPPS, AGS*WR*GSGSGGKEFGRWVI	- 1		1	1	1	ŀ	DEALBEAMPKVAKYAGGTNDKGIGMGMIV
PAPSDKSVKIEBREGITVYKY   VAQATRIRAALEGTATYRC   MKYYQATRIRAALEGTATYRC   MKYYGRRNEIWLLKT     865   2215   A   7246   559   682   RRLGAVAHAYTSSTLGGRGG   LANMAKPRLY     866   2216   A   7257   641   1310   TCTYKYLMGWIRGRRSRHSV   DLKKSDFSTRWQKQRCPVV   FCCFLAVAMGIRFILMVAIWS   QIPLTESYCGPCFKNWICYKN   WYESQASCMSQNASLLKVY   KSYHWMGLVHIPTNGSWG   UIEMQKGCALYASSFKGYIE   QRTV   SIKIIEAFGSNGPDFWFFRYW   MPFQTLWLMNANRFCSIFT   TYYHCWLSVVVCRCESHGI   PDTVIGGRGSGGKEFGRWVI   KGSCPAGGSRMVSESD*EGR   AGS*WR*GSRPAGRGTPPRS     868   2218   A   7298   3   272   PDTVIGGRGSGGKEFGRWVI   KGSCPAGGSRMVSESD*EGR   AGS*WR*GSRPAGRGTPPRS   AGS*WR*GSRPAGRGTPPRS   GFLTLCTWLLLLGPGLLATVR   YRLVRPADINFLACVMECEC   KELLQLSKPELPQDGTSTLR   KRYGGFMKKMDE   KRYGGFMKKMDE   KELLETGDNRERSHHQDGSI   FMRGLKRSPQLKEKAKELD   PQKW*MTSPQNRYGGFMKKMDE   KELLETGDNRERSHHQDGSI   FMRGLKRSPQLKEKAKELD   PQKW*MTSPQNRYGGFMKKMDE   KELLETGDNRERSHHQDGSI   FMRGLKRSPQLKEKAKELD   PQKW*MTSPQNRYGGFMKKMDE   KGLLAKRYGGFMKKMDE   KELLETGDNRERSHHQDGSI   FMSFRSQRRGCCGRRAPRF   TEEDPGPARGPRSGLAYFF   KGLQLLLSLLAFICEEVVSQ   VSCSAFLLSLLILIVYCTFFY   FYITLGTGCVFLLASIIFVSTI   GFIASFMFILDPITMLYEKRI   GFIASFMFILDPITMLYEKRI   PAFAL TEPL NA	1		1				DISEAVEPNEDGSLOKKLKVWFRIPNQFQSDP
See   2215   A   7246   559   682   RRLGAVAHAYTSSTLGGRGG   LANMAKPRLY   RRLGAVAHAYTSSTLGGRGG   LANMAKPRLY   DLKKSDFSTRWCKORCPVVM   FCCFLAVAMGIRFILMVAIWS/ OJPLTESYCGPCPKNWICYKN   WYESQASCMSQNASLLKVY.	1					1	DADSDKSVKIEEREGITVYSMOFGGYAKLAD
MKPYGRRNEIWLLKT	- 1		1		İ		YVAQATRLRAALEGTATYRGDIYFCTGYDPP
865         2215         A         7246         559         682         RRLGAVAHAYTSSTLGGRGG LANMAKPRLY           866         2216         A         7257         641         1310         TCTYKYLMGWIRGRRSRHSV DLKKSDFSTRWQKQRCPVVM FCCFLAVAMGIRFILMVAIWS/QIPLTESYCGPCPKNWICYKN WYESQASCMSQNASLLKVYM WYESQASCMSQNASLLKVYM KSYHWMGLVHIPTINGSWQW IIEMQKGDCALYASSFKGYIE QRTV           867         2217         A         7288         151         396         SIKIIEAFGSNGPDFWFFRYW MPFFQTLWLMNANRFCSIFT TPYHCWLSVVVCRCESHGI           868         2218         A         7298         3         272         PTTVIGGRGSGGKEFGRWVI KGSCPAGGSRMVSESD*EGR AGS*WR*GSRPAGRGTPPRS.           869         2219         A         7332         1223         332         PRRDAEDRDESCLNPAFIGI FLTLCTWLLLLGPGLLATVR YRLVRPADINFLACVMECEC KELLQLSKPELPQDGTSTLRI KRYGGFMKKDAE KELLETGDNERSHHQDGSI FMRGKRSPQLKEKAKELQ PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMKKDAE KELLETGDNERSHHQDGSI FMRGKRSPQLKEKAKELQ PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMKKDAE KELLETGDNERSHYGGFM KGDGL FMRGKGSGRGEG FWSPRSQRRGCCGRRAPRPI TEEDPGPARGRSGLAAYFF KGLQLLISLLAFICEEVVSQ VSCSAFLLSLLLLIVYCTPFY FYTLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI GFIASFMFLLDFITMLYEKRI PAFAI TEPI NA	1		1			1	LAUDVCDRNFIWLLKT
R65	ļ					- (82	RRI.GAVAHAYTSSTLGGRGGWIT*GQELQTS
866   2216   A   7257   641   1310   TCTYKYLMGWIRGRSRHSV DLKKSDFSTRWQKQRCPVVF FCFIAVAMGIRFIIMVAIWS, QIPLITESYCGPCPKNWICYKN WYESQASCMSQNASLLKVY: KSYHWMGLVHIPTNGSWQM IIEMQKGDCALYASSFKGYUE QRTV   QRTV   MPFFQTLWLMNANRFCSIFT TYYHCWLSVVVCRCESHGI   PDTVIGGRGSGGKEFGRWI KGSCPAGGSRMVSESD*EGR AGS*WR*GSRRAGSFDFRS.   869   2219   A   7332   1223   332   PRDAEDRDESCLNPAFPIGI FLTLCTWLLLLGPGLLATVR YRLVRPADINFLACVMECEC KELLQLSKPELPQDGTSTLR KRYGGFMKRYGGFMKMD NGSELAKRYGGFMKKMD NGSELAKRYGGFMKKMD NGSELAKRYGGFMKKMD NGSELAKRYGGFMKKMD NGSELAKRYGGFMKKMD NGSELAKRYGGFMKKMD FMRGLKRSPQLKEKAKELQ PPKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMKF GFWSPRSQRRGCCGRRAPRI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQ VSCSAFLLSLLLLVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKR	, – 1	2215	Α	7246	559	002	I ANTALK PRIV
B66   2216   A   7237   G41   DLKKSDFSTRWQKQRCPVVF   FCCFLAVAMGIRFIIMVAIWS/ QIPLTESYCGPCPKNWICYKN   WYESQASCMSQNASLLKVY: KSYHWMGLVHIPTNGSWQW   IIEMQKGDCALYASSFKGYIE QRTV   G770   G77	ļ		l			1210	TCTYKYLMGWIRGRRSRHSWEMSEFHNYNL
FCCFIAVAMGIRFIIMVAIWS;   QIPLTESYCGPCPKNWICYKN   WYESQASCMSQNASLLKVY;   KSYHWMGLVHIPTNGSWQW   IIEMQKGDCALYASSFKGYIE   QRTV   SIKIIEAFGSNGPDFWFFRYW   MPFFQTLWLMNANRFCSIFT   TPYHCWLSVVVCRCESHGI   TPYHCWLSVVVCRCESHGI   WGSCPAGGSRMVSESD*EGR   AGS*WR*GSRPAGRGTPPRS;   AGS*WR*GSRPAGRGTPPRS;   PRRDAEDRDESCLNPAFPIGI   FLTLCTWLLLLGPGLLATVR   YRLVRPADINFLACVMECEC   KELLQLSKPELPQDGTSTLRI   KRYGGFMKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   PQKW*MTSPQNRYGGFLKR   SYSKEVPEMERRYGGFMKF   KELLETGDNRERSHHQDGSI   FMRGLKRSPQLKEKAKELQ   PQKW*MTSPQNRYGGFLKR   SYSKEVPEMERRYGGFMKF   KELLETGDNRERSHHQDGSI   FMRGLKRSPQLKEKAKELQ   PQKW*MTSPQNRYGGFLKR   SYSKEVPEMERRYGGFMKF   TEEDPGPARGPRSGLAAYFF   KGLQLLLSLLAFICEEVVSQ   VSCSAFLLSLLILIVYCTFFY   FYTILGTGCVFLLASIIFVSTI   GFIASFMFLLDFITMLYEKRI   PAFAI TEPI NA	;	2216	A	7257	641	1310	DIKKSDESTRWOKORCPVVKSKCRENASPFF
Ref	1		1		ł		FCCFIAVAMGIRFIIMVAIWSAVFLNSLFNQE
867 2217 A 7288 151 396 SIKIEAFGSNGPDFWFFRYW MPFFQTLWLMNANRFCSIFT TPYHCWLSVVVCRCESHGI  868 2218 A 7298 3 272 PDTVIGGRGSGKEFGRWVL KGSCPAGGSRMVSESD*EGR AGS*WR*GSRPAGRGTPPRS:  869 2219 A 7332 1223 332 PRRDAEDRDESCLNPAFFIGI FLTLCTWLLLLGPGLLATVR YRLVRPADINFLACVMECEC KELLOLSKPELPODGTSTLRI KRYGGFMKRYGGFMKKMD NGSEILAKRYGGFMKKMD NGSEILAKRYGGFMKKMD NGSEILAKRYGGFMKKMD SYSKEVPEMEKRYGGFMF FWSPKEVPEMEKRYGGFMF AGQGRGREGAESGGSRGEG FWSPKEVPEMEKRYGGFMF TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQLVSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI PAFAL TEPL NA	1		1				OIPLTESYCGPCPKNWICYKNNCYQFFDESKN
867 2217 A 7288 151 396 SIKIIEAFGSNGPDFWFFRYW MPFFQTLWLMNANRFCSIFT TPYHCWLSVVVCRCESHGI PDTVIGGRGSGKEFGRWVL KGSCPAGGSRMVSESD*EGR AGS*WR*GSRPAGRGTPRSS AGS*WR*GSRPAGRGTPRSS AGS*WR*GSRPAGRGTPRSS AGS*WR*GSRPAGRGTPRSS CELL LILL GPGLLATVR YRL VRPADINFLAC VMECEC KELL QLSKPELPQDGTSTLRI KRYGGFMKRYGGFMKKMD NGSEILAKRYGGFMKKMD NGSEILAKRYGGFMKKDAE KELLETGDNRERSHHQDGSI FMRGLKRSPQLKEKAKELQI PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMRF SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMEKRYGGFMRF GFLKR SYSKEVPEMER GFLK SYSKEVPEMER GFLK			)	Ì	}	1	WYESQASCMSQNASLLKVYSKEDQDLLKLV
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R67   2217   A   7288   151   396   SIKIIEAFGSNGPDFWFFRYW   MPFFQTLWLMNANRFCSIFT   TPYHCWLSVVVCRCESHGI   TPYHCWLSVVVCRCESHGI   TPYHCWLSVVVCRCESHGI   PDTVIGGRGSGGKEFGRWVI   KGSCPAGGSRMVSESD*EGR   AGS*WR*GSRPAGRGTPPRS   AGS*WR*GSRPAGRGTPRS   AGS*WR*GSRPAGRGTPRS   FLTLCTWLLLGPGLLATVR   YRLVRPADINFLACVMECEG   KELLQLSKPELPQDGTSTLRI   KRYGGFMKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKKMD   NGSEILAKRYGGFMKF   SYSKEVPEMEKRYGGFMK   SYSKEVPEMEKRYGGFMK   SYSKEVPEMEKRYGGFMKP   AGQGRGREGAESGGSRGEG   FWSPRSQRRGCCGRRAPRP   TEEDPGPARGPRSGLAAYFF   KGLQLLLSLLAFICEEVVSQV   VSCSAFLLSLILLIVYCTPFY   FYITLGTGCVFLLASIIFVSTI   GFIASFMFLLDFITMLYEKRI   PAFALTEPLNA		ļ	- }	1		1	IIEMQKGDCALYASSFKGYIENCSTPNTYICM
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KGSCPAGGSRMVSESD*EGR   AGS*WR*GSRPAGRGTPPRS     869   2219   A   7332   1223   332   PRRDAEDRDESCLNPAFPIGI     FLTLCTWLLLLGPGLLATVR   YRLVRPADINFLACVMECEG   KELLQLSKPELPQDGTSTLRI   KRYGGFMKRYGGFMKKMD   NGSEILAKRYGGFMKKDAE   KELLETGDNRERSHHQDGSI   FMRGLKRSPQLKEKAKELQI   PQKW*MTSPQNRYGGFLKR   SYSKEVPEMEKRYGGFMRF   AGQGRGREGAESGGSRGEG   FWSPRSQRRGCGGRAPRPI   TEEDPGPARGPRSGLAAYFF   KGLQLLSLLAFICEEVVSQ   VSCSAFLLSLILIVYCTFFY   FYITLGTGCVFLLASIIFVSTI   GFIASFMFLLDFITMLYEKRI     GFIASFMFLLDFITMLYEKRI   PAFAI TEPLNA			1	1	1		TPYHCWLSVVVCRCESHO!
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869 2219 A 7332 1223 332 PRRDAEDRDESCLNPAFPIGIT FLTLCTWLLLLGPGLLATVR YRLVRPADINFLACVMECED KELLQLSKPELPQDGTSTLRI KRYGGFMKKMD NGSEILAKRYGGFMKKMD NGSEILAKRYGGFMKKMD FMRGLKRSPQLKEKAKELQI PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMF AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRITEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQU VSCSAFLLSLLILVYCTPFY FYITLGTGCVFLLASIIFVSTH GFIASFMFLLDFITMLYEKRI PAFAL TEPL NA	0	2210	1	, 23 -			KGSCPAGGSRMVSESD*EGRGC*A311 CAC
869 2219 A 7332 1223 FLTLCTWLLLLGPGLLATVR YRLVRPADINFLACVMECEG KELLQLSKPELPQDGTSTLRI KRYGGFMKRYGGFMKKDAEI KRYGGFMKKDAEI KELLETGDNRERSHHQDGSI FMRGLKRSPQLKEKAKELQI PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMRF AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQUVSCSAFLLSLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI PAFAI TEPLNA		1				1	AGS*WR*GSRPAGRGTPPRSLSHARPP
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PRLVRPADINFLACVMECEC KELLQLSKPELPQDGTSTLRI KRYGGFMKRYGGFMKKMDAEI KRYGGFMKRYGGFMKKDAEI KELLETGDNRERSHHQDGSI FMRGLKRSPQLKEKAKELQI PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMRF AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQVSCSAFLLSLILILVYCTPFYI FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI PAFAI TEPLNA	9	2219	A	1332	1223		FLTLCTWLLLLGPGLLATVRAECSQDCATCS
RELLQLSKPELPQDGTSTLRI KRYGGFMKRYGGFMKKMD NGSEILAKRYGGFMKKDAE KELLETGDNRERSHHQDGSI FMRGLKRSPQLKEKAKELQI PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMRF EIHQRLTERTQFLDESRKNPI AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRAPRPI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQI VSCSAFLLSLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI PAFAI TEPLNA		1	- {				VDI VRPADINFLACVMECEGKLPSLKIWEIC
RRYGGFMKRYGGFMKKMD NGSEILAKRYGGFMKKDAE KELLETGDNRERSHHQDGSI FMRGLKRSPQLKEKAKELQI PQKW*MTSPQNRYGGFLKR SYSKEVPEMEKRYGGFMRF  870 2220 A 7382 216 1018 EIHQRLTERTQFLDESRKNPI AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRPI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQI VSCSAFLLSLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI PAFALTEPLNA			1			1	KELLOLSKPELPODGTSTLRENSKPEESHLLA
870 2220 A 7382 216 IO18 EIHQRLTERTQFLDESRKNPI AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRI TEEDPGPARGPRSGLAYFF KGLQLLLSLLAFICEEVVSQL VSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKR		1	1		i	1	KRYGGEMKRYGGEMKKMDELYPMEPEEEA
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SYSKEVPEMEKRYGGFMRF  870 2220 A 7382 216 1018 EIHQRLTERTQFLDESRKNPI AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRPI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQ VSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKR			1	,	1		POKW*MTSPONRYGGFLKRFAEALPSDEEG
870 2220 A 7382 216 I018 EIHQRLTERTQFLDESRKNPI AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRPI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQI VSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI PAFALTEPLNA		1					CVCVEVPEMEKRYGGEMRE
AGQGRGREGAESGGSRGEG FWSPRSQRRGCCGRRAPRPI TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQI VSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRI			1				FIHORI TERTOFLDESRKNPNS*QANLLRGG
FWSPRSQRRGCCGRRAPRE TEEDPGPARGPRSGLAAYFF KGLQLLLSLLAFICEEVVSQ VSCSAFLLSLLILIVYCTPFYT FYITLGTGCVFLLASIIFVSTF GFIASFMFLLDFITMLYEKRO	70	2220	A	7382	216	1018	A GOOR GREGAES GGSRGEGPGSDGRLPATO
TEEDPGPARGPRSGLAAYFF  KGLQLLLSLLAFICEEVVSQ  VSCSAFLLSLLILIVYCTPFY  FYITLGTGCVFLLASIIFVSTI  GFIASFMFLLDFITMLYEKRO  PAFALTEPLNA	•		1				FWSPRSQRRGCCGRRAPRPEAMENGAVYSP
KGLQLLLSLLAFICEEVVSQ VSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRO		1	1	(			TEEDPGPARGPRSGLAAYFFMGRLPLLRRVI
VSCSAFLLSLLILIVYCTPFY FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRO PAFALTEPLNA		1	- 1				VOLOT LEGIT A FICE PVVSOCTI CGGI YFFE
FYITLGTGCVFLLASIIFVSTI GFIASFMFLLDFITMLYEKRO				1			KULULLISLIATICEE TSQUIDCOGNITTE
GFIASFMFLLDFITMLYEKR					İ		VSCSAFLLSLLLLIVICIFFIERVDIRVRSS
DAFAI TEPI NA						1	FYITLGTGCVFLLASHF VSTHDKTSAEIAAIV
RAEALTEPLNA			(	1	1	1	GFIASFMFLLDFITMLYEKRQESQLRKPENT
					i	ì	RAEALTEPLNA
921 2221 A 7403 3 393 SCAMCSGLL*LLLPIWLSWI		1000		7402	12	393	SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSV
1 871   2221   A   7403   5   DPGNMSFVKETVDKLLTGF	71	2221	A	/403	,	1	DPGNMSFVKETVDKLLTGFRCFREREAAPRI
ALRGAALPGESEAGDPESLE			-				ALRGAALPGESEAGDPESLRSSVNADWIQY

			CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D-A coartic Acid F=Glutamic Acid,
10: of	NO: of	nou		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	!	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence	1	Į.	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1			sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	}		residue of	Sequence	/=possible nucleotide deletion, \=possible
	ļ	Ì	1	peptide		nucleotide insertion
				sequence		DLWEAEVSTPRCEAGFCQECFRTPGNQEKDG
					}	PFIC
	1	}				FVDIVSVVEFPHCPEARFPAQHGQDSKRLTLC
372	2222	A	7413	1061	359	PGGS*PQATLHLDRMRVSASPTKEIQVKKYK
J / 2				1		CGLIKPCPANYFAFKICSGAANVVGPTMCFED
	1	1			· ·	CGLIKPCPAN TFAFRICSOAALTV VSI TMOLES
	1		ì		•	RMIMSPVKNNVGRGLNIALVNGTTGAVLGQ
	1	1	1		,	KAFDMYSGDVMHLVKFLKEIPGGALVLVAS
			1			YDDPGTKMNDESRKLFSDLGSSYAKQLGFRD
	1	1			į	SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE
	}	1	i		Í	CWDELL EMEGCMPPKPF
				2242	2394	ILKCAGHGGSCL*SQHFGRLRWEDRLRLGVQ
873	2223	Α	7429	2242	2374	L DUDGOUCETPSI LKIERKLE
	1				004	T POTSOUT WAT! HI PASTRKAPOAECGMISITE
874	2224	A	7468	146	894	WORLGVGITGEGIFFILFGTLLYFDSVLLAFGN
			1			THE TOTAL STREET RESTRICT RESTREET
	ļ	1	1		l	GGVVIVLLRWPLLGMFLETYGFFSLFKGFFPV
		1	Ì	į.	Ì	AFGFLGNVCNIPFLGALFRRLQGTSSMV*KTE
	- {	1	1	1	ł	MSSLNLDHWLKGAKREEWEPPPQSPALTHSP
	1	1	į	1.		TYPGPPQVQKERNGAEQLTSNPQVDSRGCQE
	1	- )		ì	ł	AEMQTPRRLGWGWYHTLTLYLWEEK
	1	ŀ	1			AEMQTPRREGWGWTHTETETEWEBRE
076	2225	A	7498	91	251	GEKPYPTWLQDEAGQWLLGFVAQPWGWPG
875	2223	1	,,			SERHEP*HGGVLFRLGPSAPPGKL
	2226	A	7544	403	587	YSCLCFLFKHITSFKNSVHIWLGTVVHAYNPN
876	2226	Α.	7,544	103		ILGGQGGWIA*GQEFKTSLGNTVRPCLYK
			7566	2	940	CCAPOTREEVPEPGGRGAAPWVALVARUUC
877	2227	A	7566	2	1,40	TEVENT VA ARRNASAVVLYNEERY GNITLY
	}	1	ł	1	l	MSHAGTGNIVVIMISYPKGREILELVQKGIPV
		- [	1			TMTIGVGTRHVOEFISGOSVVFVAIAFILMMI
						er AND TEVVIORELYTGSOIGSOSHRKETKKV
	l	1				COLLI HTVK HGEKGIDVDAENCA VCIENFA V
	ł		i			KDURIL PCKHIFHRICIDPWLLDHRICPMCKL
	1	ļ			1	DUTE AT GYWGEPGDVOEMPAPESPPGKDPAA
	1	1	ł			NLSLALPDDDGSDESSPPSASPAESEPQCDPSI
}		ı	Ì			KGDAGENTALLEAGRSDSRHGGPIS
j	1	- }	1			ERSLLCKVDVRWIYVSEGTKTQRRHRQGSLF
878	2228	A	7586	315	1232	RGRMQAACWYVLFLLQPTVYLVTCANLTNO
0/0	تعدد				(	GKSELLKSGSSKSTLKHIWTESSKDLSISRLLS
Ì		1	İ			GKSELLKSGSSKSTLKHIWTESSKDLSISICEE
)		- }	1			QTFRGKENDTDLDLRYDTPEPYSEQDLWDW
1		1		1		I PNSTDI OFPRPRAKRRPIYKI GKFKKIMFO Y
				1		COEHSNIKTVKLNLLITGKIVDHGNGIFSVII
1		1		1		PUNCTGOGNVSVSLVPPTKIVEFDLAQQIVII
)						AKDSKSFNCRIEYEKVDKATKNILCNYDPSK
1		1			1.	TCYOEOTOSHVSWLCSKPFKVICIYISFYSID
1		1				VKLVOKVCPDYNYHSDTPYFPSG
1					101	TESWKI KWWSPTCLDOLNGSAPGNVFIHG
879	2229	A	7605	479	391	DAAVAMTAQGGLVANRGRRFKWAIELSGP
880	2230	A	7612	93	659	GGSRGRSDRGSGQGDSLYPVGYLDKQVPDT
""		1		1	1	VQETDRILVEKRCWDIALGPLKQIPMNLFIM
1		1				VQETDRIL VERRC WDIALOI ERQII MINDI IM
1		Į.		1		MAGNTISIFPTMMVCMMAWRPIQALMAISA
						FKMLESSSQKFLQGLVYLIGNLMGLALAVY
	1	1		1		CQSMGLLPTHASDWLAFIEPPERMEFSGGGI
}		1				117
<u> </u>					1452	CROWTMRSHTITMTTTSVSSWPYSSHRMRFI
881	2231	A	7615	291	1434	NIJSDOPPONESATPNVTTCPMDEKLLSTVLT
1			Ì			evevtetyGLyGNHALYVFLGHKKKNSIQH
1	-	Ì	-	1		LNVAIADLLLIFCLPFRIMYHINQNKWTLGV
1	1	}			1	CKVVGTLFYMNMYISILLGFISLDRYIKINR
1	1	1		Ì		QQRKAITTKQSIYVCCIVWMLALGGFLTMII
	1	- 1	l l	]		QQRKAII IKQSII VCCIV WWILALGGI DIWII
			1	1	1	TLKKGGHNSTMCFHYRDKHNAKGEAIFNFI

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A enartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
ıucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	!	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
		Ì	}	peptide	Sequence	/=possible nucleotide deletion, \=possible
		Ì		sequence		nucleotide insertion
		<u> </u>	<del> </del>	sequence	<del> </del>	VVMEWLIELLIILSYIKIGKNLLRISKRRSKFPN
	1					SCKYATTARNSFIVLIFTICFVPYHAFRFIYISS
		1	}	1	1	OI NVSSCYWKEIVHKTNEIMLVLSSFNSCLDP
		1		ļ		VMYFLMSSNIRKIMCQLLFRRFQGEPSRSES1
		1				SEEKPGYSLHDTSVAVKIQSSSKST
		<del> </del>	7617	67	379	RQMALLKANKDLISAGLKEFSVLLNQQVFND
882	2232	A	/01/	07	3.12	DI VSEEDMVTVVEDWMNFYINYYRQQVIGE
		1		1		PQERDKALQELRQELNTLANPFLAKYRDFLK
	1	ì				CHELPSHPPPSS
	J	<del></del>	7622	400	215	KVKTCRYNPKYSAANDTGFVDIPSREKDLAK
883	2233	A	/022	1400	2.5	AVATVGPISVAVGASHVFFQFYKKGKHLSS
	1		7620	2640	2861	APVLILQMVKLSIVLTPQFLSHDQGQLTKELQ
884	2234	A	7638	2040		OHVKSVTCPCEYLRKVSECRQMGPGALEQFP
		ļ		[		CI SCHTSHSG
			7642	201	455	PSRGKMELEAMSRYTSPVNPAVFPHLTVVLL
885	2235	A.	7042	201	1.22	AIGMFFTAWFFVYEVTSTKYTRDIYKELLISL
	1	ì	ļ			VASLFMGFGVLFLLLWVGIYV
		<del>  </del>	7692	61	569	APENPFSRQHFNSETKVKLSLKTGTWLGNHA
886	2236	A	1092	101	302	LIL GEHESTHHELGLSGKVVGFLVKNILEVIKN
		}				GGMETRHPGKVSSWFHRWDSRAEQHNHAE
	ĺ			1	İ	HHEDVPQGDEDSKVSEAQQEFPDVVTCAGLE
		i		1		GLLPKALRVLLFQLKVQHRPGIHQQRPEQQD
				Ĭ		VSDHRYGRSVRQNRK
007	2237	A	7693	85	315	NPGCCLPVAMRTSYLLLFTLCLLLSEMASGG
887	2237	^	1073			NFLTGLGHRSDHYNCVSSGGQCLYSACPIFTI
		-				IQGTCYRGKAKCCK
000	2238	A	7702	242	1298	APSHRRRYLSPSRSAGQLGNMALERLCSVLK
888	2238	^	1			VLLITVLVVEGIAVAQKTQDGQNIGIKHIPAT
!		- 1		ł		QCGIWVRTSNGGHFASPNYPDSYPPNKECIY
	Ì					LEAAPRQRIELTFDEHYYIEPSFECRFDHLEVI DGPFGFSPLIDRYCGVKSPPLIRSTGRFMWIK
						SSDEELEGLGFRAKYSFIPDPDFTYLGGILNPI
i		]	}			DCQFELSGADGIVRSSQVEQEEKTKPGQAVE
ĺ		i	ł			CIWTIKATPKAKIYLRFLDYQMEHSNECKRN
						VAVYDGSSSIENLKAKFCSTVANDVMLKTG
			1	l		GVIRMWADEGSRLNRFRMLFTSFGGASPAQ.
	- [	-	1			ALSFCHSNMCINNSLVCNGVQNCAYPWDEN
1						
		1				HC CHYIMNPSTHHPASAGGSILGLFDFFGLGLGI
889	2239	A	7707	185	2911	MTMDALLARLKLLNPDDLREEIVKAGLKCG
007		1				ITSTTRFIFEKKLAQALLEQGGRLSSFYHHEA
1		}	ì	1	{	GVTALSQDPQRILKPAEGNPTDQAGFSEDRL
ł			ŀ	}		GYSVGLNPPEEEAVTSKTCSVPPSDTDTYRA
<b>!</b>						ATASKEPPLYYGVCPVYEDVPARNERIYVYI
Į.					}	NKKEALQAVKMIKGSRFKAFSTREDAEKFA
i	ĺ	f				GICDYFPSPSKTSLPLSPVKTAPLFSNDRLKD
1		1		}		LCLSESETVNKERANSYKNPRTQDLTAKLRI
		1				AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIV
1		1			(	EGCRYNVMHVAAKENQASICQLTLDVLENI
1		1				DFMRLMYPDDDEAMLQKRIRYVVDLYLNT
1		Ì				DKMGYDTPLHFACKFGNADVVNVLSSHHL
		1				VKNSRNKYDKTPEDVICERSKNKSVELKER
	1	1	1			EYLKGHYYVPLLRAEETSSPVIGELWSPDQT
1						EASHVSRYGGSPRDPVLTLRAFAGPLSPAKA
	ļ					DFRKLWKTPPREKAGFLHHVKKSDPERGFE
	1	}		1	- 1	VGRELAHELGYPWVEYWEFLGCFVDLSSQI
1	1	-				GLQRLEEYLTQQEIGKKAQQETGEREASCRI
						GLQRLEEYLTQQEIGRRAQQETGEREADCR KATTSGSNSISVRAFLDEDDMSLEEIKNRQN
1	j					
						ARNNSPPTVGAFGHTRCSAFPLEQEADLIEA

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	'		}	amino acid	of peptide	T=Threonine, V=Vaine, W=Tryptophian,
i			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
į.		[	1	peptide		/=possible nucleotide deletion, \=possible
1		1	1	sequence		nucleotide insertion
				sequence		EPGGPHSSRNGLCHPLNHSRTLAGKRPKAPR
_		(	ĺ	(		GEFAHI PPVSDLTVEFDKLNLQNIGRSVSKTP
	ļ	Į.	1			DESTKTKDQILTSRINAVERDLLEPSPADQLG
	ļ	1	1			NGHRRTESEMSARIAKMSLSPSSPRHEDQLEV
	İ	1	}	1	1	TREPARRLFLFGEEPSKLDQDVLAALECADV
	1		1			TREPARKLITUTET SKLDOD V DA LEDOTE V
	1	1	ł	1		DPHQFPAVHRWKSAVLCYSPSDRQSWPSPAV
		1	ł	ļ	1	KGRFKSQLPDLSGPHSYSPGRNSVAGSNPAKP
	İ	1	ĺ		ì	GLGSPGRYSPVHGSQLRRMARLAELAAL
		<del> </del> _		1260	269	RHMPVIPALWEAEVGGLLEPRSSRSAWATE
890	2240	A	7711	360	1175	KLPWEPSFLIKMQIIRHSEQTLKTALISKNPVL
891	2241	A	7721	61	11/3	VSQYEKLDAGEQRLMNEAFQPASDLFGPITL
	1	1		1	)	HSPSDWITSHPEAPQDFEQFFSDPYRKTPSPN
	1	1	1	1	1	KRSIYIQSIGSLGNTRIISEEYIKWLTGYCKAYF
		1			1	KRSI YIQSIGSLUNI KUISEETIK WETO TCKATT
					1	YGLRVKLLEPVPVSVTRCSFRVNENTHNLQIH
		1	}	{	1	AGDILKFLKKKKPEDAFCVVGITMIDLYPRDS
		1		1		WNEVEGOASLTDGVGIFSFARYGSDFYSMHY
	1		1	1		KGKVKKLKKTSSSDYSIFDNYYIPEITSVLLLK
	1		-	]		SCKTT THEIGHIFGLRHCOWLACLMQGSNHL
			i	1		FEADRREI NLCPICLHKLOCAVGFSIVERYKA
	1		l	1		LVRWIDDESSDTPGATPEHSHEDNGNLPKPV
	1	1	l l			EAFKEWKEWIIKCLAVLQK
	ŀ	İ	[ .	<u> </u>		SAPTAPARPCRAERGSGGGMLALLAASVALA
892	2242	A	7723	2	1650	VAAGAQDSPAPGSRFVCTALPPEAVHAGCPL
0/2			İ	ļ		PAMPMQGGAQSPEELRAAVLQLRETVVQQ
	1	1	Ì	ł		PAMPMQGGAQSPEEELRAAVEQLICET V QQ
			ł		ļ	KETLASARAIRELTGKLARCEGLAGGKARGA
	1		1	1		GATGKDTMGDLPRDPGHVVEQLSRSLQTLK
	1	1	ļ	)	1	DRLESLEPLPAMPMQGGAQSPEEELRAAVLQ
	1	ĺ			Ì	I RETVVOOKETLASARAIRELTGKLARCEGL
i	1	i				AGGK ARGAGATGKDTMGDLPRDPGHVVEQ
	1	ì		ļ	}	LSRSLQTLKDRLESLEHQLRANVSNAGLPGD
i	1		į			FREVLQQRLGELERQLLRKGAELEDEKSLLH
	1		1			NETSAHRQKTESTLNALLQRVTELERGNSAF
		1	1	ì		KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT
	ļ		1			ICLWLRSSASPGMGTPFSYAVPGQANEIVLIE
	Į.	-	1			ICLWLRSSASPUMUTFF5TAVI OQIAVBIVEDI
	Ì			1		WGNNPIELLINDKVAQLPLFVSDGKWHHICV
İ	1					TWTTRDGMWEAFQDGKKLGTGENLAPWHP
1					1	KPGGVLILGQEQDTVGGRFDATQAFVGELSQ
1	1	1			1	FNIWDRVLRAQEIVNIANCSTNMPGNIIPWVD
ļ		1			1	NNVDVFGGASKWPVETCEERLLDL
					2410	L TAGTAMNYPLTLEMDLENLEDLFWELDRL
893	2243	Α	7729	3554	2419	DNYNDTSLVENHLCPATEGPLMASFKAVFVP
1						VAYSLIFLLGVIGNVLVLVILERHRQTRSSTET
					1	FLFHLAVADLLLVFILPFAVAEGSVGWVLGTI
		Ì				FLFHLAVADLLLVFILFFAVAEGSVGWVDGT
}			1	1	į	LCKTVIALHKVNFYCSSLLLACIAVDRYLAIV
1		1		1	1	HAVHAYRHRRLLSIHITCGTIWLVGFLLALPE
1		1				I FAKUSOGHHNNSLPRCTFSQENQAETHAWI
				1		TSRFLYHVAGFLLPMLVMGWCYVGVVHRLF
[					1	OAORRPOROKAVRVAILVTSIFFLCWSPYHIV
				1	1	IFLDTLARLKAVDNTCKLNGSLPVAITMCEFL
1						GLAHCCLNPMLYTFAGVKFRSDLSRLLTKLG
1		i				OTODACI COLEDOUIDDECI CECENATCI TTE
					<u></u>	CTGPASLCQLFPSWRRSSLSESENATSLTTF
904	2244	A	7738	670	287	FVTRAGRWGAGARVRGGAGGMASGAARW
894	2244	A	1,138	5.5		VLAPVRSGALRSGPSLRKDGDVSAAWSGSG
1			1		Ì	SLVPSRSVIVTRSGAILPKPVKMSFGLLRVFSI
1				1	1	VIPFLYVGTLISKNFAALLEEHDIFVPEDDDD
1		1			}	ח
1	1	- 1	1			D APYAHSQVHCLDKVCGLLPFLNPEVPDQFYF
1	t .		7753	119	I 278	APTAMOQVICLURACGERITEMENTO
895	2245	A	1133	11.	1	THE CLE HACKEADUCDDTDDI
895	2245	A	1133		372	LWLSLFLHAGKEAPHCPRTRPL SPAWWNSQQRVVSPFLALLTLEPTFHHLLPIN

	DEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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iucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496		acid residue	O=Glutamine R=Arginine, S=Serine,
ence	1	1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	Ì	!	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	l	l	residue of	sequence	/=possible nucleotide deletion, \=possible
	{	1	1	peptide		/=possible flucteonide detection, / possible
	ļ	1	1	sequence	1 _	nucleotide insertion
	<del>                                     </del>	<del> </del>	<del></del>	<del> </del>		QVSTAALAVLLCTMALCNQVLSAPLAADTPT
	1		1	ļ		ACCFSYTSRQIPQNFIADYFETSSQCSKPSVIFL
	1		i	}	1	TERCROVCADPSEEWVOKYVSDLELSA
	Ī	l			116	PPRRGTHHESCYLGSFRVSAMFPRVSTFLPL
897	2247	A	7761	1725	445	RPLSRHPLSSGSPETSAAAIMLLTVRHGTVRY
	1		1			RSSALLARTKNNIQRYFGTNSVICSKKDKQSV
	ì	ì	1			RTEETSKETSESQDSEKENTKKDLLGIIKGMK
	1	Ì				RTEETSKEISESQUSERENTRADELGIINGINI
	1	1	-		1	VELSTVNVRTTKPPKRRPLKSLEATLGRLRRA
	}	ł		İ	1	TEYAPKKRIEPLSPELVAAASAVADSLPFDKQ
				İ	1	TTKSELLSQLQQHEEESRAQRDAKRPKISFSNI
	1	1	-	Ì	1	LISTARY ARSATARYR SRPELRIOF DEGYDNYR
	1	1	ł	1	Ĭ.	GOEKTODI KKRKNIFTGKRLNIFDMMAVIKE
	l l	ľ	l		]	APETDTSPSLWDVEFAKQLATVNEQPLQNGF
	ļ	-	1			EELIQWTKEGKLWEFPINNEAGFDDDGSEFH
	}		i			EHIFLEKHLESFPKQGPIRHFMELVTCGLSKNF
	1		l l	1		EHIFLEKHLESPPKUGPIKHFWELVICOBSIGN
	1					YLSVKQKVEHIEWFRNYFNEKKDILKESNIQF
		1		)		KLRPWKFLFRNN
		4	7775	• 85	496	SCOTTOPPAQSCSTGTMRIMLLFTAILAFSLA
898	2248	Α	7775	60	1 7,0	- LOSEGAVCKEPOEEVVPGGGRSKRDPDLYQLL
	1	}	ł	1	į	ODI EKSHSSLEGLI.KALSOASTDPKESTSPEK
	1	1	<b>,</b>	1	1	RDMHDFFVGLMGKRSVQPDSPTDVNQENVP
	1	1	}	1		SFGILKYPPRAE
						PFHLGASSNTFRLQVQTQESKAQKEVKMGFI
899	2249	A	7785	179	703	PFHLGASSNIFKLQVQIQESKAQKLVKINGI
899	2249	1	1 ,,,,,,			FSKSMNESMKNQKEFMLMNARLQLERQLIM
		1	1		4	QSEMRERQMAMQIAWSREFLKYFGTFFGLA
	1	-	- 1		Į.	A 101 TAGAIKKKKPAFLVPIVPLSFILLI YQ YDL
	ı	- 1	} .	ļ	· ·	GYGTLLERMKGEAEDILETEKSKLQLPRGMI
		1	1	1		FESIEKARKEOSRFFIDK
	l l				1200	VIVI PLKSYKIRSPSLHCOCEIFREEFLFSSLQE
900	2250	Α	7789	1465	300	GRDKDTFSKMAMVSEFLKQAWFIENEEQEY
	İ	1	{		<b>\</b>	VQTVKSSKGGPGSAVSPYPTFNPSSDVAALH
				İ	1	KAIMVKGVDEATIIDILTKRNNAQRQQIKAA
		ı			}	KAIMVKGVDEATIDILTKKINAQIQQIIBUT
	į	- 1	1	{		LQETGKPLDETLKKALTGHLEEVVLALLKTP
	ļ	Ì	l l			AQFDADELRAAMKGLGTDEDTLIEILASRTN
i	i	1				KEIRDINRVYREELKRDLAKDITSDTSGDFRN
	1		i	Į.		ALLSI AKGDRSEDFGVNEDLADSDARALYE
		ļ	1	ļ		GERRIGITOVNVFNTILTIRSYPQLKKVFQKI
	(	Í	•			TKYSKHDMNKVLDLELKGDIEKCLTAIVKC
		1	1		ļ	TSKPAFFAEKLHQAMKGVGTRHKALIRIMV
	Ì	- 1				RSEIDMNDIKAFYQKMYGISLCQAILDETKG
	-	1	1			RSEIDMNDIKAF TUKWI GISLOQALDDITTO
			1			YEKILVALCGGN
			7796	<del>-   2</del>	807	VEFHPQRARAGARAPSMGVLLTQRTLLSLVI
901	2251	A	1/96	1 4	00.	ATTERSMASMASMAAIGSCSKEYRVLLGOLOKU
		1	-			DI MODTSRI I DPYTRIOGLDVPKLREHCKEK
				1		CAPPERTIRGI GRRCFLOTLNATLUCVLER
l			1	l		ADLEQRLPKAQDLERSGLNIEDLEKLQMARI
l			1	1		NILGLRNNIYCMAQLLDNSDTAEPTKAGRG
	ļ	1				MILULKINITI CIMAQELDISDI ALI TIGICICI
					- (	SQPPTPTPASDAFQRKLEGCRFLHGYHRFMI
1	1	1			1	SVGRVFSKWGESPNRSRRHSPHQALRKGVR
			1			TRPSRKGKRLMTRGQLPR
l					721	TAARROKGTAARRLOKGTAARRRQKGTA
902	2252	A	7802	2	121	DDDOKGTAARRPOKGTAARRROKGTAAKK
		}	1		1	QKGTAARRQKGTAARRPQKGTAARRRQK
1			1	İ		QKGIAAKKKQKGIAAKKTQKGIAAKGQK
		1				TAARRQKGTAARRQKGLAIASRGCPCAS
		i		1	Ì	AGGVRGAGSRLRAMAPKVFRQYWDIPDGI
	1	- 1			į	CURK A VSTTSIASVAGLTAAAYRVTLNPPG
ļ		1		1		LEGVAKVGOYTFTAAAVGAVFGLTTCISAH
	1			- !		DEKONDO NYFLGGCAGGLTLGARTHNYGI
	1		1	1	1	I BURL DDI DITTI DOCUMENTO
		i	i	İ		AAACVYFGIAASLVKMGRLEGWEVFAKPK

	CTO TD	1400	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	1	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	Dence	{	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	i .	peptide	Joque	/=possible nucleotide deletion, \=possible
	1	1	1	1	}	nucleotide insertion
		<u> </u>	<del> </del>	sequence	584	PWI PWSDGRAARSSRKCPRSRFPVQVGKMA
903	2253	A	7807	1	364	VSTVFSTSSLMLALSRHSLLSPLLSVTSFRRFY
	į.	1	1			RGDSPTDSQKDMIEIPLPPWQERTDESIETKR
	Į	}				ARLLYESRKRGMLENCILLSLFAKEHLQHMT
	1	<b>!</b>	1			EKQLNLYDRLINEPSNDWDIYYWATEAKPAP
		1	Ì			EIFENEVMALLRDFAKNKNKEQRLRAPDLEY
			j	}		LFEKPR
		<u> </u>			1001	GAGRALGHLETGAGDVAAALPARKFPRSLLG
904	2254	A	7813	40	821	AGARLTGWTMNVFRILGDLSHLLAMILLLGK
	]	ì				IWRSKCCKGISGKSQILFALVFTTRYLDLFTNF
	1	1	ì	1	1	ISIYNTVMKVVFLLCAYVTVYMIYGKFRKTF
	1	j	1			DSENDTFRLEFLLVPVIGLSFLENYSFTLLEIL
			ļ		1	WTFSIYLESVAILPQLFMISKTGEAETITTHYL
,		1	ļ			FFLGLYRALYLANWIRRYQTENFYDQIAVVS
			1			GVVQTIFYCDFFYLYVTKGRSWDDSNADTGL
		1	ĺ			
•			l			RSYSSI LSNKDVLSPQLKDENSKLRRKLNEVQSFSEA
905	2255	Α	7817	1399	881	QTEMVRTLERKLEAKMIKEESDYHDLESVVQ
			1			QVEQNLELMTKRAVKAENHVVKLKQEISLL
						QAQVSNFQRENEALRCGQGASLTVVKQNAD
			- (			VALQNLRVVMNSAQASIEQLVSGAETLNLVA
	1			1	1	AVECUE AND PROCESS AND
	-		1		<u> </u>	EILKSIDRISEVKDEEEDS DSPRNRFEILGRPTRTPTRPGPRPAMEDLDAL
906	2256	A	7822	3	1462	DSPRNRFEILGRPIKIPIRPORKFAMEDEDAE
, , ,		1	ł		İ	LSDLETTTSHMPRSGAPKERPAEPLTPPPSYG
	ł		1			HQPQTGSGESSGASGDKDHLYSTVCKPRSPK
	į.		1	į	1	PAAPAAPPFSSSSGVLGTGLCELDRLLQELNA
	1		- 1	Į.	ì	TOFNITDEIMSOFPSSKVASGEQKEDQSEDKK
			l		1	RPSLPSSPSPGLPKASATSATLELDRLMASLSD
	1					FRVQNHLPASGPTQPPVVSSTNEGSPSPPEPTG
	İ	1				KGSLDTMLGLLQSDLSRRGVPTQAKGLCGSC
	1	ļ				NKPIAGQVVTALGRAWHPEHFVCGGCSTAL
						GGSSFFEKDGAPFCPECYFERFSPRCGFCNQPI
		ŀ	-			RHKMVTALGTHWHPEHFCCVSCGEPFGDEG
	ı		ł			FHEREGRPYCRRDFLQLFAPRCQGCQGPILDN
	ł	1	l	1	1	YISALSALWHPDCFVCRECFAPFSGGSFFEHE
			İ			GRPLCENHFHARRGSLCATCGLPVTGRCVSA
	1					LGRRFHPDHFTCTFCLRPLTKGSFQERAGKPY
			1			CQPCFLKLFG
007	2257	A	7828	1792	1671	FIYVNQSFAPSPDQEVGTLYECFGSDGKLVLH
907	2231	1	, 020	1		YCKSQAWG
000	2250	A	7842	110	1172	KLSCPCSHGTRVTAVRGPRLKAGVQWHDLG
908	2258	A	1042	1	1	SI OPPRSGI KOSSHI SLSSSWDFRHAPTHPET
		1		1	1	YTCPKMIEMEOAEAOLAELDLLASMFPGENE
	1					LIVNDOLAVAELKDCIEKKTMEGRSSKVYFII
1	1					NMNLDVSDEKMAMFSLACILPFKYPAVLPEI
		1	1			TVRSVLLSRSOOTOLNTDLTAFLQKHCHGDV
				1	1	CILNATEWVREHASGYVSRDTSSSPTTGSTVQ
			1		1	SVDLIFTRLWIYSHHIYNKCKRKNILEWAKEL
						SLSGESMPGKPGVVCVEGPOSACEEFWARLR
						KI NWKRILIRHREDIPFDGTNDETERQRKFSIF
]	1					EEKVFSVNGARGNHMDFGQLYQFLNTKGCG
}		1	1	Í		DVFQMFLWV
1					2022	EGICVYTFIYVHMYTRTCMHTYPYMYMNSV
909	2259	A	7870	3067	2923	LISSEILLIPSKYLFESK
1						GALTWSHPLLAVCPQGVWLGSTPSGSPALLP
		A	7884	212	4874	PSHRVNAEPGCVVTNACASGPCPPHANCRDL
910	2260	1 1				
_	2260	^				WOLLD OCALL CONTROL OF THE CONTROL
_	2260	A				WOTESCTCOPGYYGPGCVDACLLNPCQNQG
_	2260					WQTFSCTCQPGYYGPGCVDACLLNPCQNQG SCRHLPGAPHGYTCDCVGGYFGHHCEHRMD QQCPRGWWGSPTCGPCNCDVHKGFDPNCNK

WO 01/57188

			·	<del></del>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	•	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	1=150 eucine, K=Lysine, L-Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ucrice		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Ì	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1 1	'	peptide	Joquini	/=possible nucleotide deletion, \=possible
1		1			ļ	nucleotide insertion
				sequence		TNGQCHCKEFHYRPRGSDSCLPCDCYPVGST
					1	SRSCAPHSGQCPCRPGALGRQCNSCDSPFAEV
1					1	SKSCAPHSGQCPCKFGALGRQCHSCDSITIET
ł					1	TASGCRVLYDACPKSLRSGVWWPQTKFGVL
ļ	1	1		ì		ATVPCPRGALGLRGAGAAVRLCDEAQGWLE
1	1		i	l .		PDLFNCTSPAFRELSLLLDGLELNKTALDTME
}	1		l			AKKLAQRLREVTGHTDHYFSQDVRVTARLL
1			ľ		,	AHLLAFESHQQGFGLTATQDAHFNENLLWA
		Ì	l			GSALLAPETGDLWAALGQRAPGGSPGSAGLV
}		}		}		RHLEEYAATLARNMELTYLNPMGLVTPNIML
1	Ļ	1		ì		SIDRMEHPSSPRGARRYPRYHSNLFRGQDAW
	1	1	1	ļ	Ì	DPHTHVLLPSQSPRPSPSEVLPTSSSIENSTTSS
		1				VVPPPAPPEPEPGISIILLVYRTLGGLLPAQFQ
		1		1		AALLACTER DONING WIGHT AND TOTAL OF THE PARTY OF THE PART
	1	J		1	1	AERRGARLPQNPVMNSPVVSVAVFHGRNFLR
		1	}		1	GILESPISLEFRLLQTANRSKAICVQWDPPGLA
			1			EQHGVWTARDCELVHRNGSHARCRCSRTGT
		1	1	1	ļ	FGVLMDASPRERLEGDLELLAVFTHVVVAVS
ľ	l l		1	1	1	VAALVLTAAILLSLRSLKSNVRGIHANVAAA
1			ļ	i		LGVAELLFLLGIHRTHNQLVCTAVVILLHYFF
	ł	}		ļ		LSTFAWLFVQGLHLYRMQVEPRNVDRGAMR
		1	1		,	FYHALGWGVPAVLLGLAVGLDPEGYGNPDF
ì				1		CWISVHEPLIWSFAGPVVLVIVMNGTMFLLA
1	i	1		1		ARTSCSTGQREAKKTSALTLRSSFLLLLLVSA
1	1					SWLFGLLAVNHSILAFHYLHAGLCGLQGLAV
1			1			LLLFCVLNADARAAWMPACLGRKAAPEEAR
1			ļ.		1	PAPGLGPGAYNNTALFEESGLIRITLGASTVSS
		Ì	1			PAPGLGPGAYNNIALFEESGLIGILGASIVSS
1	į.	1	{	1	1	VSSARSGRTQDQDSQRGRSYLRDNVLVRHGS
l	1		1			AADHTDHSLQAHAGPTDLDVAMFHRDAGA
	· ·	i	1	}		DSDSDSDLSLEEERSLSIPSSESEDNGRTRGRF
l l	1 .		1	ļ		QRPLCRAAQSERLLTHPKDVDGNDLLSYWPA
1			1	1		LGECEAAPCALQTWGSERRLGLDTSKDAAN
1	1		1	1	ĺ	NNOPDPALTSGDETSLGRAQRQRKGILKNRL
	i		1	1	<b>\</b>	OYPLVPOTRGAPELSWCRAATLGHRAVPAAS
1		1	-			YGRIYAGGGTGSLSQPASRYSSREQLDLLLRR
			j	1		QLSRERLEEAPAPVLRPLSRPGSQECMDAAPG
	1				1	RLEPKDRGSTLPRRQPPRDYPGAMAGRFGSR
	1		1	1		DALDLGAPREWLSTLPPPRRTRDLDPQPPPLP
		1	}	l		DALDLUAFREWLSTEITI ROTROEDI QITTEI
	ì		1			LSPQRQLSRDPLLPSRPLDSLSRSSNSREQLDQ
- 1	ł		1		ı	VPSRHPSREALGPLPQLLRAREDSVSGPSHGP
ſ			1			STEQLDILSSILASFNSSALSSVQSSSTPLGPHT
l l	ŀ					TATPSATASVLGPSTPRSATSHSISELSPDSEPR
		1	1			DTQALLSATQAMDLRRRDYHMERPLLNQEH
		1	1			LEFLGRWGSAPRTHOWRTWLQCSRARAYAL
		j	1	Į.	)	LLOHLPVLVWLPRYPVRDWLLGDLLSGLSVA
			1		,	IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY
				1	}	FLFGTSRHISVESLCVPGPVDT
		1			<del> </del>	EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG
911	2261	A	7890	21	806	SCRPKARSSSARWALTCCLVLLPFLAGLTTYL
						2CKLVAV222AK MATICCTATCLLTVQCIIIT
		1	1		ì	LVSQLRAQGEACVQFQALKGQEFAPSHQQV
	1			1	1	YAPLRADGDKPRAHLTVVRQTPTQHFKNQFP
		ļ			1	ALHWEHELGLAFTKNRMNYTNKFLLIPESGD
			1	1	1	YFIYSOVTFRGMTSECSEIRQAGRPNKPDSITV
		1			1	VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ
					1	PIYLGAMFSLQEGDKLMVNVSDISLVDYTKE
			1		1	DKTFFGAFLL
	]	_1_			<del></del>	ACGIRHEGALPGLTATPEAMLRFLPDLAFSFL
912	2262	A	7891	1263	111	ACUIRTEUALFULTATFEANUAFEFDEAGUE
			1	ł	1	LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ
						PVPYILKKIFQDREAAATTGVSRDLCYVKELG
		1				VRGNVLRFLPDQGFFLYPKKISQASSCLQKLL
						YFNLSAIKEREQLTLAQLGLDLGPNSYYNLGP
	]			1		ELELALFLVQEPHVWGQTTPKPGKMFVLRSV
1	1	i				

	- 650 FM T	1/2	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
₹O: of	NO: of	hod	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		1	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	ng to first	acid residue	O=Glutamine R=Arginine, S=Serine,
ence			914		of peptide	T=Threonine V=Valine, W=Tryptophan,
			1	amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
		]	l .	residue of	sequence	/=possible nucleotide deletion, \=possible
	Ì	ł		peptide		-volectide insertion
		·		sequence		DWPOGAVHENLLDVAKDWNDNPRKNFGLFL
			-			FILVKEDRDSGVNFOPEDTCARLRCSLHASLL
			İ	1	}	ANTI NPDOCHPSRK RRAAIPVPKLSCKNLCH
	Ì	1	1			RHOLFINFROLGWHKWIIAPKGFMANYCHGE
		1	1	1		CPFSLTISLNSSNYAFMQALMHAVDPEIPQAV
						CIPTKLSPISMLYQDNNDNVILRHYEDMVVD
		1		1		
	İ	1	1			ECGCG ASRLPRGPGCGADMRPLLGLLLVFAGCTFAL
913	2263	TA-	7892	15	849	YLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAE
913	2203	1		į.		YLLSTRLPRGRRLGSTEEAGGRSEWTTODELC
		1	1			LRELSEVLREYRKEHQAYVFLLFCGAYLYKQ
	1	Į.			}	GFAIPGSSFLNVLAGALFGPWLGLLLCCVLTS
			1		1	VGATCCYLLSSIFGKQLVVSYFPDKVALLQR
				Ļ	}	KVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPI
						LNIPIVQFFFSVLIGLIPYNFICVQTGSILSTLTS
	1		1			LDALFSWDTVFKLLAIAMVALIPGTLIKKFSQ
		1	1			KHLQLNETSTANHIHSRKDT
		<del> </del>	7893	815	959	KSGWVWWLTPLIPALWEAQTEGSLRPEVKN
914	2264	Α	1693	015		DI CAUTE PEESKKKKILV
	<u> </u>	+	7909	3	641	HASGPGGLLRRRGSGANMPVARSWVCRKT
915	2265	A	7909	3	1	UNITED DEFENSELDOELKLIGEY GLKNKKEY
	1	1	ŀ		l l	WOVETT AKIRKAARELLTLDEKDPRKLEEG
			- 1	}		NALI RRI VRIGVLDEGKMKLDYILGLKIEDEL
		1	- {			EDDI OTOVEKI GLAKSIHHAHVLIQQCHIKVK
			1			FOVVNIL FETVRLDSOKHIDFSLCFPIGVANPS
		1			1	INVERNASKGOGGAGARDDEEEE
					967	TAUTOWUTCORI SOLTHRSILKYLLIDIHAC
916	2266	A	7914	3	967	OVER THE STATE OF
			i			UDUDDDSDRWGOTPEGLPAASPCGPGPRSCFS
			1			on propswgmlaci.ctvlwhlpavpalnki
		Ì	- (	1	1	CDBCBCBSIOKTYDI TRYLEHOLKSLAGI YLN
		į	1			VI CODENIEDDENPPRI GAETLPRATVULEV W
			ł		ì	DOLNINKI BI TONYEAYSHLLCYLKGLNKUAA
		1	ļ.			TART DOST A HECTSI OGLLGSLAGYMAALGI
			- 1			I DI DODI DOTEPTWTPGPAHSDFLOKMDUF WL
		1	Į.			LKELQTWLWRSAKDFNRLKKKMQPPAAAVI
		ļ	1			LUICAHGE
1	1	1	}			PROPERCYCL VOEVOTENVTVAEGGVAEITCKL
917	2267	$\overline{A}$	7921	2	1166	HQYDGSIVVIQNPARQTLFFNGTRALKDERFO
71/		1				LEEFSPRRVRIRLSDARLEDEGGYFCQLYTED
		1				THHQIATLTVLVAPENPVVEVREQAVEGGEV
ì		1				ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ
1			]			ELSCL VPRSRPAATLKWIRDREDGGIIGE AON
(					}	ENGKVWSVASTVRFRVDRKDDGGIIICEAQN
			1	1		QALPSGHSKQTQYVLDVQYSPTARIHASQAV
1		i				I VERCETT VI TCAVTGNPKPNUKWNKUNESI
]		}				DED AT A VIGITITIE POLVS ADNOTYT CLASNA
1		1		1		TIGHAD AT VVI VVYGESRLRPTEGGGGAPUP
						L CAVVE A OTSVPYATVGGILALLVFLIICVLVG
1	1		1	- 1		MVWCSVRQKGSYLTHEASGLDEQGEAREAR
1		}				LACCOCUVDYFFFFI
1					2653	PRRI PRASPESSVSSSLSPSAVVMACRWSTK
918	2268	A	7938	3	2000	PERRUPEALLITE AGVYGNGALAEMSENVI
		1	1	1	}	ISCUST A COETPEOTRAPS GITTS POWYSE I PA
1		1	1	(		DICEMBED ANDCENTISE())F1)IOGSKKCNLD
1			1	- 1		WLTIETYKNIESYRACGSTIPPPYISSQDHIWI
		1				WUTTET Y KNIEST KACOSTILIT TISSONITAL
1		1		1		FHSDDNISRKGFRLAYFSGKSEEPNCACDQFI CGNGKCIPEAWKCNNMDECGDRSDEEICAK
1						CGNGKCIPEAWKUNNMUECUURSUEEICAK
İ	ı	- 1	1	}	1	ANPPTAAAFQPCAYNQFQCLSRFTKVYTCLF
						ODIMECCOUNT PY
			ļ	ļ		ESLKCDGNIDCLDLGDEIDCDVPTCGQWLKY FYGTFNSPNYPDFYPPGSNCTWLIDTGDHRK

NO: of NO: of hod ID NO: beginning nucleotide D=Asp	acid sequence (A=Alanine C=Cysteine,
NO. 01 NO. 01 NO. 01 NO.	ertic Acid, E=Glutamic Acid,
nucl- peptide in nucleotide location F=Pher	nylalanine, G=Glycine, H=Histidine,
nucl- peptide   LISSN   Location   Corresponding   I=Isole	ucine, K=Lysine, L=Leucine,
00/496 correspondi to last amino M=Mc	thionine, N=Asparagine, P=Proline,
Old so to first soid residue O=Glu	tamine, R=Arginine, S=Serine,
amino acid of pentide T=Thre	eonine, V=Valine, W=Tryptophan,
residue of sequence Y=Tyr	osine, X=Unknown, *=Stop codon,
peptide /=possi	ible nucleotide deletion, \-possible
sequence nucleo	tide insertion
VILRE	TDFKLDGTGYGDYVKIYDGLEENPHK
LLRV	LTAFDSHAPLTVVSSSGQIRVHFCADKV
NAAR	GFNATYQVDGFCLPWEIPCGGNWGCY RCDGYWHCPNGRDETNCTMCQKEEFP
TEQQ	GVCYPRSDRCNYQNHCPNGSDEKNCFF
CSRN	NFHCKNNRCVFESWVCDSQDDCGDGS
CQPO	CPVIVPTRVITAAVIGSLICGLLLVIALG
CTCV	LYSLRMFERRSFETQLSRVEAELLRREA
DDGV/	GQLIAQGLIPPVEDFPVCSPNQASVLENL
DI AV	RSQLGFTSVRLPMAGRSSNIWNRIFNFA
RSRH	SGSLALVSADGDEVVPSQSTSREPERNH
THRS	LESVESDDTDTENERRDMAGASGGVAA
PLPO	KVPPTTAVEATVGACASSSTQSTRGGH
ADNO	GRDVTSVEPPSVSPARHQLTSALSRMTQ
	vvrftlgrssslsonosplrqldngvsg
	DDDVEMLIPISDGSSDFDVNDCSRPLLDL
ASDC	QGQGLRQPYNATNPGVRPSNRDGPCERC
GIVH	TAQIPDTCLEVTLKNETSDDEALLLC
919 2269 A 7951 1674 1839 VVRV	VTCCPPARSTTERTNAYDEEDCVEMVAS
GGW	NDVACHTTMYFMCEFDKKNM
920 2270 A 7953 47 572 GGRA	ASWPEQAKEPRREGHTDKQQTEDVLAA
GLRC	CLPHLPAICARRMSPAFRAMDVEPRAKG
VLLE	EPFVHQVGGHSCVLRFNETTLCKPLVPRE
HQFY	YETLPAEMRKFTPQYKGKSQLLEGLPHW VRDRGHGRPWQPSLEPSLPPTLCFPSLSS
RGDV	WPSAQHLTPSVFNPW
DE GP	RTVVTGIGYSKALQSSNRNTKSLLQNEF
921 2271 A 7957 612 812 RSGR	YSFRALSFKESTWATFQHGGEATKSRSL
l l ssto	)
1660 FNIT	FKWKEIWMCRGNKKSCCWTFIKDRHLT
922 2272 A 7967 1443 1660 ENTIT	CKSKSGETLLICIFCSNLVGFFFFGIRGFSN
l l wei	VKPN
923 2273 A 7981 1 3023 GSAF	PRAATAMARARPPPPPSPPPGLLPLLPPLL
923   2273   A   7301   1.1.PL	LLLPAGCRALEETLMDTKWVTSELAWT
SHPE	SGWEEVSGYDEAMNPIRTYQVCNVRES
SQN	NWLRTGFIWRRDVQRVYVELKFTVRDC
NSIPI	NIPGSCKETFNLFYYEADSDVASASSPFW
MEN	PYVKVDTIAPDESFSRLDAGRVNTKVRS
FGPL	SKAGFYLAFQDQGACMSLISVRAFYKK
CAST	TTAGFALFPETLTGAEPTSLVIAPGTCIPN
AVE	VSVPLKLYCNGDGEWMVPVGACTCATG
HEPA	AAKESQCRPCPPGSYKAKQGEGPCLPCPP
NSR1	TSPAASICTCHNNFYRADSDSADSACTT
VPSP	PRGVISNVNETSLILEWSEPRDLGVRDD
LLYY	NVICKKCHGAGGASACSRCDDNVEFVPR
QLGI	LSEPRVHTSHLLAHTRYTFEVQAVNGVS
GKSI	PLPPRYAAVNITTNQAAPSEVPTLRLHSS
SGSS	SLTLSWAPPERPNGVILDYEMKYFEKSEG VTSQMNSVQLDGLRPDARYVVQVRART
IAST	YGQYSRPAEFETTSERGSGAQQLQEQLP
VAG	GSATAGLVFVVAVVVIAIVCLRKQRHGS
LIVG	YTEKLQQYIAPGMKVYIDPFTYEDPNEA
	FAKEIDVSCVKIEEVIGAGEFGEVCRGRL
DSEY	PARCIDVSC VRICE VIDAUEFUE VCKURE
VREI	CHRESTATIVE VICOTED OUDDING SEA
VREI	GRREVFVAIKTLKVGYTERQRRDFLSEA
VREI KQPC SIMC	GOFDHPNIIRLEGVVTKSRPVMILTEFME
VREI KQPC SIMC NCA	GOFDHPNIIRLEGVVTKSRPVMILTEFME LDSFLRLNDGOFTVIOLVGMLRGIAAGM
VREI KQPC SIMC NCA KYI.	GQFDHPNIIRLEGVVTKSRPVMILTEFME LDSFLRLNDGQFTVIQLVGMLRGIAAGM SEMNYVHRDLAARNILVNSNLVCKVSDF
VREI KQPC SIMC NCA KYL:	GOFDHPNIIRLEGVVTKSRPVMILTEFME LDSFLRLNDGOFTVIOLVGMLRGIAAGM

	GEO ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	Hon	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	1	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	-	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1		Sequence	/=possible nucleotide deletion, \=possible
			1	peptide		nucleotide insertion
	i	L	<u> </u>	sequence	<u> </u>	WDMSNQDVINAVEQDYRLPPPMDCPTALHQ
	1		1	Į.	1	LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA
			İ			SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD
		1	· ·			WLDAIKMGRYKESFVSAGFASFDLVAQMTA
		1	ŀ			EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT
	Ì	Į	1			•
	ł	-	i	1		LPVQV
924	2274	A	7985	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNF
747	/.		1	1		QLMRELDQRTEDKKAEIDILAAEYISTVKTLS
		1	1	1		PDQRVERLQKIQNAYSKCKEYSDDKVQLAM
				1	)	QTYEMVDKHIRRLDADLARFEADLKDKMEG
	1			i		SDFESSGGRGLKKGRGQKEKRGSRGRGRRTS
		ł	1			EEDTPKKKKHKGG
	2075	A	7994	447	589	LPCSFCAQCMSSFERVWLQQSHFHNPRWNSR
925	2275	A	7994	447	301	SPIRCYCOHWPHCVHC
		<del>                                     </del>	7996	925	582	GPCKVCCITLAIMLOCHSFYRKDVQVEHPKS
926	2276	Α	/990	923	302	I NPK YSOIENEL SADMALKRKCLLSISDLDFW
			1		1	IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQI
		İ		i		POTOPII PLGGRYYITIRO
				<del>                                     </del>	353	RIORPLNSRSPNHSLFVKAELTAKQATMKLSV
927	2277	Α	7998	2	333	CLLLVTLALCCYQANAEFCPALVSELLDFFFI
		1	į			SEPLFKLSLAKFDAPPEAVAAKLGVKRCTDQ
		ļ	Ì			MSLQKRSLIAEVLVKILKKCSV
	İ	1	_l			LAPLRCQPGTRTQPRSHPAANDPSAAMSAAG
928	2278	Α	8004	130	588	ARGLRATYHRLLDKVELMLPEKLRPLYNHPA
	ļ					GPRTVFFWAPIMKWGLVCAGLADMARPAEK
	1	ł	1			LSTAQSAVLMATGFIWSRYSLVIPKNWSLFA
ļ	Į.	- }	1	i		VNFFVGAAGASQLFRIWRYNQELKAKAHK
	l		ļ	<u> </u>		EFARRVFIAAREMSLLRSLRVFLVARTGSYP
929	2279	A	8007	2	1016	EFARRAVIIAAREMSLLRSLRVILVARIUSII
32)		1	}	1		AGSLLRQSPQPRHTFYAGPRLSASASSKELLM
1		1	l			KLRRKTGYSFVNCKKALETCGGDLKQAEIWI
	}	1	ļ			HKEAQKEGWSKAAKLQGRKTKEGLIGLLQE
			1		1	GNTTVLVEVNCETDFVSRNLKFQLLVQQVAL
		1	İ	,		GTMMHCQTLKDQPSAYSKGFLNSSELSGLPA
1		1			ì	GPDREGSLKDQLALAIGKLGENMILKRAAW\
		1	L			KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG
1					1	ALVICETSEQKTNLEDVGRRLGQHVVGMAPI
1		- 1	1			SVGSLDDEPGGEAETKMLSQPYLLDPSTTLGQ
		1				YVOPOGVSVVDFVRFECGEGEEAAETE
					1679	NSRVWGPWTEPSAGSLRPMARKQNRNSKEL
930	2280	A	8008	3	1077	GLVPLTDDTSHAGPPGPGRALLECDHLRSGV
Į.	]	ļ	j	}		PGGRRRKDWSCSLLVASLAGAFGSSFLYGYN
				}		LSVVNAPTPYIKAFYNESWERRHGRPIDPDTL
	1	1	1			TLLWSVTVSIFAIGGLVGTLIVKMIGKVLGRK
				1		HTLLANNGFAISAALLMACSLQAGAFEMLIV
1		1		1		GRFIMGIDGGVALSVLPMYLSEISPKEIRGSLO
}		1		1	1	GKFIMGIDGG VALS VLPNI I CZEGFKEIROŚLI
		1		1		QVTAIFICIGVFTGQLLGLPELLGKESTWPYLI
				<b>.</b>		GVIVVPAVVQLLSLPFLPDSPRYLLLEKHNEA
						RAVKAFQTFLGKADVSQEVEEVLAESRVQR
		- 1				IRI VSVLELLRAPYVRWOVVTVIVTMACYQI
1		1	Ì	1		CGLNAIWFYTNSIFGKAGIPPAKIPYVTLSTGG
1		1	ļ	}		IETLAAVFSGLVIEHLGRRPLLIGGFGLMGLF
		1			1	GTLTITLTLODHAPWVPYLSIVGILAIIASFCS
		ĺ	}		1	PGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSN
		1				FAVGLLFPFIQKSLDTYCFLVFATICITGAIYL
1		- 1			1	YFVLPETKNRTYAEISQAFSKRNKAYPPEEKI
	İ					DSAVTDGKINGRP
						AAGAVVSAMPKAKGKTRRQKFGYSVNRKR
		Ā	8009	861	300	AAGAVVSAMPKAKUKI KKQKFU I SVIKKK
931	2281					
931	2281	^	0007	}		NRNARRKAAPRIECSHIRHAWDHAKSVRQN AEMGLAVDPNRAVPLRKRKVKAMEVDIEER

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
aucl-	peptide	,	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence	l l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}	]	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		Ì	1		sequence	/=possible nucleotide deletion, \-possible
	1	İ	1	peptide		nucleotide insertion
	l		<u> </u>	sequence	ļ	PKELVRKPYVLNDLEAEASLPEKKGNTLSRD
		1				LIDYVRYMVENHGEDYKAMARDEKNYYQD
		1			1	FIDA AKAMA ENUGED I WANTAKDERA I JÁD
	1	1	1		1	TPKQIRSKINVYKRFYPAEWQDFLDSLQKRK
		ļ	Į.			MEVE SYDE
932	2282	A	8011	412	1	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG
732	2202	1	1.00		}	DIRGSHFSSPQRQRSQRVPGKETARVLRAGK
		1	· t		İ	OGRGQIPIPCPWPPPPPPPPPPGSPGPGCRQFHQ
				•		SLEAKARHPASVREMRGKVKMRRALRRAPA
		1	1			STRASSRQPNPK
		<del></del>	<del></del>	1.15	1077	PPVPPASRSDMAQNLKDLAGRLPAGPRGMGT
933	2283	A	8012	147	1077	ALKLLLGAGAVAYGVRESVFTVEGGHRAIFF
		1		1		NRIGGVQQDTILAEGLHFRIPWFQYPIIYDIRA
		1		1		NKIGOVQQDTILAEGLAFKIF WFQTFIITDIKA
	1	1		1	}	RPRKISSPTGSKDLQMVNISLRVLSRPNAQEL
		}		1		PSMYQRLGLDYEERVLPSIVNEVLKSVVAKF
		1				NASQLITQRAQVSLLIRRELTERAKDFSLILDD
		1	1			VAITELSFSREYTAAVEAKQVAQQEAQRAQF
	Ì	•		1		LVEKAKQEQRQKIVQAEGEAEAAKMLGEAL
	j			1		SKNPGYIKLRKIRAAQNISKTIATSQNRIYLTA
	l		ļ			DNLVLNLODESFTRGSDSLIKGKK
		<b>_</b>		255	982	SQFSLSQVLVDSAEEGSLAAAAELAAQKREQ
934	2284	Α	8023	255 .	702	RLRKFRELHLMRNEARKLNHQEVVEEDKRL
		1	1			KLPANWEAKKARLEWELKEEEKKKECAARG
		{	1		1	EDYEKVKLLEISAEDAERWERKKKRKNPDLG
		\ \				FSDYAAAQLRQYHRLTKQIKPDMETYERLRE
		Į.	ì			FSDYAAAQLKQ HACTIVDCTEEIDPMVIDLE
	ł				}	KHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLE
	ĺ				ļ.	KQIEKRDKYSRRRPYNDDADIDYINERNAKF
	i		1			NKKAERFYGKYTAEIKQNLERGTAV
935	2285	A	8027	59	310	LVSSTVNLLTEKAPWNSLAWTVTSYVFLKFL
933	2203	1.	002		1	QGGGTGSTGMRDSALTLLGIGPSHRHSLSIRL
		1				SQHSSPAPMYSQTFHILVLG
		<del></del>	8032	1	639	SGRECNMAKTYDYLFKLLLIGDSGVGKTCVL
936	2286	A	8032	1	037	FRESEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ
		ı	ł	Í		IWDTAGQERFRTITTAYYRGAMGIMLVYDIT
				l <sub>e</sub>		NEKSFDNIRNWIRNIEEHASADVEKMILGNKO
	i i	1	· ·			DVNDKRQVSKERGEKLALDYGIKFMETSAK
			-			ANINVENAFFTLARDIKAKMDKKLEGNSPQG
	l	1	1	1		ANIII V ENALL I LAKDIKARINDIREBONO QU
	1.	1				SNQGVKITPDQQKRSSFFRCVLL
937	2287	A	8039	393	311	EETIHSENSYILEKYIPISANLTLTIA
938	2288	- A	8052	675	-1334	LHPAATSTAWLHVPPGLSMALSWVLTVLSLI
730	2200	^	3032	1		PLLEAOIPLCANLVPVPITNATLDRITGKWFYI
1			1		1	ASAFRNEEYNKSVQEIQATFFYFTPNKTEDTI
İ						LREYOTRODOCIYNTTYLNVORENGTISRYV
					ĺ	GGQEHFAHLLILRDTKTYMLAFDVNDEKNW
İ					1	GLSVYADKPETTKEQLGEFYEALDCLRIPKSI
			J		1	VVYTDWKKDKCEPLEKQHEKERKQEEGES
1			1	1		VVIIIWKKUKCEPLEKUREKEKKUEGES
939	2289	A	8055	12	1039	SSVAEFPERVQLSQPQNWNFSGAGGAWSLDF
137	====	1				AEQLKWSAELARLGESIMDGKQGGMDGSKP
1					1	AGPRDFPGIRLLSNPLMGDAVSDWSPMHEAA
[						IHGHOLSLRNLISQGWAVNIITADHVSPLHEA
ļ		-				CLGGHLSCVKILLKHGAQVNGVTADWHTPL
	-			1	1	FNACVSGSWDCVNLLLQHGASVQPESDLASF
		}	1			IHEAARRGHVECVNSLIAYGGNIDHKISHLGT
1		1				PLYLACENQQRACVKKLLESGADVNQGKGQ
		1				PLYLACENQUACYANLESUADYNQUACY
	1	- 1		ĺ		DSPLHAVARTASEELACLLMDFGADTQAKN
		1	j	1		AEGKRPVELVPPESPLAQLFLEREGPPSLMQL
		1			1	
			1			CRLRIRKCFGIQQHHKITKLVLPEDLKQFLLH
						L
940	2290	A	8058	2	1203	i

		T	1 000	Deadined	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:		location	F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	Ì	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ì	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		}		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	Į.	1	]	residue of	sequence	Y=1 yrosine, X=0ikilowii, 'stop codon,
	Î	ļ	ì	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del> </del>	┼	<del> </del>	<del></del>		VVDTVMCPNMPNKSVLLYTLSFIYIFIFVIGMI
	1	<b>\</b>	1	ļ.		ANSVVVWVNIQAKTTGYDTHCYILNLAIADL
	i	1	Į.			WVVLTIPVWVVSLVQHNQWPMGELTCKVTF
	l	1			ļ	LIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS
		1	ì	1	ļ	RKKMVRRVVCILVWLLAFCVSLPDTYYLKT
	Ì	1		,	]	VTSASNNETYCRSFYPEHSIKEWLIGMELVSV
			1			VI GEAVPESHAVEYELLARAISASSDQEKHSS
	1	ļ	1	1		RKIIFSYVVVFLVCWLPYHVAVLLDIFSILHYI
	i			}		PFTCRLEHALFTALHVTQCLSLVHCCVNPVL
	1.	1	· I		}	YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA
	1		[			YSFINKNYKYELMKAFIFKISAKIOLIKEIDI
	}	1	ì			SRVSETEYSALEQSTK
941	2291	A	8059	73	432	DMAGLMTIVTSLLFLGVCAHHIIPTGSVVLPS
741	2271	1"	5555		1	PCCMFFVSKRIPENRVVSYQLSSRSTCLKAGY
	1	1				IFTTKKGQQFCGDPKQEWVQRYMKNLDAKC
		1				KKASPRARAVAVKGPVORYPGNOTTC
	1	<del></del>	0007	278	1262	GGIGEIKORPSCLGRCLDPSLSVLMNISLGLG
942	2292	Α	8067	210	1202	VESAVISOK PSRDICORGTSLTIQCQVDSQVT
	ŀ	1	1			MMEWYROOPGOSLTLIATANQGSEATYESG
		l			1	VIDKFPISRPNLTFSTLTVSNMSPEDSSIYLCS
	1	ļ	ł	1	1 .	GRQGTYEQYFGPGTRLTVTEDLKNVFPPEVA
	1				1	VFEPSEAEISHTQKATLVCLATGFYPDHVELS
	1	l	1		1	WWVNGKEVHSGVSTDPQPLKEQPALNDSRY
	l.					WWYNGKEVHSUVSIDPQFLKEQIAENDOK
	1		1		· I	CLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
				ĺ		NDEWTQDRAKPVTQIVSAEAWGRADCGFTS
		1		İ		ESYQQGVLSATILYEILLGKATLYAVLVSAL
ı	-		i		1	LMAMVKRKDSRG
943	2293	A	8070	1	879	MVKVVPATRGNLPRSQLTGTHQHCQPREPK
943	2293	1.	00,0	1		TASERLRRRPRATARLRAHAAPPEPPLAVFA
			1			PSDRKELLALPVACDPVIASVMSWVQAASLI
	1					OGPGDKGDVFDEEADESLLAQREWQSNMQ
	1	1	1			RVKEGYRDGIDAGKAVTLOOGFNQGYKKG.
	i					EVILNYGRLRGTLSALLSWCHLHNNNSTLIN
		Ì				INNILDAVGOCEEYVLKHLKSITPPSHVVDL
						DSIEDMDLCHVVPAEKKIDEAKDERLCENN
	1				Ì	EFNKNCSKSHSGIDCSYVECCRTQEHAHSGR
	l l	-	1			PKDII (DECTDSOF
						PKPHMDFGTDSQF ESARWSRQLRRTLIRLSFPISCGRSHAFGGCK
944	2294	A	8073	1	797	EDAKWOKŲLKKILIKLOFI ISCURSITAI OUCE
` ` `		1				MAATSGTDEPVSGELVSVAHALSLPAESYG
						DPDIEMA WAMRAMQHAEVYYKLISSVDPQ
						LKLTKVDDQIYSEFRKNFETLRIDVLDPEEL
		1				SESAKEKWRPFCLKFNGIVEDFNYGTLLRLI
		1		i		CSOGYTEENTIFAPRIOFFAIEIARNREGYNK
					1	VVISVODKEGEKGVNNGGEKRADSGEEENT
1					1	KNGGEKGADSGEEKEEGINREDKTDKGGEK
Į.		}		1		GKEADKEINKSGEKAM
						GAATLLRSASSAARKAAEAEQVWLHLHRY
945	2295	A	8074	↓ 2	505	SADRRVLGLREWGRPASERECSLCQRLKRE
ł			1			NMGDVEKGKKIFIMKCSQCHTVEKGGKHK
l		ĺ				GPNLHGLFGRKTGQAPGYSYTAANKNKGII
]		1			1	GEDTLMEYLENPKKYIPGTKMIFVGIKKKEE
1					<b>\</b>	
ļ			]	ĺ		ADLIAYLKKATNE
946	2296	A	8081	42	590	EGRRGKFGGKLCNFLFYFHSNSAESRMDVL
940	2296	^	0001			VAIFAVPLILGQEYEDEERLGEDEYYQVVY
	1					YTYTPSYDDFSADFTIDYSIFESEDRLNRLDK
		1	1			DITEATETTISLETARADHPKPVTVKPVTTEP
						SPRSEAMPCPVLRSPIPLPPVRVPLFRWGCIS
1		J			1	KKVGRRLLMTLWMGVWQEEIGR
)	1	- 1		1		GGGSSPRELAGAAGLTVTSQAVAARRQQPS
l	l.	1				
947	2297	A	8084	322	549	SRARAPAHSLRAALSLASSARSWGAVSRDR

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Olycine, 11- Institute,
	seq-	į	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide		[	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ì	}	1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	ì			sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide	Į	nucleotide insertion
		1	1	sequence	<u> </u>	nucleotide inscribit
	<del> </del>	+	1			PCPPAIMYQSSNKC
	2298	В	8093	3905	846	MEPGEVKDRILENISLSVKKLQSYFAACEDEI
948	2298		0075	3502	1	PAIRNHDKVLQRLCEHLDHALLYGLQDLSSG
		1		i	l,	VWVI VVHFTRREAIKOIEVLOHVATNLGRSK
	1	1				A WI VI AT NENSLESYLRLFOENLGLLHKYYY
	1	1			1	KNALVCSHDHLTLFLTLVSGLEFIRFELDLDA
	1		1			PYLDLAPYMPDYYKPQYLLDFEDRLPSSVHG
	ļ	1	ļ			PYLDLAPYMPDI IRFQ I LEDI EDICE SOTTI
	ļ	)				SDSLSLNSFNSVTSTNLEWDDSAIAPSSEDYD
	1	1				FGDVFPAVPSVPSTDWEDGDLTDTVSGPRST
	1	i	1		1	ASDLTSSKASTRSPTQRQNPFNEEPAETVSSS
		j	- }	1	1	DTTPVHTTSOEKEEAQALDPPDACTELEVIKV
	1	1	1		1	TKKKKIGKKKKSRSDEEASPLHPACSQKKCA
	1	1		1		KOGDGDSRNGSPSLGRDSPDTMLASPQEEGE
		1			1	GPSSTTESSERSEPGLLIPEMKDTSMERLGQPI
	1	t		1		OKSSI I ESSERSEI GEETI EMIES ISMERIEGE
				1		SKVIDQLNGQLDPSTWCSRAEPPDQSFRTGSF
		į		1	1	GDAPERPPLCDFSEGLSAPMDFYRFTVESPST
		ļ			ľ	VTSGGGHHDPAGLGQPLHVPSSPEAAGQEEE
	1	1		1	1	CGGGEGOTPRPLEDTTREAOELEAQLSLVKE
	1			<b>\</b>		GPVSEPEPGTOEVLCOLKRDQPSPCLSSAEDS
	1			}	ļ	GVDEGQGSPSEMVHSSEFRVDNNHLLLLMIF
		4		1		VFRENEEQLFKMIRMSTGHMEGNLQLLYVL
	Ì	1	1	1	İ	TDCYVYLLRKGATEKPYLVEEAVSYNELDY
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			i		1	PTDESLGPTPCHCSPPEGTITKEGMLHYKAG.
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	1		1		1	EQFETELKYKMTINGKIAVLYLKKNKNLLA
		1	1		}	GYTETYYNSTGKEITTSPQIMDDCYYQGHIL
		1			1	FKVSDASISTCRGLRGYFSOGDQRYFIEPLSI
				1		LIBDGOFHALFKYNPDEKNYDSTCGMDGVL
	1	1		1	1	WAHDLQQNIALPATKLVKLKDRKVQEHEK
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						GISEECINICCDARICKIRATIOCIBORO
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						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFOVNGFPCHHGKGHCLMGTCPTLQEG
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKO
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHA
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHA CDHELQCQCEEGWIPPDCDDSSVVFHFSIVV VI FPMAVIFVVVAMVIRHOSSREKQKKDQI
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHIGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHA CDHELQCQCEEGWIPPDCDDSSVVFHFSIVV VI EPMAVIFVVVAMVIRHOSSREKQKKDQF
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHA CDHELQCQCEEGWIPPDCDDSSVVFHFSIVV VLFPMAVIFVVVAMVIRHQSSREKQKKDQF
						CQFKKAGMVCRPAKDECDLPEMCNGKSGN PDDRFQVNGFPCHHGKGHCLMGTCPTLQEC CTELWGPGTEVADKSCYNRNEGGSKYGYC RVDDTLIPCKANDTMCGKLFCQGGSDNLPV KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHA CDHELQCQCEEGWIPPDCDDSSVVFHFSIVV VI FPMAVIFVVVAMVIRHOSSREKQKKDQI

Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVTRSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSLSSCKPGFGVDQLRDDNLETYWQ
F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MGLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
sponding stamino residue stamino residue eptide ence Provide Encourage encourse
M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKGRTQKEKKAARASKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNIILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
residue Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNIILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNIILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MGLLLMILASAVLGSFLTLLAQFFLLYRQPE PPADEAARAGEGFRYIKPVPGLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPF WGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
/=possible nucleotide deletion, \=possible nucleotide insertion  MGLLLMILASAVLGSFLTLLAQFFLLYRQPE PPADEAARAGEGFRYIKPVPGLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNIILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNIILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
PPADEAARAGEGFRYIKPVPGLLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGFEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
GRDEEPSGAAPEGGATPTAAPETPAPPIREIC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVFFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGTQKEKKAARASKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGTQKEKKAARASKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI
RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARASKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARASKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
CPG  EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK  VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSI SSCKPGFGVDOLRDDNLETYWQ
GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
PRCSQERKKK  PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSOAVWSI SSCKPGFGVDOLRDDNLETYWQ
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LYKYFALOPDDVYYCGIKYIKDDVILNEPSAD
APAALYOTIEENIKIFEEEEVEFISVPVPEFADS
DPANIVHDFNKKLTAYLDLNLDKCYVIPLNT
SIVMPPRNLLELLINIKAGTYLPQSYLIHEHMV
ITDRIENIDHLGFFIYRLCHDKETYKLQRRETI
KGIOKREASNCFAIRHFENKFAVETLICS
VESRSAWHEGEDOIDRLDFIRNQMNLLTLDV
KKKIKEVTEEVANKVSCAMTDEICRLSVLVD
EFCSEFHPNPDVLKIYKSELNKHIEDGMGRNL
ADRCTDEVNALVLOTOOEIIENLKPLLPAGIQ
DKLHTLIPCKKFDLSYNLNYHKLCSDFQEDIV
FRESLGWSSLVHRFLGPRNAQRVLLGLSEPIF
OLPRSLASTPTAPTTPATPDNASQEELMITLVT
GLASVTSRTSMGIIIVGGVIWKTIGWKLLSVS.
LTMYGALYLYERLSWTTHAKERAFKQQFVN
VATEKI RMIVSSTSANCSHOVKQQIATTFARL
COOVDITOKQLEEEIARLPKEIDQLEKIQNNS
CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS KLLRNKAVQLENELENFTKQFLPSSNEES
CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS KLLRNKAVQLENELENFTKQFLPSSNEES ASGSPAPSSSSAMAAACGPGAAGYCLLLGLH LFLLTAGPALGWNDPDRMLLRDVKALTLHY

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		ł				504	/=possible nucleotide deletion, \=possible
DRYTTSREUPPPOLKCYGGTAGCDSYTPKY   QCQNKGWGYDGYWQWECKTDLDYAFYGKI   VYSCEGYESSEDGYWLRGSCGLEYNLDYTE    GLQKLKESGKQHGFASTSDYYYKWSSADSC     MSGLITIVYLGIAFVYYKLFLSDGQYSFFF     SEPPERH YQREFTSAGPPPPGFKSEFTGP     NTGHGATSGFGSATTGQQGYENSGFGFWTG     TGGLGWLFGSNRAATPPSGSWYYFSYPPS     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSYSVCSNSDTKTRT.     GTGWIRAYSPLHGGGSTNAWAGAVY     GTGAALDVIRGSLSLTNLSSSMAGYYVCK     HNEWGTAQCONTLEVSTGMAAAVAGAAV     TLYGGLGLAGI.VLHTBRGKALEPANDK     GTGAALDVIRGSLSLTNLSSSMAGYYVCK     HNEWGTAQCONTLEVSTGMAAAVAGAAV     TLYGGLGLAGI.VLHTBRGKALEPANDK     GARRINGTHE GARRINGT	l	ļ	1			ļ	
QCQNKGWDGYDVQWECKTDLDAYKFGGL   VYSEGYESSEDQYVLRGSGCLBYNLDYTE    GLQKLKESGKQHGFASFSDYYYKWSSADSC    MSGLITTV/LIGHAFVYKLLTSDGQYSPP    YSEYPPFSHRYQRFTNSAGPPPGFKSETTG    NTGHGATSGFGSATGQQGYENSGFGWTG   GTGGLGYLFGSNRAATPPSDSWYYFSYPPS    PGTWNRAYSPLHGGSGSYSVCSNSDTKTRT.   SGYGGTRR    THVWMTOMCYAPHQVLSYNGVTSKPGV    VYSWPSRNLSIR.EGLQEKDSGYSVCSNSDTKTRT.   SGYGGTRR    THVWMTOMCYAPHQVLSYNGVTSKPGV    VYSWPSRNLSIR.EGLQEKDSGYSVCSNSDTKTRT.   GYGGTRR    GYGGTARR    THVWMTOMCYAPHQVLSYNGVTSKPGVSSWNVD   DKQGKSRGJSIKILELNVLYPPAPPSCHLOG   PHVGANVILSCQSFSKFAVQYQWDRQLPS    QTFFAPALDVIRGSLSITNLSSSNAGYYVKN   HNEWGTAQCNYLLEVSTIGGAAVYAGAW   TLVGLGLLAGLVLLYHRRGKALEPANDIK   APPHGPPRFGALTPTPSLSSQALPSRRLPTTD    APPHGPSPSIPGGVSSSSGLSRMGAVYWMPAQ   QAGSLV    APPHGPSPSIPGGVSSSGLSRMGAVYWMPAQ   QAGSLV    APPHGPSPSIPGGVSSSGLSRMGNVNLTHEIFFELKL   EKCESSYSLTYPPVVKLENGSSTNVSLTLRPT    LVATYLTPETTRSKNTILLELPDEVVYPGWNSSGVTSQNWQQLTVYLHGNBSNOTGPRI    LVATYLTPETTRSKNTILLELPDEVVYPGWNSSGVTSQNWGQLTVYLHGNBSNOTGPRI    LVATYLKGFGLKYFNOVPVYNSNVDVSLLAWPNSSSGLSRMGAVYSVFNILL   LVATYLKGFGLKYFNOVPVYNSNVDVFSLAWVLTHUTGDFTGSSLGSTBATAWAYSVFNICH   AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILILIIVQCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AVAILITITICCCLYERGGGRVSWPAIGFLV    AV			L	<b></b>	sequence		DRYTTSPRI DPIPOLKCYGGTAGCDSYTPKVI
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NMSGLITIVVLLGIAFVYYKLFLSDGYGYST   SPETPSSHRYOPSTRINAGPPFOFKSEFTOF   NTGHGATSGFGSAFTGQGYSNSCPGFWTC   GTGGLGYLFGSRAAPPRSDAYPSSPFSPFTORMARASPELHGGSGSYSVCSNSDTKTRT.   SCYGGTRRR   SCYGGTRRR   SCYGGTRRR   STANDAYTISCOSPRSSPAVQYQWDYRQLPSTYSPFSCRLOG   PHVGANVTLSCOSPRSSPAVQYQWDRQLPSTYCHARASPELTION   DKQKSRGHSKILLELNVLVPPAPPSCRLOG   PHVGANVTLSCOSPRSSPAVQYQWDRQLPSTYTD   ABPQRISPPGGSSSTAVGAVYAWAYAQ   LOCAL LITERACA CONTILEVISTOFGAAVVAGAV   TLVGLGLLAGULAL LITERACA CHERADOK   DALAPRTLPWFSSDTISKNGTLSSVTASAL   RPPHGPPRFGALTFPTISSSAGALFSRLPTTD   AAHPQRISPPGGVSSSGLSMGAVPVMVPAQ   QAGSLV		1	]		ļ		VASCEGAESSEDGA ALKOSCOLETAED LED
		1				Ì	GLQKLKESGKQHGFASFSDYYYKWSSADSC
NTGHGATSGFGSAFTGQQGYENSCPGWTC   GTGGLGYLFGSNRATPFEDSYNYYSYPSYPS    PCTWNRAYSPLHGSGSSYSVCSNSDTKTRT.   SCYGGTRRR    P57   2307   A   8159   1492   528   TIVVATGMCYAPHQVLSYINGVTTSKPG   SCYGGTRRR    VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_SLR_LEGLGEKDSGPSCSVNV   VYSMPSRN_LEGLGEKDSVNL   DAQGKSRGHSISLLINLSSSMAGVPVVRVA   AMPPGRSPRGGSSSGSLSMAGAVVVVPAQA   AMPPGRSPRGGSSSSSLSMAGAVVVVPAQA   AMPPGRSPRGGVSSSGLSMAGAVVVVPAQA   AMPPGRSPRGGVSSSGLSMAGAVVVVVPAQA   AMPPGRSPRGGVSSSGLSMAGAVVVVVPAQA   AMPPGRSPRGGSSSSSLSMAGAVVVVVPAQA   AMPPGRSPRGGSSSSSLMMGAVVVVVPAQA   AMPPGRSPRGGSSSSSLMMGAVVVVVPAQA   AMPPGRSPRGGSSSSLMMGAVVVVVPAQA   AMPPGRSPRGGSSSSSLMMGAVVVVVPAQA   AMPPGRSPRGGSSSSLMMGAVVVVPAQA   AMPPGRSPRGGSSSSLMMGAVVVVPAQA   AMPPGRSPRGGSSSSLMMGAVVVVPAQA   AMPPGRSSSLLQMFLSSGSSNVSLTLRF   AMPPGRSSSLLQMFLSSSSLVFLSGGSSSLAGGSVNSVPADAV   AMPPGRSSSLLQMFLSSSSLVFLSGGSSSLAGGSVNSVPADAV   AMPPGRSSSLVFLSGGSSSLAGGSVNSVPADAV   AMPPGRSSSLVFLSGGSSSLAGGSVNSVPADAV   AMPPGRSSSLVFLSGGSSDLGSSMAGNSVNSVPADAV   AMPPGRSSSLVTSGSSSDLGSSDLAGGSSMAGNSVNSVPADAV   AMPPGRSSSLVTSGSSSDLGGLRAGALLEG   AMPPGRSSSLVTSGSSSDLGGLRAGALLEG   AMPPGRSSSVSLGGSSDLFSSSDLFFRFSSSSLVSSSVNSVPADAVANDFVNSDGSFMAGNSVNSVPADAVANDFVNSDGSSDLGGLRAGALLEG   AMPPGRSSSSDLFFRFSSSDLGGLRAGALLEG   AMPPGRSSSSDLFRRSSVTVNHMSSNSVNSSSSDLFNSSSDLFNGGSSDLAGGSFMANNAGNSVNSVNSGSSSDLFRSSSVTVNHMSSSSNLFSSSDLFNGGSFMANNAGNSVNSVNSGSSSDLFSSSNLF			1	Ì	1		NMSGLITIVVLLGIAFVVYKLFLSDGQYSPPP
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VYSMPSRNLSLR.IEGI.QEKDSSPYSCSVNW DKOQKSRGSHKITLELNVLVPPAPPSCRLQG PHYGANYTLSCQSPRSKPAVQVYQWDRQLPS QTFFAPALDVIRGSLSLTNLSSSMAGVYVCK HNEVGTAQCNVTLEVSTGPGAAVVAGAVY TLVGLGLLAGI.VLLYHRRGKALEEPANDIK DAIPPRITHPWFKSSDTISKNGTLSSVTSARAI RPPHGPPRPGALTPIPSLSSQALPSPRLPTTO AHPOPISPIPGGVSSSGSLSRMGAVPVMVPAQ QAGSLV  ELARPPKQGSSEKSRNMIRNWLTIFILFPLKI EKCESSVSLTVPPVVKLENGSSTNVSLTLRP LNATLVITFEITFRSKNITILELPDBVVVPPGV NSSFQVTSGNVGQLTVYLHGNHSNQTGPRI FLVIRSSAJSINQVIGWIYFVAWSVSTNVSLT AVVLTLIIIVQCCLYERGGGRVSWPAIGFLV AWLFAFVTMIVAAVGVITWLGFLFCSSYKK AVVLTLIIIVQCCLYERGGGRVSWPAIGFLV AWLFAFVTMIVAAVGVITWLGFLFCSSYKK AVTLKYPPQAYMNFYSTEGWSIGNVL DFTGGSFSLLQMFLQSYNNDQWTLIFGDPT FGLGVFSIVFDVVFQAYMNFYSTEGWSIGNVL DFTGGSFSLLQMFLQSYNNDQWTLIFGDPT FGLGVFSIVFDVVFQAYMPFVGPLAVLF MOPPGPPPAYAPINGDFTEVSSADAEDLSG ASPDVKLNLGGDFIKESTATIFLRQRGYGW LEVEDDDPEDNKPLLEELDDLKDTYKIRG LMPMPSI GFRRQVVRDNPDFWGPLAVLF MISLYGQFRVSWHITIWFGSLTFLLARVL GEVAYGQVLGVIGYSLLPLIVIAPVLLVAVG EVYSTLIKLFGVFWAAYSAASLLVGEEFKT KPLLYPFLLYTYFLSLYTIGV MTCFRGGRGEGRSHAFEANKDHKAKVPSP LYSQLNALQFTVDERSI WLOQPTSLTALSQU SVYSTLIKLFGVFWAAYSAASLLVGEEFKT KPLLYPFLLTYTFLSLYTIGV MTCFRGGRGGGRSSBATATNT CPNCRHSDLEALFQDFKDCDFFSKTYTISFP CPNCRHSDLEALFQDFKDCDFFSKTYTISFP CPNCRHSDLEALFQDFKDCDFFSKTYTISFP CPNCRHSDLEALFQDFKDCDFFSKTYTISFP CPNCRHSDLEALFQDFKDCDFFSKTYTISFP CDNNNLHPIFGRHAHEQDTKMHEIYKGNI QLNKNTLKTSAATDVWAVYFSSSSDLAGRKKKILLKE YSTESELTINGGQKPSSSDTFFRFSSSEAH HLLVHVHKHYSMQNHYQVLLLIFLHESLI SENLRKDVAAVTGSPASQTISICIGIGLRSAEI LLLHPVDQANTLKSPYSESSSVVYDPYLPTI GDFLSSKRKQISRDINRRSVIVNHSDNRS SVDLSHPIKAPDLFXDSSSVINFREDSSILISFDSSOLOY	l	1					SG 1 GG 1 RKK
VYSMPSRINI.SI.RIEGIQERUSSIPTSSVINVS DKQGKSRGHSIKTLEILNU.VPPAPPSCRIQG PHYGANVTI.SCQSPRSKPAVQVYQWDRQLPS QTFFAPALDVIRGSI.SI.NI.SSSMAGVYVCK HNEVGTAQCNVTLEVSIGPGAAVVGAVYQVCK HNEVGTAQCNVTLEVSIGPGAAVVAGAVY TI.VGLGLLAGI.VI.YHRGKALEEPANDIK DALAPRTLPWPKSSDTISKNGTI.SSVTSARAI RPPHGPPRPGALTPTPSI.SSQALPSPRLPTTD AHPQPISPIGGVSSESIGSRMGAVPVMVPAQ QAGSLV  ELARRPKQQSSEKSRNMIRNWLTIFILFPLKI EKCESSVSI.TVPPVVKLENGSSTIVISI.TLEP LNATI.VITTETITPSKNITILEI.PDEVVVPPGV NSSFQVTSQNVGQLTVVI.HGNHSNQTIGPBL TI.VIRSSAJSIINQVIGWIYFVAWSISFYPQVII NWRRKSVIGS.FDFVALNI.TGPVATSVFNIC LWVPYIKEOFLLKYPRGVNFVNSDVFFSL AVVILTIIIVQCCLYERGGGRVSWPAIGFLV AWLFAFVTMIVAAVGVTIVLQFLCFCSYIK AVTLVKYPQAYMNFYKSTEGWSIGNVL DFTGGSFSI.LQMFLQSYNDQWTI.FGDPT FGLGVFSIVPDVVFFIGCT.YRKRPGVDQL AWLFAFVTMIVAAVGVTIVLQFLCFCSYIK AVTLVKYPQAYMNFYKSTEGWSIGNVL DFTGGSFSI.LQMFLQSYNDQWTI.FGDPT FGLGVFSIVPDVVFFIGCT.YRKRPGVDQL EVEDDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLEELDDI.KDTYKIRC LEVEDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLLEELDDI.KDTYKIRC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNKPLTETTI.KDCC LEVEDDPEDNCHTTTI.KDCC LEVEDDPEDNCHTTI.KDCC LEVEDDPEDNCHTTTI.KDCC LEVEDDPLTTTI.KDCC LEVEDDPLTTTI.KDCC LEVEDDPLTTTI.KDCC LEVEDDPLTTTI.KDCC LE	957	2307	A	8159	1492	528	THYVMTUMCTAPHQVLSTINGVTTSAFGVSL
PHYGANYTLSCQSPRSKPAQVYQWDRQLPS  OTFLAPALDVIRGSLSLTNLSSSMAGYYVCK HNEVGTAQCNYTLEVSIGPGAAVVGAVYQVCK HNEVGTAQCNYTLEVSIGPGAAVVGAVYQVCK HNEVGTAQCNYTLEVSIGPGAAVVGAVYQVCK HNEVGTAQCNYTLEVSIGPGAAVVGAVYQAQ DAGSLV  ELARPKPOGSSEKSRNMIRNWLTIFILFPLKI EKCESSVSLTVPPVVKLENGSSTRMGAVPVMVPAQ QAGSLV  ELARPKQGSSEKSRNMIRNWLTIFILFPLKI EKCESSVSLTVPPVVKLENGSSTNVSLTLRP INATLYTTEFITFSKNITLELPDEVVVPPGV NSSFQVTSQNVGQLTVVLHGNHSNQTGPRI FLVIRSSAJSINQVIGWIYFVAWSISFYPQVI NWRKSKYGLSFDFVALNLTGPVATSVFNIC LWVPYIKEOFLLKYPRGVNPVNSDVFFSLI AVVLTLIIVQCCLYERGGQRVSWPAIGFLV AWLFAFVTMIVAAVGVTTWLQFLCFCSYNK AVTLVKYPQAYMNFYKSTEGWSIGNVL DFTGGSFSLLQMFLQSYNDQWTLIFGDPT FGLGVFSIVPDVVFFIQHFCLYBKRPGVDQL AWLFAFVTMIVAAVGVTTWLQFLCFCSYNK AVTLVKYPQAYMNFYKSTEGWSIGNVL DFTGGSFSLLQMFLQSYNDQWTLIFGDPT FGLGVFSIVPDVVFFIQHFCLYBKRPGVDQL AWLFAFVTMIVAAVGVTTWLQFLCSYNSW AVTLVKYPQAYMNFYKSTEGWSIGNVL DFTGGSFSLLQMFLQSYNDQWTLIFGDPT FGLGVFSIVPDVVFIQHFCLYBKRPGVDQL AWLFAFVTMIVAAVGVTTWLQFLYFCSSYNT MQPPGPPPAYAPINGDFTFVSSADAEDLSG ASPDVKLNLGGDFIKESTATTHLRQRGVGW LEVEDDDPEDNKPLLELDDLKDYTKIRG LWPMPSLGFNRQVVRQNPDFWGPLAVVLF MISLYGGFRVSWITTIWFGSLTSTLLARVL GEVAYGQVLGVIGYSLLPLIVLAPVLLVVG EVYSTLIKLFGVPWAAYSAASLLVGEFKT KPLLYPFLLYTYFLSLYTIGV MTCFRGGGGGGGSEMATNTT CPNCRHSDLEALFQDFKXDGFFKYTSFP CDNNNLHPIFGRHAHEQDTKMHEIYKGNI QLNKNTLKTSAATDVWAVYFSGSMATNTT CPNCRHSDLEALFQDFKXDGFFKYTSFP CDNNNLHPIFGRHAHEQDTKMHEIYKGNI QLNKNTLKTSAATDVWAVYFSGWIDTPG KSGGGRFSTVDSFFLSWICQFTRYAESQKI QTCNQVSLNTSQSESSDLAGRKKNLLKW YSTESELTINGGQKSSSDTLAGRKKNLLKW YSTESELTINGGGCNSSSDTLAGRKKNLLKW YSTESELTINGGGCNSSSSTFFRFSNSSEAL HLLVHVHKHYSMQNHYQVLLLILLEHESLI SENLRKDVEAVTGSPASQTSICIGILLBSLI SENLRKDVEAVTGSPASQTSICIGILLBSLI SENLRKDVEAVTGSPASQTSICIGILGRSLI SENLRKDVEAVTGSSSNIFTRSSSSSLAGRKKNLLKW SVDLSHPILKDPLLFKASSDTNLQKGISFMD SVDLSHPILKDPLLFKASSDTNLQKGISFMD SVDLSHPILKDPLLFKASSDTNLQKGISFMD SVDLSHPILKDPLLFKASSDTNLQKGISFMD SVDLSHPILKDPLLFKASSDTNLQKGISFMD SVDLSHPILKDPLLFKASSDTNLQKGISFMD	131	1 230,	1		1		VYSMPSRNLSLRLEGLQEKDSGPYSCSVNVQ
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			L CEC	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	i=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	{	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience	ļ		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	ļ		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	l	Į.	1		sequence	/=possible nucleotide deletion, \-possible
		1		peptide	1	nucleotide insertion
				sequence		DISKEETPPVRTLKSQSSLSGKPKERCPPNLAP
		Ī	Ì			LCVSYKNMKRSSSQMSLDTISLDSMILEEQLL
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		1	1	1		EFLTSSLMNIQHFLEDETVATVMPMKIQVSNT
		1	1	<b>\</b>		KINLKDDSPRSSTVSLEPAPVTVHIDHLVVER
			1			KINLKDDSPRSSIVSLEFAFVIVIIDIEVVDR
		1				SDDGSFHIRDSHMLNTGNDLKENVKSDSVLL
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		ļ			Į	GLGTDELRLLYGMALVRFVNLISERKTKFAK
	- [	1				VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI
	1	j	- 1			NDCRRGCYFVLDWLQKTYWCRQLENSLRET
•						WELEEFREGIEEEDQEEDKNIVVDDITEQKPE
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		1	l l			PODDGKSTESDVKADGDSKGSEEVDSHCKK
	1		<b>!</b>	1		ALSHKELYERARELLVSYEEEQFTVLEKFRY
	ļ		ļ.	1		PKAIKAWNNPSPRVECVLAELKGVTCENREA
	1		- 1			VLDAFLDDGFLVPTFEQLAALQIEYEENVDL
	ľ				· ·	NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE
						RMLSELPALGISGIRPTYILRWTVELIVANTK
	1		1	į.	İ	GRNARRFSAGQWEARRGWRLFNCSASLDW
		ļ		1		RMVESCLGSPCWASPQLLRIIFKAMGQGLPE
	l				]	FEOEKI LRICSIYTOSGENSLVQEGSEASPIGE
ł	1	- 1	ł	j	1	COUTT DSI YWSVKPASSSFGSEAKAQQQEEQ
ĺ						GOVNDVKEEEKEEKEVLPDOVEEEEENDDQ
	i		İ			FEEEDEDDEDDEEEDRMEVGPFSTGQESFIA
}	ì			İ		ENARLLAQKRGALQGSAWQVSSEDVRWDT
		1	1		•	PLGRMPGQTEDPAELMLENYDTMYLLDQP
	1	-	}	}	1	LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSS
1	1	1			1	NFEGLLWSQGQLHGLKTGLQLF
		1				EPRRNFRDDSTRPRTRGRTRGRRRACRSAE
964	2314	A	8184	6	1393	GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSP
1	-21,	1		1		GIGLRSLLLYPKLQLPAUPTORCR WDF VSSI
					1	PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGL
}			1			NVGKSTFFNVLTNSQASAENFPFCTIDPNESF
1		İ				VPVPDERFDFLCQYHKPASKIPAFLNVVDIA
1				- [		LVKGAHNGQGLGNAFLSHISACDGIFHLTRA
	į			}		FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEN
	i	1	1			GPUDKI EKVAVRGGDKKLKPEYDIMCKVKS
1						WVIDOKKPVRFYHDWNDKEIEVLNKHLFL1
		1				KPMVYLVNLSEKDYIRKKNKWLIKIKEWVL
	1	1	1	1		, Am 174 7 4 20 17 - T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-
ì		{	i i			KYDPGALVIPFSGALELKLQELSAEERQKYL

			1 000	D 11-4-4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	(	USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	]	/=possible nucleotide deletion, \=possible
	Ì	1		sequence		nucleotide insertion
		<del> </del>	· <del> </del> -	Sequence		ANMTQSALPKIKAGFAALQLEYFFTAGPDEV
					1	RAWTIRKGTKAPQAAGKIHTDFEKGFIMAEV
	}	ł	ł	}		MKYEDFKEEGSENAVKAAGKYRQQGRNYIV
			-	İ		EDGDIIFFKFNTPQQPKKK
066	2315	A	8195	1437	594	RSFSLSFSLLSPSEMMALGAAGATRVFVAMV
965	2313	^	0175	1.5.		AAALGGHPLLGVSATLNSVLNSNAIKNLPPPL
		1		1		GGAAGHPGSAVSAAPGILYPGGNKYQTIDNY
		1				QPYPCAEDEECGTDEYCASPTRGGDAGVQIC
						LACRKRRKRCMRHAMCCPGNYCKNGICVSS
	]	1			1	DQNHFRGEIEETITESFGNDHSTLDGYSRRTT
					1	LSSKMYHTKGQEGSVCLRSSDCASGLCCARH
						FWSKICKPVLKEGQVCTKHRRKGSHGLEIFQ
		İ				RCYCGEGLSCRIQKDHHQASNSSRLHTCQRH
966	2316	A	8207	416	4082	KFKLIKIMLLTLIILLPVVSKFSFVSLSAPQHW
900	2510	1	0207			SCPEGTLAGNGNSTCVGPAPFLIFSHGNSIFRI
			1			DTEGTNYEQLVVDAGVSVIMDFHYNEKRIY
}	1			1		WVDLERQLLQRVFLNGSRQERVCNIEKNVSG
	Î					MAINWINEEVIWSNQQEGIITVTDMKGNNSHI
	1		-	•		LLSALKYPANVAVDPVERFIFWSSEVAGSLY
:		1	1			RADLDGVGVKALLETSEKITAVSLDVLDKRL
}						FWIQYNREGSNSLICSCDYDGGSVHISKHPTQ
	1	1	l			HNLFAMSLEGDRIFYSTWKMKTIWIANKHTG
	İ					KDMVRINLHSSFVPLGELKVVHPLAQPKAED
		Ì			ł	DTWEPEQKLCKLRKGNCSSTVCGQDLQSHLC MCAEGYALSRDRKYCEGNDWKYCEDVNEC
		1		1		AFWNHGCTLGCKNTPGSYYCTCPVGFVLLPD
ľ				1		GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF
					1	CPEGSVLERDGKTCSGCSSPDNGGCSQLCVPL
	İ	1	1			SPVSWECDCFPGYDLQLDEKSCAASGPQPFL
j			1	l	1	LFANSQDIRHMHFDGTDYGTLLSQQMGMVY
ļ	ł					ALDHDPVENKIYFAHTALKWIERANMDGSQ
1				-		RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK
				ļ		SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK
1	İ	1	1	1		RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW
		į		ļ		PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK
i						RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP
}			1			SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP
		1		1		LAKPGADPCLYONGGCEHICKKRLGTAWCS
						CREGEMKASDGKTCLALDGHQLLAGGEVDL
1						KNOVTPLDILSKTRVSEDNITESQHMLVAEIM
				1		VSDODDCAPVGCSMYARCISEGEDATCQCLK
1			1			GFAGDGKLCSDIDECEMGVPVCPPASSKCINT
1	1			1		EGGYVCRCSEGYQGDGIHCLDIDECQLGVHS
						CGENASCINTEGGYTCMCAGRLSEPGLICPD
	1	1		1		STPPPHI REDDHHYSVRNSDSECPLSHDGYCL
	1	- (	1	1	· 	HDGVCMYIEALDKYACNCVVGYIGERCQYR
						DLKWWELRHAGHGQQQKVIVVAVCVVVLV
						MULLUSLWGAHYYRTQKLLSKNPKNPYEESS
				1	1	RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD
	1			}		LKNGGOPVAGEDGOAADGSMQPTSWRQEPQ
		ļ				LCGMGTEOGCWIPVSSDKGSCPQVMERSFH
1				}		MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL
						DPPHOMELTO
0(5			8210	$\frac{1}{3}$	601	SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL
967	2317	A	8210	3	001	RLHHRFRALDRNKKGYLSRMDLQQIGALAV
		1		1		NPL GDRIJESFFPDGSORVDFPGFVRVLAHFRP
					1	VEDEDTETODPKKPEPLNSRRNKLHYAFQLY
						DI DRDGKISRHEMLOVLRLMVGVQVTEEQL
1						ENIADRTVQEADEDGDGAVSFVEFTKSLEKM
1		1				DVEHKMSIRILK
1					_1	

			T===	D 4:-004	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ĺ	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, 1-1 forme,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uciicc	<b>\</b>	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	İ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ			peptide	1 *	/=possible nucleotide deletion, \=possible
	ļ	Ì				nucleotide insertion
	<u> </u>		<u> </u>	sequence	409	ISSCPHTAYEGSMSTLSNFTQTLEDVFRRIFIT
968	2318	A	8211	2	409	YMDNWRQNTTAEQEALQAKVDAENFYYVIL
	1	1	1	İ		YLMVMIGMFSFIIVAILVSTVKSKRREHSNDP
	1	1		ì		YEMVMIGMESTHATILE STARSMIGHT THE NIG
	1		1	1		YHQYIVEDWQEKYKSQILNLEESKATIHENIG
	•	ì		Į.		AAGFKMSP
0.60		<del>                                     </del>	8215	1	1938	GMPRSRGGRAAPGPPPPPPPPPGQAPRWSRWR
969	2319	A	0213	} *	1.330	VPGRLLLLLLPALCCLPGAARAAAAAAAGAGN
		1	1			RAAVAVAVARADEAEAPFAGQNWLKSYGY
	1	Ì	-		ļ	LLPYDSRASALHSAKALQSAVSTMQQFYGIP
	1		-	]		VTGVLDQTTIEWMKKPRCGVPDHPHLSRRRR
	į.	1	1		1	VIGVLDQI IEWWIKKI KCOVI DILI IEDIGGG
						NKRYALTGQKWRQKHITYSIHNYTPKVGELD
	1			1	1	TRKAIRQAFDVWQKVTPLTFEEVPYHEIKSDR
			1	1	1	KEADIMIFFASGFHGDSSPFDGEGGFLAHAYF
	1	1	1	1	1	PGPGIGGDTHFDSDEPWTLGNANHDGNDLFL
	1					VAVHELGHALGLEHSSDPSAIMAPFYQYMET
		1		1		HNFKLPODDLOGIOKIYGPPAEPLEPTRPLPTL
	1		1	1		PVRRIHSPSERKHERQPRPPRPPLGDRPSTPGT
	1		1	1	}	KPNICDGNFNTVALFRGEMFVFKDRWFWRL
	1	1				RNNRVQEGYPMQIEQFWKGLPARIDAAYER
			1			ADGRFVFFKGDKYWVFKEVTVEPGYPHSLG
		}	1	1	·	ADGREVERGORYWYREVIVERVGERV
			1			ELGSCLPREGIDTALRWEPVGKTYFFKGERY
	1	1	-			WRYSEERRATDPGYPKPITVWKGIPQAPQGA
	1				1	FISKEGYYTYFYKGRDYWKFDNQKLSVEPGY
		1		1		PRNILRDWMGCNOKEVERRKERRLPQDDVDI
1	1	1	i			MVTINDVPGSVNAVAVVIPCILSLCILVLVYTI
	}	1	ì		İ	FQFKNKTGPQPVTYYKRPVQEWV
1	1 _				0000	SRLSLQFYVSFRRTGLFTCKLIVEIFFRNYMN
970	2320	Α	8216	1235	2223	DSLRTNVFVRFQPETIACACIYLAARALQIPLP
		1	İ	}		TRPHWFLLFGTTEEEIQEICIETLRLYTRKKPN
			-			I RPH WELLFUL TELETIQUE CIETE TO THE THE THE TELETION OF A VICE AND DETERMINED TO THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETION OF THE TELETIO
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]	ļ	}	}		İ	ALSTLGGFSPASKPSSPREVKAEEKSPISINVK
1		1				TVKKEPEDRQQASKSPYNGVRKDSKRSRNSR
	l	l	1		i	SASRSRSRTRSRSRSHTPRRHYNNRRSRSGTY
	- 1	ł	ł	İ		SSRSRSRSRSHSESPRRHHNHGSPHLKAKHTR
ł	l	- 1	1		1	DDLK SSNR HGHKRKKSRSRSQSKSRDHSDAA
1	Ì	-	ļ			KKHRHERGHHRDRRERSRSFERSHKSKHHGG
		1	1			SRSGHGRHRR
1		1				DCRLQAAMPTNFTVVPVEAHADGGGDETAE
971	2321	A	8217	3	3274	DCKLQAAMYINTIV YY VEARADOOODETAD
1		-		1		RTEAPGTPEGPEPERPSPGDGNPRENSPFLNN
1	1		Į	1		VEVEQESFFEGKNMALFEEEMDSNPMVSSLL
1	1		i	1	1	
		ļ	1		]	NKLANYTNLSQGVVEHEEDEESRRREAKAPR
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KI ALVFLACVVLSILAIYAGVIKSAFDPPDIPV.
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSOPSAACDEYFIQNNVTEIQGIPGA
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AFESRASTLPYVLTDIAASFTLLVGIYFPSVTG
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AFESRASTLPYVLTDIAASFTLLVGIYFPSVTG
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAOKSIPTGTILAIVTTSFIY
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM I AWPSPWVIVIGSFFSTCGAGLOTLTGAPRLL
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL OAIARDGIVPFLOVFGHGKANGEPTWALLLT
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VI ICFTGILIASLDSVAPILSMFFLMCYLFVNL
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VLICETGILIASLDSVAPILSMFFLMCYLFVNL ACAVOTLLRTPNWRPRFKFYHWTLSFLGMSL
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VLICETGILIASLDSVAPILSMFFLMCYLFVNL ACAVOTLLRTPNWRPRFKFYHWTLSFLGMSL
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV. CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VLICETGILIASLDSVAPILSMFFLMCYLFVNL ACAVQTLLRTPNWRPRFKFYHWTLSFLGMSL CLALMFICSWYYALSAMLIAGCIYKYIEYRG
						MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESFLIVAMCCTCTMLTAISMSAIATNGVVP AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VLICETGILIASLDSVAPILSMFFLMCYLFVNL ACAVOTLLRTPNWRPRFKFYHWTLSFLGMSL

ectide seq- uence	seq- uence		USSN 09/496 914	location correspondi ng to first amino acid residue of peptide sequence	corresponding to last amino acid residue of peptide sequence	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LKAGKGLTIVGSVLEGTYLDKHMEAQRAEE NIRSLMSTEKTKGFCQLVVSSSLRDGMSHLIQ SAGLGGLKHNTVLMAWPASWKQEDNPFSW KNFVDTVRDTTAAHQALLVAKNVDSFPQNQ ERFGGGHIDVWWIVHDGGMLMLLPFLLRQH KVWRKCRMRIFTVAQVDDNSIQMKKDLQMF LYHLRISAEVEVVEMVENDISAFTYERTLMM EQRSQMLKQMQLSKNEQEREAQLIHDRNTAS HTAAAARTQAPPTPDKVQMTWTREKLIAEK YRSRDTSLSGFKDLFSMKPDQSNVRRMHTAV KLNGVVLNKSQDAQLVLLNMPGPPKNRQGD ENYMEFLEVLTEGLNRVLLVRGGGREVITIYS TSRRVTMKFNPFVTSDRSKNRKRHFNAPSHV
972	2322	A	8224	701		RKKIMSSPLSKELRQKYNVRSMPIRKDDEVQ VVRGHYKGQQIGKVVQVYRKKYVIYIERVQ REKANGTTVHVGIHPSKVVITRLKLDKDRKKI LERKAKSRQVGKEKGKYKEELIEKMQE GCPHAGGKGRVPTGGLTGGRTWSPSAAPRSC
973	2323	A	8237	873	4610	PRPGPTPAPGAMDKLPPSMRKRLY SLPQUVG AKAWIMDEEDAEEEGAGGRQDPSRRSIRLR PLPSPSPSAAAGGTESRSSALGAADSEGPARG AGKSSTNGDCRRFRGSLASLGSRGGGSGGTG SGSSHGHLHDSAEERRLIAEGDASPGEDRTPP GLAAEPERPGASAQPAASPPPPQQPPQPASAS CEQPSVDTAIKVEGGAAAGDQILPEAEVRLG QAGFMQRQFGAMLQPGVNKFSLRMFGSQKA VEREQERVKSAGFWIIHPYSDFRFYWDLTML LLMVGNLIIIPVGITFFKDENTTPWIVFNVVSD TFFLIDLVLNFRTGIVVEDNTEIILDPQRIKMK YLKSWFMVDFISSIPVDYIFLIVETRIDSEVYK TARALRIVRFTKILSLLRLLRLSRLIRYIHQWE EIFHMTYDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMLQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSHMLCIGYGRQAPVGMSDV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRIHD YYEHRYQGKMFDEESILGELSEPLREEIINFNC RKLVASMPLFANADPNFVTSMLTKLRFEVFQ PGDYIIREGTIGKKMYFIQHGVVSVLTKGNKE TKLADGSYFGEICLLTRGRRTASVRADTYCR LYSLSVDNFNEVLEEYPMMRRAFETVALDRL DRIGKKNSILLHKVQHDLNSGVFNYQENEIIQ QIVQHDREMAHCAHRVQAAASATPTPTPVIW TPLIQAPLQAAAATTSVAIALTHIPRLPAAIFR PPPGSGLGNLGAGGTPRHLKRLQSLIPSALGS ASPASSPSQVDTPSSSSFHIQQLAGFSAPAGLS PLLPSSSSSPPPGACGSPSAPTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGSGGGGSSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL
974	2324	A	8247	279	700	LVPVKDASRICSLTYLLGSHWNNLVVRSPVL

					5 V 4 4 4 4	Amino acid sequence (A=Alanine C=Cysteine,
SEQ II	D   SEQ ID	Met	SEQ	Predicted	Predicted end	De Accordic Acid E=Glutamic Acid.
NO: of	1 -	hod	ID NO:	beginning	nucleotide	F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
1			USSN	location	corresponding	l=Isoleucine, N=Lysine, L=Leucine,
eotide			09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ł	1	ì	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
}	}	}			sequence	/=possible nucleotide deletion, \=possible
1		1		peptide	•	nucleotide insertion
	ļ	l	l	sequence		LVALKNWKPKGTNIPAPQSPVFGEAVSGVYM
975	2325	A	8249	62	1571	MTKVLGMAPVLGPRPPQEQVGPLMVKVEEK
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ł	1	1	1			EEKGKYLPSLEMPRORPROTELL VI FOFLT
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	1					GEKPYKCKECGKAFNHSSNFNKHHRIHTGEK
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						- C C Mains
	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	seq-	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
otide	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
seq- uence	denice	ļ	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
JCIICC		1	}	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì			residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		nucleotide insertion
			-	sequence		LPAVFVCIALVFSLIVPPFGKYPSLELQPWMY
	<del> </del>	+	<del>                                     </del>		Ì	NEQYTFVSNDAPEDTGTLELLNALTKDPGFG
		1		ì	1	TRCMEGNPIPDTPCQAGEEEWTTAPVPQTIM
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			l			EALCTRMAIMVNGRFRCLGSVQHLKNRFGD
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		1				EKHRNMLQYQLPSSLSSLARIFSILSQSKKRLH
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		Ì	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
ucuc	1	ļ	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	Ì	1	residue of	sequence	/=possible nucleotide deletion, \=possible
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	<del> </del>	<del> </del>	<del> </del>			MRLSGPQAFDKNEINSLQSSEGLLEKIIKQAK
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						COSTONA SOLOGIO OMOLOLERO HAGA ARO
		-			1	LNSSGPSASQLQQLQMQLQLERQHAQAARQ
	1	}			1	QLETARNATRRINTSSVITITIQSTATTNIAN
		1			1	TESSQOTLQNSQFLLTRLNDPKMSETERQSM
	ļ				1	ESERADRSLFVQELLLSTLVREESSSSDEDDR
	1	1	1			GEMADFGAMGCVDIMPLDVALENLNLKESN
1				į	}	KGNEPPPPPL
			0215		1004	GSTHASADAWAOWFCTEALVMGAPVWYLV
982	2332	Α	8315	1	,,,,,	A A A I I VOFTI FLTRSRGRAASAGQEPLHNEEL
1		1		1	}	AGAGRVAOPGPLEPEEPRAGGRPRRRRDLGS
		Í				DI OAORRAORVAWAEADENEEEAVILAQEE
		- 1	1			EGVEKPAFTHI SGKIGAKKLRKLEEK QAKKA
		1		}		ODEAEEAERFERKRIESOREAEWKKEEEKLK
	ļ	- 1		1		1 FEFOKEFFERK AREEOAOREHEEYLKLKEA
			1		1	FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK
	1	1	}	İ	1	VVLLEDLASQVGLRTQDTINRIQDLLAEGTTT
1		- 1		1		GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA
- 1		1	1	- [		GAIDDEGE TVACEBEDY OVER
1						ELAQASNSLIAWGRESPAQAPA
693	2222	-	8320	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKP
983	2333	^	0320	1		DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD
		- 1				PHKIVEFVNSGVGDFSOPDTSPDTNGGGS15D
1						TOEDIT DELLGNMVLAPLPDPGPPSLAVAPEP
	1	ĺ	1	ì		CPQPLRSPSLDNPTPFPNLGPSENPLKRLLVPG
į.	1		1	1		CPOPERSFSEDINI III III EGI GEI II EI
						EEWEFEVTAFYRGRQVFQQTISCPEGLRLVGS

						( ) ( ) ( ) ( ) ( ) ( )
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		ļ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	peptide		/=possible nucleotide deletion, \=possible
	Ì	1		sequence		nucleotide insertion
		<del> </del>	<del> </del>	Sequence		EVGDRTLPGWPVTLPDPGMSLTDRGVMSYV
	1	1				RHVLSCLGGGLALWRAGOWLWAQRLGHCH
	ļ					TYWAVSEELLPNSGHGPDGEVPKDKEGGVF
			İ			DLGPFIVGSLGPPDLITFTEGSGRSPRYALWFC
		İ	1			VGESWPQDQPWTKRLVMVKVVPTCLRALVE
		١.				MARVGGASSLENTVDLHISNSHPLSLTSDQY
		1		1		KAYLQDLVEGMDFQGPGES
		l			<del></del>	ANMAPVEHVVADAGAFLRHAALQDIGKNIY
984	2334	Α	8321	1	1243	TIREVVTEIRDKATRRLAVLPYELRFKEPLPE
	·	ł				YVRLVTEFSKKTGDYPSLSATDIQVLALTYQL
						YVKLVIEFSKKIGDIFSCSAIDIQVLALIIQE
		1		1	1	EAEFVGVSHLKQEPQKVKVSSSIQHPETPLHIS
		1	İ	1	1	GFHLPYKPKPPQETEKGHSACEPENLEFSSFM
	l.					FWRNPLPNIDHELQELLIDRGEDVPSEEEEEEE
		1	1		1	NGFEDRKDDSDDDGGGWITPSNIKQIQQELE
	1					QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV
			]	1		LAVNGMLIREARSYILRCHGCFKTTSDMSRV
					ļ	FCSHCGNKTLKKVSVTVSDDGTLHMHFSRNP
1						KVLNPRGLRYSLPTPKGGKYAINPHLTEDQRF
						PQLRLSQKARQKTNVFAPDYIAGVSPFVENDI
			1			SSRSATLQVRDSTLGAGRRRLNPNASRKKFV
l		1				KKR
985	2335	A	8322	352	529	RRNNIRQFIMKVCISGQARWLTPVVPVLWET
303	2555	^	032		Ì	EAGRSLELKSLRPAWATWGNPISTKINK
986	2336	A	8325	89	1172	KMNPTDIADTTLDESIYSNYYLYESIPKPCTKE
986	2330	Α	0525	"		GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL
	1		ł		ĺ	FKYKRLRSMTDVYLLNLAISDLLFVFSLPFWG
	1	İ	İ			YYAADQWVFGLGLCKMISWMYLVGFYSGIF
						FVMLMSIDRYLAIVHAVFSLRARTLTYGVITS
			1			LATWSVAVFASLPGFLFSTCYTERNHTYCKT
				1		KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCY
}	1	1	1		1	SMIRTLQHCKNEKKNKAVKMIFAVVVLFLG
						FWTPYNIVLFLETLVELEVLQDCTFERYLDYA
			ļ	1		IQATETLAFVHCCLNPIIYFFLGEKFRKYILQL
İ			i	1		FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS
	ļ					TMDHDLHDAL
L				1	470	SLSAMRFLAATFLLLALSTAAQAEPVQFKDC
987	2337	Α	8326	3	470	GSVDGVIKEVNVSPCPTQPCQLSKGQSYSVN
				1	1	VTFTSNIQSKSSKAVVHGILMGVPVPFPIPEPD
						GCKSGINCPIQKDKTYSYLNKLPVKSEYPSIK
		Ì			1	LVVEWQLQDDKNQSLFCWEIPVQIVSHL
		1				LA AEMONDALIAGONICA AND DEDA
988	2338	A	8335	1205	323	VIKMALAARLLPQFLHSRSLPCGAVRLRTPA
1		1				VAEVRLPSATLCYFCRCRLGLGAALFPRSAR
		1			1	ALAASALPAQGSRWPVLSSPGLPAAFASFPAC
1						PQRSYSTEEKPQQHQKTKMIVLGFSNPINWV
		1				RTRIKAFLIWAYFDKEFSITEFSEGAKQAFAH
		1				VSKLLSQCKFDLLEELVAKEVLHALKEKVTS
		1		1	1	LPDNHKNALAANIDEIVFTSTGDISIYYDEKG
				1		RKFVNILMCFWYLTSANIPSETLRGASVFQVK
		1	i			LGNQNVETKQLLSASYEFQREFTQGVKPDWT
		1				IARTEHSKLLE
000	0220	<del> </del>	8349	67	185	MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL
989	2339	Α	6349	0'	103	KSLHPMS
			+		1115	ASPFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ
990	2340	A	8361	210	1112	ITLQGSRRRQGRTAFPASGKKRETDYSDGDPL
			1	1		DVHKRLPSSTGEDRAVMLGFAMMGFSVLMF
1	1	1				FLLGTTILKPFMLSIQREESTCTAIHTDIMDDW
	1				1	THE COLUMN RECIVILIZION RECOLUMN CONTRACTOR AND A STREET
						TOCATTOCAMOUGOCKADOLI UAEAMI CADO
						LDCAFTCGVHCHGOGKYPCLQVFVNLSHPG
						LDCAFTCGVHCHGQGKYPCLQVFVNLSHPG QKALLHYNEEAVQINPKCFYTPKCHQDRNDL LNSALDIKEFFDHKNGTPFSCFYSPASQSEDVI

			LCEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D-A enartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	USSN	location	corresponding	I-Isoleucine K=Lysine L=Leucine,
otide	seq-		1	correspondi	to last amino	M=Methionine, N=Asparagine, P=Profine,
eq-	neuce		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience	}	Į	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ļ	ì		sequence	V=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	sequence	/-possible nucleotide deletion, \-possible
	1	1	Į.	peptide		nucleotide insertion
	]	· _	1	sequence		LIKKYDQMAIFHCLFWPSLTLLGGALIVGMV
	<del></del>				1	RLTQHLSLLCEKYSTVVRDEVGGKVPYIEQH
	}	1	ļ			QFKLCIMRRSKGRAEKS
	1	1	ł		L	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVL
991	2341	A	8369	9	921	EGFLSAEECVAMQQRIGEIVAEMDVPLHCRT
771	25.17	1	1			EGFLSAEECVAMQQRIGETVALMDVIETEEK
	l	1	1			EFSTQEEEQLRAQGSTDYFLSSGDKIRFFFEK
	ŀ	1	}			GVFDEKGNFLVPPEKSINKIGHALHAHDPVFK
	l	1	İ			SITHSFKVQTLARSLGLQMPVVVQSMYIFKQP
	1	1	ì	1		HFGGEVSPHQDASFLYTEPLGRVLGVWIAVE
	ļ		1			DATLENGCLWFIPGSHTSGVSRRMVRAPVGS
	1		j		)	APGTSFLGSEPARDNSLFVPTPVQRGALVLIH
		Į	i		1	GEVVHKSKQNLSDRSRQAYTFHLMEASGII
	1	-	1		1	WSPENWI OPTAELPFPOLYT
	İ				4	MALSGNCSRYYPREOGSAVPNSFPEVVELNV
992	2342	A	8370	906	*	CGOVYFTRHSTLISIPHSLLWKMFSPKKDIAN
	1	1	ļ			DIAKDSKGREFIDRDGELFRYILDYLKDKQVV
	1	1			İ	1 PDHEPEK GRI KREAEYFOLPDLVKLLIPDEI
		j	1		ļ	L COSPDEECHSDEEDASOGSDTRICPPSSLLPAD
	ĺ	l l	1			RKWGFITVGYRGSCTLGREGQADAKFRRVPR
			i			ILVCGRISLAKEVFGETLNESRDPDRAPERYTS
	}	1		1		RFYLKFKHLMGAPASNFILGFWGLGQNQDK
	1		1		ŀ	HPVNIYLQQRSVIRPDLTSKKAGDLKGKGDA
	1	- 1	ł			HPVNIYLQQKSVIKI DEISKIEROZZKIOTET
		ļ	ļ	_		QEVSRRRRWLGDPEHL MRMQRHKNDTMDFGDSGKRIGGGVLCLLHQ
993	2343	A	8379	1	2794	MRMQRHKND1 MDFGD3GRIGGGGVEGDS14
993	2545	' *		Į		SNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIE
			1		1	DMVTTASTYLFEATEKRFFFKNVSILIPENWK
•	ŀ		1	İ	Ĭ	ENPOYKRPKHENHKHADVIVAPPTLPGRDEP
		i	1			YTKQFTECGEKGEYIHFTPDLLLGKKQNEYG
	1		1			PPGKLFVHEWAHLRWGVFDEYNEDQPFYRA
1	1	- 1	1	-		KSKKIEATRCSAGISGRNRVYKCQGGSCLSRA
		1	<b>j</b> .			CRIDSTTKLYGKDCQFFPDKVQTEKASIMFM
1		1	1		Ì	1 OCTORVIVERCNEKTHNOEAPSLUNIKUNIKSI
	1		1		}	WEVICKISEDEKNTIPMVTPPPPPVFSLLKIRQK
ļ	ì	1	1	i	İ	VCI VI DKSGSMGGKDRLNRMNQAAKHFLLV
	l l					TVPNCSWVGMVHFDSTATIVNKLIQIKSSUCI
	İ	l	Ì	ļ		NITI MAGI PTYPI GGTSICSGIKYAFQVIGELH
	1	1			1	SOI DESEVELL TOGEDNIASSCIDE VKQSGAJ
1	1	Ì		1		VUELAT GRAADEAVIEMSKITGGSHFY VODEA
	l l	1	l			QNNGLIDAFGALTSGNTDLSQKSLQLESKGL
		1	ĺ			LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPI
		- 1	ŀ			SISLWDPSGTIMENFTVDATSKMAYLSIPGTA
1	1		1			SISLWDPSGIIMENTI VDATSIQUETTESE A ANSSI
1	1			1		KVGTWAYNLQAKANPETLTITVTSRAANSS\
1		}		1		PPITVNAKMNKDVNSFPSPMIVYAEILQGYV
1		ļ	ļ	1		VLGANVTAFIESQNGHTEVLELLDNGAGADS
1		1				FKNDGVYSRYFTAYTENGRYSLKVRAHGGA
1			}			NTARLKLRPPLNRAAYIPGWVVNGEIEANPP
			[		1	PREIDED TOTTLEDES RTASGGAFVVSQVPSL
			- }			DI POOVPPSOITDI DATVHEDKILI WI APGU
1	1		1			MEDVGKVORYIIRISASILDLRDSFDDALQVN
		1		1		TTDI SPKEANSKESFAFKPENISEENATHIFIA
1	Į.		}	}	1	R SIDK SNI TSK VSNIAOVTLFIPQANPDDIDPI
		- 1				PTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIV
		- 1				
}		)	1			NFILSTTI INSSPRTGRDHQELNLHTERDSRSQRAVLKIF
994	2344	$\overline{A}$	8385	231	644	RONPGIFYWIFLPSRSHSASHGSRQRQVSCQC
774	2344	17		į.		RONPOLL AND THE PROPERTY CONTRACTOR
1	Ì	1	1	}		TODEILKMRNTFAELKNSLEALSSRMDQAEL
	-	1	1			RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSI
i		1	- 1			PSSWDYRACLS AWRKSSVVPPRGTRRGEKSDQDKSGQKNKI

PCT/US01/03800 WO 01/57188

					11 Almin C-Custeine
SEO ID	Met	SEO	Predicted	Predicted end	Amino scid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	1	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
		in			I=Isoleucine, K=Lysine, L=Leucine,
				corresponding	M=Methionine, N=Asparagine, P=Proline,
uence		No. 1			O-Glutamine R=Arginine, S=Serine,
		914			T-Threonine V=Valine W=Tryptophan,
1				or behine	V=Tyrosine, X=Unknown, *=Stop codon,
				Sequence	/=possible nucleotide deletion, \=possible
					-volectide insertion
<u> </u>		ļ	sequence		DEL SMK OSPAL APEERCRRAGSPKPVLKADD
	1	1	1		NINIM CNGCSOKI ATANLLRELLVLIPCICAL V
			1		TITER I SVVGTI OKVYFKSNGSEPLVIDGEL
	1				QGSDVILTNTIYNQSTVVSTAHPDQHVPAWT
					TDASLPGDQSHRNTSACMNITHSQCQMLPYH
ì	1	}	1	1	ATLTPLLSVVRNMEMEKFLKFFTYLHRLSCY
		1	1		QHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCE
					AAKEGCESVLGMVNYSWPDFLRCSQFRNQT ESSNVSRICFSPQQENGKQLLCGRGENFLCAS
	Ì				GICIPGKLQCNGYNDCDDWSDEAHCNCSENL
				1	FHCHTGKCLNYSLVCDGYDDCGDLSDEQNC
					DCNPTTEHRCGDGRCIAMEWVCDGDHDCVD
			1		ventialcechengl.VECRNGOCIPSTFQCDG
			1		PEDCYDGEDFFNCSVIOTSCOEGDORCLINE
			}		LOT DOCCOSSI COPNISLINICSOCEPTILELOM
İ		1			AND DATA TO THE PROPERTY OF TH
		ļ			I VOTNOVKVI MFFSCTILVPKCDVN I GEHIFF
	l	1	1		LODAT CERCEPCIONICIDATEDIDOS
	ĺ		ļ	1	FPEENSDNQTCLMPDEYVEECSPSHFKCRSGQ
			<b>\</b>		CVLASRRCDGQADCDDDSDEENCGCKERDL
ĺ			}		WECPSNKQCLKHTVICDGFPDCPDYMDEKN CSFCQDDELECANHACVSRDLWCDGEADCS
					DSSDEWDCVTLSINVNSSSFLMVHRAATEHH
l			1		LUCADOWOFII SOT ACKOMGLGEPSVIKLIQE
	Ì				1 APPEDDUATI HONWESLNGI ILHELLVNOQS
			1		- LODGE CRICK I CTRODOGERPAARMINERILUUR
ļ	į.				TCDDGR WPWOCSLOSEPSGHICGCVLIANA W
					LVITVAHCEEGRENAAVWKVVLGINNLUHPS
	}	Ì			VEMOTREVKTIII HPRYSRAVVDY DISIVELSE
					DISETGV/DPVCI PNPE()WLEPDI ICIIIOW
		1			CUMCNEMPER LOEGEVRUSLEHCUS I PUMA
					TITTRMICAGYESGTVDSCMGDSGGPLVCEK
					PGGRWTLFGLTSWGSVCFSKVLGPGVYSNVS
	- 1				YFVEWIKRQIYIQTFLLN KVILSSEMSKTNKSKSGSRSSRSRSRSRSRSRSRSRSRSRSRSRSRSRSRSR
2346	- A	8392	199	3085	FSKSRSRSRSLSRSRKRRLSSRSRSRSYSPAHN
2540	1	"	ł		RERNHPRVYQNRDFRGHNRGYRRPYYFRGR
		1	ł		NRGFYPWGQYNRGGYGNYRSNWQNYRQAY
	١.		1		CDDDCDQQQQQXXXXXXXXXXXXXXXXXXXXXXXXXXXX
		)			DDCDDCCCRCCRCCNHSRVESSKRKSAKEKKDS
i					L V D C D D C O A C D N O C D E V K E O T F S G U 1 S Q U 1 F
1	}				A CECCUPWINATYGTGSASRASAVSELSPRE
	i	1			CDAI KCDI OSVVVRRRSPRPSPVPKPSPPLSSI
		ĺ	İ		COMCCTI PSGAGYOSGTHOGOFDHOSOSLSF
			į		CVVCDVCKSPPSTGSTYGSSOKEESAASUUA
1	ļ	}	- 1		YTKRYLEEQKTENGKDKEQKQTNTDKEKIKI
ļ	ļ			<b>\</b>	V CORONTGI GDGKMKSDSFAPKIDSENFING
					SQSPKRYKLRDDFEKKMADFHKEEMDDQDI
1			ļ		DKAKGRKESEFDDEPKFMSKVIGANKNQEE
					KSGKWEGLVYAPPGKEKQRKTEELEEESFPE RSKKEDRGKRSEGGHRGFVPEKNFRVTAYK
	1		1	}	RSKKEDRGKRSEGGHRUFVFERMIKVIATIK AVQEKSSSPPPRKTSESRDKLGAKGDFPTGK
İ	1				AVQEKSSPPPRKTSESRDALDARODITTOIL SFSITREAQVNVRMDSFDEDLARPSGLLAQE
Ì	ì				SFSITREAQVNVRMDSFDEDLAIG SGENZE KLCRDLVHSNKKEQEFRSIFQHIQSAQSQRSI
	1				SELFAQHIVTIVHHVKEHHFGSSGMTLHERF
		1			KYLKRGTEQEAAKNKKSPEIHRRIDISPSTFR
		1		1	KYLKKU I EVERARITAKU BILINGEDIN DI
	1		l l		LUCI AUDEMESPREPGYKAEGKYKDUPYDLI
					HGLAHDEMKSPREPGYKAEGKYKDDPVDLE LDIERRKKHKERDLKRGKSRESVDSRDSSHS
					HGLAHDEMKSPREPGYKAEGKYKDDPVDLE LDIERRKKHKERDLKRGKSRESVDSRDSSHS ERSAEKTEKTHKGSKKQKKHRRARDRSRSS SSSQSSHSYKAEEYTEETEEREESTTGFDKSR
	SEQ ID NO: of peptide seq- uence	NO: of peptide sequence	NO: of peptide sequence USSN 09/496 914	NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  NO: of peptide sequence  No: of peptide sequence	

					ra rada	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Americ Acid E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	1=Isoleucine K=Lysine, L=Laucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	ļ	09/496	ng to first	acid residue	Glutamine R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T-Threonine V=Valine, W=Tryptophan,
1			1	residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	į	1		peptide	304	/=possible nucleotide deletion, \=possible
	ļ	l		sequence	1	aucleotide insertion
	ļ	<b>├</b> -	<del> </del>	sequence		GTKDFVGPSERGGGRARGTFQFRARGRGWG
			}			RGNYSGNNNNSNNDFQKRNREEEWDPEYT
			ļ		1	PKSKKYYLHDDREGEGSDKWVSRGRGRGAF
			1			PRGRGRFMFRKSSTSPKWAHDKFSGEEGEIE
				Į.	_	DDESGTENREEKDNIQPTTE
005	2347	A	8398	202	552	CPALGGRQDLQGTRLLWAHDSGVGGQKAKS
997	2347	^	0370			KQENLESLEATGREEEGGQGPPVTTKGVLLA
		1	1			LLMAGLALQPGTALLCYSCKAQVSNEDCLQ
			1			VENCTQLGEQCWTARIREWGDDSRQA
000	2348	A	8400	697	301	NPPSACTPGSCDSCSGRGRDLAFDSVWSTNN
998	2340	1 11	10.00	1		MSDPRRPNKVLRYKPPPSECNPALDDPTPDY
	1.	ì			1	MNLLGMIFSMCGLMLKLKWCAWVAVYCSFI
	Ì			}	ł	SFANSRSSEDTKQMMSSFMLSISAVVMSYLQ
				1		NPQPMTPPW
999	2349	A	8401	93	1126	ASASHITSGHLRCFPGSEGVGTMARCFSLVLL
999	2349	1.	1			LTSIWTTRLLVQGSLRAEELSIQVSCRIMGITL
		ŀ	Ì		1	VSKKANQQLNFTEAKEACRLLGLSLAGKDQ VETALKASFETCSYGWVGDGFVVISRISPNPK
		İ				VETALKASFETCS TOW VODOL V VISION TO
		1	}	1	ŀ	CGKNGVGVLIWKVPVSRQFAAYCYNSSDTW
	1	_ ]				TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYS VASPYSTIPAPTTTPPAPASTSIPRRKKLICVTE
						VASPYSTIPAPITIPPAPASISIF KIKKELEVIE
		4		1		VFMETSTMSTETEPFVENKAAFKNEAAGFGG
				1		VPTALLVLALLFFGAAAGLGFCYVKRYVKAI VPTALLVLALLFFGAAAGLGFCYVKRYVKAI
				}		PFTNKNQQKEMIETKVVKEEKANDSNPNEES
						KKTDKNPEESKSPSKTTMRCLEAEV KERCQFVVKPMLSTVGSFLQDLQNEDKGIKT
1000	2350	A	8406	2	777	AAIFTADGNMISASTLMDILLMNDFKLVINKI
1000	250	1		{	1	AYDVQCPKREKPSNEHTAEMEHMKSLVHRL
		1		į	1	FTILHLEESQKKREHHLLEKIDHLKEQLQPLE
,	+	}				QVKAGIEAHSEAKTSGLLWAGLALLSIQGGA
		}			<b>,</b>	LAWLTWWVYSWDIMEPVTYFITFANSMVFF
ĺ		-				AYFIVTRQDYTYSAVKSRQFLQFFHKKSKQQ
1						HFDVQQYNKLKEDLAKAKESLKQARHSLCL
1						HEDYQQYNKEKEDEAKAGEBBIQAGGE
1	}	1	}	İ		QMQVEELNEKN VGFWERPLRSSRWFRRSLRRWEMLARAARO
1001	2351	A	8410	1400	264	TGALLLRGSLLASGRAPRRASSGLPRNTVVL
1001	233.		İ			VPQQEAWVVERMGRFHRILEPGLNILIPVLD
		Į.	1	- 1		IRYVQSLKEIVINVPEQSAVTLDNVTLQIDGV
1				1	1	LYLRIMDPYKASYGVEDPEYAVTQLAQTTM
				}	į	RSELGKLSLDKVFRERESLNASIVDAINQAAI
		l		į	ł	CWGIRCLRYEIKDIHVPPRVKESMQMQVEAL
		l	ł		]	CWGIRCLRYEIRDIHVFFRVRESMQMQVE
ł	-	1	(			RRKRATVLESEGTRESAINVAEGKKQAQILA EAEKAEQINQAAGEASAVLAKAKAKAEAIR
1						EARKAEQINQAAGEASAYLARARARALAR
			İ			LAAALTQHNGDAAASLTVAEQYVSAFSKLA
1			1	1		KDSNTILLPSNPGDVTSMVAQAMGVYGALT
1	1			1		KAPVPGTPDSLSSGSSRDVQGTDASLDEELD
1	1			1		VKMS CONCOUNTINECHKTY
1003	2352	A	8421	134	941	NRENLLESRMMDPCSVGVQLRTTNECHKTY
1002	2332	^	3,21	-		YTRHTGFKTLQELSSNDMLLLQLRTGMTLS
1				1	ĺ	NNTICFHHVKIYIDRFEDLQKSCCDPFNIHKK
L .						AKKNLHVIDLDDATFLSAKFGRQLVPGWKL
			1		1	PKCTQIINGSVDVDTEDRQKRKPESDGRTAK
		1		}		ALRSLQFTNPGRQTEFAPETGKREKRRLTKN
		1		l		ATAGGOROVIPAKSKVYDSOGLLIFSUMDLI
			l	Į.		
						DCLDEDCLGCFYACPACGSTKCGAECRCDF
					ļ	WI VEOTETEGGETIHNKHAG
			9427	12	1416	WLYEQIEIEGGEIIHNKHAG TEWGI SGSCPGCSPLEPGSRGRGAAAWRILI
1003	2353	A	8427	3	1416	WI VEOTETEGGETIHNKHAG

					D. distand and	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid. E=Glutamic Acid,
IO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	İ	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
ence		ł	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	}		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		{	İ	peptide		
	1	l		sequence		nucleotide insertion SLDTENIDEILNNADVALVNFYADWCRFSQM
	<del> </del>	<del>                                     </del>	<del> </del>			SLDTENIDEILNNADVALVNI TADWCIG DQIII
		1		{		LHPIFEEASDVIKEEFPNENQVVFARVDCDQH
	ì	1				SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ
	<b>\</b>	1	ì	ļ		RSVKALADYIRQQKSDPIQEIRDLAEITTLDRS
		1	l			KRNIIGYFEQKDSDNYRVFERVANILHDDCAF
		}		1		LSAFGDVSKPERYSGDNIIYKPPGHSAPDMVY
		1		Į.		LGAMTNFDVTYNWIQDKCVPLVREITFENGE
	1	1			Ì	ELTEEGLPFLILFHMKEDTESLEIFQNEVARQL
	1	}				ISEKGTINFLHADCDKFRHPLLHIQKTPADCP
	1			ì		VIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDL
	1	ļ				HSGKLHREFHHGPDPTDTAPGEQAQDVASSP
	}	1			1	DESSEOKI APSEVRYTLLRDRDEL
		<del></del>	8432	910	387	CI SPKI RAGEL PGFCRVSPCGSWVVETLVKM
1004	2354.	Α	6432	710	1	ACAAARSPADODRFICIYPAYLNNKKTIAEGR
				1	1	PIPISK AVENPTATEIODVCSAVGLNVFLEKN
						KMVSREWNRDVOYRGRVRVQLKQEDGSLC
	1	ì		}		LVOFPSRKSVMLYAAEMIPKLKTRTQKTGGA
	1	{				DOST OOGEGSKKGKGKKKKK
					530	OCHETE MOSCITHWR VI.GLCLLSVGVWGQD
1005	2355	Α	8453	90	330	CNEEMGGITOTPYKVSISGTTVILTCPQYPGSE
		1	1	ľ		II WOHNDKNIGGDEDDKNIGSDEDHLSLKER
	1	1	1	İ		SELEOSGYYVCYPRGSKPEDANFYLYLRARG
		1				NPGLONRYHRLFREDHSKGHSQ
					307	AVORIBHEMNIERLTGDLSHLAAIVILLLKIW
1006	2356	Α	8458	3	307	VTRSCAGISGKSOLLFALVFTTRYLDLF1SF1S
	1					LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC
	1				1	OI CIEN
	l				553	GAGAGGDWAAMDKLKKVLSGODTEDRSGL
1007	2357	A	8459	43	333	SEVVEASSLSWSTRIKGFIACFAIGILCSLLGT
		l		ļ		VI I WYPRKGLHI FAVFYTFGNIASIGSTIFLM
	- {	1				GPVKOLKRMFEPTRLIATIMVLLCFALTLCSA
	-	- 1	ì			FWWHNKGLALIFCILQSLALTWYSLSFIPFAR
				1		DAVKKCFAVCLA
					<del></del>	AQDIRSVHSLGQKSTFVKHFRTLSHLHGLPDI
1008	2358	A	8462	487	150	DDU WDDOER SPPSHPCMPSHRPOIPOLSNSGP
	}	}		}		DPRWGCVGPSMPTSTCLPGAVEASTTKASLP
		Ì				KCPVDSSLPTPEACFL
	l l	İ		l		ETRVKTSLELLRTQLEPTGTVGNTIMTSQPVF
1009	2359	A	8465	134	954	NETIIVLPSNVINFSQAEKPEPTNQGQDSLKKI
1005	-					LHAEIKVIGTIQILCGMMVLSLGIILASASFSPI
	ŀ	i	!			FTQVTSTLLNSAYPFIGPFFFIISGSLSIATEKR
	ļ	i		1		TKLLVHSSLVGSILSALSALVGFIILSVKQATI
ĺ		ì				NPASLQCELDKNNIPTRSYVSYFYHDSLYTTI
		- 1				CYTAKASLAGTLSLMLICTLLEFCLAVLTAV
	1		l l			CYTAKASLAGI ESLIVILICI ELEPCEA SINT
1	ļ	]	]			RWKQAYSDFPGSVLFLPHSYIGNSGMSSKM
1						HDCGYEELLTS
1010	2360	- A	8468	2	473	KYRYRRPYPVMRKICQVGPAGLAFILNISPV
1010	2300	' '	0.00	1		HRVALCHLAGCQEQAAWYHTLQILFFLVSA
		1		İ		FFSCPVPEKYFPGSCDIVGHGHQIFHAFLSICT
{		1	i			LSQLEAILLDYQGRQEIFLQRHGPLSVHMAC
	ľ			1		SFFFLAACSAATAALLRHKVKARLTKKDS
	ľ		1	i		TEL COLEVAUDDADMGDDKSKRKPPPKKKM
	0361		0470		409	IET26TEVVULLYDMOMOMOMOMOM
1011	2361	A	8478	5	409	GTI ETOFTOPECNHEK SCDVKMDRARNIGV
1011	2361	A	8478	5	409	GTLETQFTCPFCNHEKSCDVKMDRARNIGV
1011	2361	A	8478	5	409	GTLETQFTCPFCNHEKSCDVKMDRARNIGV
1011	2361	A	8478	5	409	GTLETQFTCPFCNHEKSCDVKMDRARNIGV SCTVCLEEFQTPITCILGNLGFFQRVGRGLES PCSSGPLCALVQGQSRPEEQVPPSDFCGVRR
						GTLETQFTCPFCNHEKSCDVKMDRARNTGV SCTVCLEEFQTPITCILGNLGFFQRVGRGLES PCSSGPLCALVQGQSRPEEQVPPSDFCGVRR RAGFQCQ
1011	2361	A	8478	2810	1652	TELSQLEKAHPPADMGRRKSKRKPPPKKKM GTLETOFTCPFCNHEKSCDVKMDRARNTGV SCTVCLEEFQTPITCILGNLGFFQRVGRGLES PCSSGPLCALVQGQSRPEEQVPPSDFCGVRR RAGFQCQ RTSTQKWQSVFNDSQEHLERFYCNPENDRM RMKYGGQEFWADLNAMNVYETTEFDQLRF LSTPPSSNVNSIYHTVWKFFCRDHFGWREYI

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/-possible nucleotide deletion, \-possible
		1		sequence		nucleotide insertion
	<del> </del>	+	1			SVIRLIEEANSRGLKEVRFMMWNNHYILHNS FFRREIKRRPLFRSCFILLPYLQTLGGVPTQAP
			l .			PPLEATSSSQUCPDGVTSANFYPETWVYMHP
				1		SQDFIQVPVSAEDKSYRIIYNLFHKTVPEFKYR
				Į.		ILQILRVQNQFLWEKYKRKKEYMNRKMFGR
				1		DRIINERHLFHGTSQDVVDGICKHNFDPRVCG
		1			j	KHATMEGOGSYFAKKASYSHNFSKKSSKGV
		1	1			HEMELAKVLTGRYTMGSHGMRRPPPVNPGS
			İ			VTSDLYDSCVDNFFEPQIFVIFNDDQSYPYFVI
		1	į	1	1	OVEEVSNTVSI
		+	8488	2	517	TENCETEL ROAWHEVCGNKMAAPIPQGFSCL
1013	2363	Α	0400	2	1 3.7	SRFIGWWFROPVLVTOSAAIVPVRTKKRFIP
		1				PIYQPKFKTEKEFMQHARKAGLVIPPEKSDRS
		1				IHLACTAGIFDAYVPPEGDARISSLSKEGLIER
		ļ		ì		TERMKKTMASQVSIRRIKDYDANFKIKDFPE
			ļ			KAKDIFIEGSPLY
1014	2364	A	8501	363	17	YIRTGYVYICIIYAQLMYTYYIRTAYVYICILY AQLMYTYVLYTHSLCIHMYSIRTAYVYICIIY
		[	1		ļ	AQIMYTYVFYTHRLCIHMYSIRTDYVYICILY
		1.				AQLMYTYVFYTHSYMSDE
		1			10100	NSSEHFSQAPQRLSFYSWYGSARLFRFRVPPD
1015	2365	A	8504	3	2190	AVILEWILOVSRESGAACTDAEITVHFRSGA
						PPVINPLGTSFPDDTAVOPSFQVGVPLSTTPRS
		Ì		ļ		NASVNVSHPAPGDWFVAAHLPPSSQKIELKG
		1				I APTCAYVEOPELLVTRVVEISIMEPDVPLPQ
			1	1	1	TLLSHPSYLKVFVPDYTRELLLELRDCVSNGS
		l			İ	LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPC
1				1		RLLLPSPPWDRWLQVTAESLVGPLGTVAFSA
		1				VAALTACRPRSVTIQPLLQSSQNQSFNASSGL
1				1		LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL
1		ŀ		İ		NTGMDSGGSLTISLRANKTEMRNETVVVACV
						NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR
		}	1		1	RANLIPYPETDNWYLSLQLMCPENAEDCEQ
				İ		AVVHVETTLYLVPCLNDCGPYGQCLLLKKHS
ļ		ļ			1	VI VASCSCKAGWRGWSCIDNSIAQIVAQQI
			1		•	AATLLITI SNI MFLAPIAVSVRRFFLVEASVY
				1		AVTMFFSTFYHACDOPGEAVLCILSYDILQI
1				1		CDFLGSGAAIWVTILCMARLKTVLKYVLFLL
ļ	]	1		1		GTI VIAMSLOLDRRGMWNMLGPCLFAFVIM
				1	1	A SMWAYRCGHRROCYPTSWORWAFYLLPG
				- [		VSMASVGIAIYTSMMTSDNYYYTHSIWHILL
					1	AGSAALLLPPPDQPAEPWACSQKFPCHYQIC
		1	1	1		KNDREELYAVT
1016	2366	-	8511	1	453	KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAI
1 .0.0	2.00	1		J	1	KGGEKKKGRSAINEVVTREYTINIHKRIHGVOFKKRAPRALKEIRKFAMKEMGTPDVRIDTRL
1		1				NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSF
						NKAVWAKGIRNVFYRIKVKESKRANEDEDSI NKLYTLVTYVPVTTFKNLQTVNVDEN
						LERTPASADMAWTKYQLFLAGLMLVTGSIN'
1013	2367	A	8513	54	1196	LSAKWADNFMAEGCGGSKEHSFQHPFLQAV
1017	1 /					GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC
1017	ĺ		1			QPFNPLLFLPPALCDMTGTSLMYVALNMTSA
1017				1	1	
1017						SECONI RGAVIIFTGI ESVAFI GRRLVLSOWI
1017						SSEOMLEGAVIIFTGLFSVAFLGRRLVLSQWL
1017						SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GU ATIAGLVVVGLADLLSKHDSQHKLSEVII
1017						SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVII GDI LIIMAOIIVAIOMVLEEKFVYKHNVHPLF
1017						SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVII GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLF AVGTEGLFGFVILSLLLVPMYYIPAGSFSGNP RGTI FDALDAFCOVGOOPLIAVALLGNISSIA
						SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI GILATIAGLVVVGLADLLSKHDSQHKLSEVI GDI LIIMAOIIVAIOMVLEEKFVYKHNVHPLI

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	}	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	Sequence	/=possible nucleotide deletion, \=possible
		ł		sequence		nucleotide insertion
		<u> </u>	<del> </del>	sequence	<del> </del>	SLALGWEAFHALQILGFLILLIGTALYNGLHR
			1	1		PLLGRLSRGRPLAEESEQERLLGGTRTPINDA
		Ì		Į	1	18
1010	2368	Ā	8518	324	694	SPFWTEKRRMEKPLFPLVPLHWFGFGYTALV
1018	2300	^	0510	1 224		VSGGIVGYVKTGSVPSLAAGLLFGSLAGLGA
			Ì			YQLYQDPRNVWGFLAATSVTFVGVMGMRS
		j	j	)		YYYGKFMPVGLIAGASLLMAAKVGVRMLM
				Į.		TSD
1019	2369	A	8526	2	1787	VSAAAVNMEPPDAPAQARGAPRLLLLAVLL
1019	2509	1 "	0520	-		AAHPDAQAEVRLSVPPLVEVMRGKSVILDCT
		1		1	İ	PTGTHDHYMLEWFLTDRSGARPRLASAEMQ
		1				GSELQVTMHDTRGRSPPYQLDSQGRLVLAEA
				1		QVGDERDYVCVVRAGAAGTAEAAARLNVF
	ı	1				AKPEATEVSPNKGTLSVMEDSAQEIATSNSRN
						GNPAPKITWYRNGQRLEVPVEMNPEGYMTS
			1			RTVREASGLLSLTSTLYLRLRKDDRDASFHC
			-	1		AAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQ
	1		1			FWVGSPSTPAGWVREGDTVQLLCRGDGSPSP
						EYTLFRLQDEQEEVLNVNLEGNLTLEGVTRG
		1				QSGTYGCRVEDYDAADDVQLSKTLELRVAY
		į.	1			LDPLELSEGKVLSLPLNSRAVVNCSVHGLPTP
	1					ALRWTKDSTPLGDGPMLSLSSITFDSNGTYVC
	ł					EASLPTVPVLSRTQNFTLLVQGSPELKTAEIEP
		ł				KADGSWREGDEVTLICSARGHPDPKLSWSQL
	į.					GGSPAEPIPGRQGWVSSSLTLKVTSALSRDGI
1	ļ	-				SCEASNPHGNKRHVFHFGTVSPQTSQAGVAV MAVAVSVGLLLLVVAVFYCVRRKGGPCCRQ
ł	İ		İ			
i	<b></b>	<u> </u>			1200	RREKGAP PRVRLLRPSRSRSCRGLLSTRAPGPSPFRSLHS
1020	2370	A	8530	2	1200	SPLLPHAMKSPFYRCQNTTSVEKGNSAVMGG
	1			<b>,</b>		VLFSTGLLGNLLALGLLARSGLGWCSRRPLR
(		1	ĺ			PLPSVFYMLVCGLTVTDLLGKCLLSPVVLAA
		Į				YAQNRSLRVLAPALDNSLCQAFAFFMSFFGL
į		- }	1			SSTLQLLAMALECWLSLGHPFFYRRHITLRLG
						ALVAPVVSAFSLAFCALPFMGFGKFVQYCPG
						TWCFIQMVHEEGSLSVLGYSVLYSSLMALLV
	Ì	}	1			LATVLCNLGAMRNLYAMHRRLQRHPRSCTR
ļ	ł	ł			1	DCAEPRADGREASPQPLEELDHLLLLALMTV
	İ					LFTMCSLPVTYRAYYGAFKDVKEKNRTSEEA
-						EDLRALRFLSVISIVDPWIFIIFRSPVFRIFFHKI
{	1					FIRPLRYRSRCSNSTNMESSL
100		<del></del>	8536	<del>   </del>	237	RRGEIDMATEGDVELELETETSGPERPPEKPR
1021	2371	A	8330	1	23,	KHDSGAADLERVTDYAEEKEIQSSNLETAMS
	1	}				VIGDRRSREQKAKQER
105=			0527	94	541	RKERRRRRRRMEAVVFVFSLLDCCALIFLSV
1022	2372	A	8537	74	1 34.	YFIITLSDLECDYINARSCCSKLNKWVIPELIG
		1	-	ì		HTIVTVLLLMSLHWFIFLLNLPVATWNIYRYI
1				1		MVPSGNMGVFDPTEIHNRGQLKSHMKEAMI
1						KLGFHLLCFFMYLYSMILALIND
L.			0540	+36	431	RMMKCPOALLAIFWLLLSWVSSEDKVVQSPL
1023	2373	A	8540	26	451	SLVVHEGDTVTLNCSYEVTNFRSLLWYKQEK
				1		KAPTFLFMLTSSGIEKKSGRLSSILDKKELSSIL
						NITATOTGDSAIYLCAVEAQCSLVTCSLYSNS
1				1		TAEALQL
				<del>   </del>	742	GVRLRYSPIAVVMVGEAGRDLRRRAVAVT
1024	2374	Ā	8544	1731	743	AEKMAVLAPLIALVYSVPRLSRWLAQPYYLL
1						SALLSAAFLLVRKLPPLCHGLPTQREDGNPCD
1			1	1	1	T SALLSAME LL TRALE LOUISE LA CRESCHI CE
1		ĺ				EDWINEVEIL MEI CATVMMKNIRRSITVEOHIGN
						FDWREVEILMFLSAIVMMKNRRSITVEQHIGN IFMFSKVANTILFFRLDIRMGLLYITLCIVFLM

			1000	Dendistad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	1 -	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	!=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	l		Sequence	/=possible nucleotide deletion, \=possible
	!		1	peptide		nucleotide insertion
				sequence		TCKPPLYMGPEYIKYFNDKTIDEELERDKRVT
		1	}		į	WIVEFFANWSNDCQSFAPIYADLSLKYNCTG
	1		}	1		LNFGKVDVGRYTDVSTRYKVSTSPLTKQLPT
			ļ		ı	LILFQGGKEAMRRPQIDKKGRAVSWTFSEEN
		1				VIREFNLNELYQRAKKLSKAGDNIPEEQPVAS
		}	1	}		TPTTVSDGENKKDK
					1707	TVSFHKTMASLKCSTVVCVICLEKPKYRCPA
1025	2375	Α	8546	2194	1707	CRVPYCSVVCFRKHKEQCNPETRPVEKKIRS
	1	1				ALPTKTVKPVENKDDDDSIADFLNSDEEEDR
			l l		1	VSLQNLKNLGESATLRSLLLNPHLRQLMVNL
			ì		1	DQGEDKAKLMRAYMQEPLFVEFADCCLGIV
			1		Ì	EPSONEES
1					<u> </u>	VGMELPAVNLKVILLGHWLLTTWGCIVFSGS
1026	2376	A	8547	1078	594	YAWANFTILALGVWAVAQRDSIDAISMFLGG
]		1	1	į	}	LLATIFLDIVHISIFYPRVSLTDTGRFGVGMAIL
	}	1	i			SLLLKPLSCCFVYHMYRERGGELLVHTGFLG
			l l			SSQDRSAYQTIDSAEAPADPFAVPEGRSQDAR
		1	l			GY
1			·		1	DFLGPASPQEEGGSESSTMTELETAMGMIIDV
1027	2377	A	8557	1	340	FSRYSGSEGSTQTLTKGELKVLMEKELPGFLQ
1			1	į	ļ	SGKDKDAVDKLLKDLDANGDAQVDFSEFIVF
		1				VAAITSACHKYFEKAGLK
}	1		1			KMAATLGPLGSWQQWRRCLSARDGSRRLLL
1028	2378	A	8569	20	963	LLLLGSGQGPQQVGAGQTFEYLKREHSLSKP
1			ì			YQGEAPRPCFLRDWELQVHFKIHGQGKKNL
			1			HGDGLAIWYTKDRMQPGPVFGNMDKFVGLG
		1			1	VFVDTYPNEEKQQERVFPYISAMVNNGSLSY
	İ	1	1			DHERDGRPTELGGCTAIVRNLHYDTFLVIRY
		-	1	1		VKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
ļ	1		l l			YYFGTSSITGDLSDNHDVISLKLFELTVERTPE
						EEKLHRDVFLPSVDNMKLPEMTAPLPPLSGL
}	1			1		ALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK
-		-				RFY
					J	AAAASHRSRARSRPRRVSSGPAPRRAQSSAG
1029	2379	Α	8572	1	578	RVASGLDSAPLCTMARALCRLPRRGLWLLLA
		ļ				HHLFMTTACQEANYGALLRELCLTQFQVDM
		)	1			EAVGETLWCDWGRTIRSYRELADCTWHMAE
		1	1	.		KLGCFWPNAEVDRFFLAVHGRYFRSCPISGR
			}			AVRDPPGSILYPFIVVPITVTLLVTALVVWQS
				1	1	KRTEGIV
					1000	DSSTVKGGSESRHLCLIPDLKGKARTREASSG
1030	2380	A	8574	1352	372	SRTCGRRTSLCTSAKSSWTYRSGRLSWQSIKG
				- 1	1	THLTITQALRQPLHRAPLLPGQLCWSPRPLEK
	1			1		NKAMGRPLLLPLLLLLQPPAFLQPGGSTGSGP
}	1			1	1	SYLYGVTQPKHLSASMGGSVEIPFSFYYPWEL
1		1		1	ľ	AIVPNVRISWRRGHFHGQSFYSTRPPSIHKDY
			Ì	1		VNRLFLNWTEGQESGFLRISNLRKEDQSVYF
		1				CRVELDTRRSGRQQLQSIKGTKLTITQAVTTT
						TTWRPSSTTTLAGLRVTESKGHSESWHLSLDT
			ì			AIRVALAVAVLKTVILGLLCLLLLWWRRRKG
	1		1			
						SRAPSSDF
1031	2381	A	8580	905	340	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQL
1001	201	1	1 1			AFDDFQESCAMMWQKYAGSRRSMPLGARIL
		1			1	FHGVFYAGGFAIVYYLIQKFHSRALYYKLAV
	1				1	EQLQSHPEAQEALGPPLNIHYLKLIDRENFVDI
1						VDAKLKIPVSGSKSEGLLYVHSSRGGPFQRW
	1		1		1	HLDEVFLELKDGQQIPVFKLSGENGDEVKKE
		1		ļ	1	The state of the s
1032	2382	A	8593	2558	961	RRRPRLLPGAEPCEPRVGPRRADMGCSAKAR WAAGALGVAGLLCAVLGAVMIVMVPSLIKQ

No. of nucleotide populate sequence and the properties of populate sequence and the populate sequence and the populate sequence and the populate sequence and the populate sequence and the populate sequence and the populate sequence and the population an							Amino acid sequence (A=Alanine C=Cysteine,
NO. of bright colds of USSN period of Period of	SEQ ID	SEQ ID	Met	_			Amino acid sequence (A-Arianine C Cysteme)
uence course ending sequence      Sequence		NO: of	hod	ID NO:			D-Aspartic Acid, D-Olddamic Rold,
USSN	nucl-	peptide	{				r=pnenylalamile, 0=0lycine, r=ristiame,
1036   2385   A   8605   1   2364   Septiment   Sept			1	USSN	location		l=isoleucine, K=Lysine, L=Lcucine,
senice    914   m go first station acid residue of peptide sequence   value value of peptide   value of pept		· -	Ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Profine,
### amino acid residue of peptide sequence   ### amino acid peptide   ### sequenc	•	dones	1			acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of peptide   sequence	uence	1	1	)		of peptide	T=Threonine, V=Valine, W=Tryptophan,
Pepside   Peps				ì			Y=Tyrosine, X=Unknown, *=Stop codon,
					ľ	Joquene	/=possible nucleotide deletion, \=possible
0,000   0,00		1	}	1		ł	nucleotide insertion
VMMPSEILKOEKPQVREERGFYVYREFRIKKS   TENNIDTVSEILEYRTFGCPOSKSHOSSDYIV   MPNILVLGAAVMMENRFMTLKLIMTLAFTI-   GERAFMNRTVGEMWGYKDPLVNLNNYFP   GMPPFKDRFGLFAELNNSDGLTTGFTOVOM   SIJHLVDKWNGLSKVOFWHSDOCMMINGTS   GOMPPFKDRFGLFAELNNSDGLTTGFTOVOM   SIJHLVDKWNGLSKVOFWHSDOCMMINGTS   GOMPPFKDRKVDFWFNFOGCP   CLESCIONVSTCRFSAPILSHPHFLNADPY-   AEAVTOLHPNOEANSLEYSPPEGCRO   CLESCIONVSTCRFSAPILSHPHFLNADPY-   AEAVTOLHPNOEANSLEYSPPEGCRO   CLESCIONVSTCRFSAPILSHPHFLNADPY-   AEAVTOLHPNOEANSLEYSPPTOT   CHESCION   AEAVTOLHPNOEANSLEYSPPTOT   CHESCION   SIZHLVAN   CHESCION			l		sequence		OVI KNIVEIDESSI SENIMWKEIPIPEYI SVYFFD
TENNINDTYSFLEYRTFGFGFEKSHGSESDY    MPNILVIGAAVMBENKPMILKIMTIAFTIT    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GERAFMINTVGEIMWGYKDPL/NILDINYTP    GOMPPFEMPESSLETYSPEACHSHEMILMYKE    SGYFEGIPTYRFVAPKTLANOSIYPPNEGFC    CLESIGION-YSTGTSAPLI-SHPHEINADPVL    AEA-VTGLIHPNGEAHSLFLDHIPYTGIPMNCSV    KLOLSLYMKSVAGGGTKGERPVLPLLWFA    ESGAMEGETI HITEYTOL VLMFKVMSHYADFVL    LALGC-VLLI-PHOEAHSLFLDHIPYTGIPMNCSVLFK     KLOLSLYMKSVAGGGTKGERPVLPLLWFA    ESGAMEGETI HITEYTOL VLMFKVMSHYADFVLLKYQ    LALGC-VLLI-PHOEAHSLFLDHIPYTGFFRASSK     CSKDERALGAYSSSLMTSAPKGSVLOEAKL     CSKDERALGAYSSSLMTSAPKGSVLOEAKL     CSKDERALGAYSSSLMTSAPKGSVLOEAKL     CSKDERALGAYSSSLMTSAPKGSVLOEAKL     VTISCLIPFAGGLOVRASSERLAEIDMPYLLXYQ    PMMGTIGGKYCMDA VLAGVASSKAFSSS     FLLISLVSSSLVSLSLCPPLTQA    FLANTSCHIPFAGGLORASSENALEIDMPYLLXYQ    PMMGTIGGKYCMDA VLAGVASSSLATSSENDOLAR VLAGVASSAGAGSTIS WEBSQQVPTI     FUND							UVERIOV RIDI SOCIA INTURBILITATION INTURBILITA
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SRIHLVDK WNGLSK VDF WHSDQCMMINGTS   GQMWPFPMTESSLEFYSPEASMLLMYKE   SGVFEGIPTYRFV APKTLF ANGSIVPPWEGFC   CLESGIQN VSTCRPSAPIFLISH PHINADPVL   AEAVTGHPNQEAHSLFLDHPVTQIPMNCSV   KLQLSLYMKSVAGIGQTOKLEVLPLLWFA   ESGAMEGETHHTYTQL VLMPKVAHTYAQYV   LLALGCVLLLVPVTQIRSQEKCYLFWSSSKK   GSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAPRGSVLQEAKL   SGSKDKEAQAYSESLMTSAFGSVLTG   SGSKDKEAQAYSESLMTSAFGSVLTG   SGSKDKEAQAYSESLMTSAFGSTVTA   SGSTDFAFT   SGSTDFA							GERAFMNRTVGEIMWGYKDPLVNLINKYFP
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GQMMPPFMTPESSLEFYSPEACRSMKLMYKE   SGMPEGIPTYREFYAPRITIFANGSYPPMEGFC   CLESGIQNUSTCRFSAPLFLSHPHFUADPUL   AEA/TGLHPNQEAHSLELDHPVTGIPMNCSV   KLQLSLYMKSVAGIGOTGKIEPVULPLLWFA   ESGAMEGEITHITYTQLVLMPKVMPHAQYV   LLALGCVLLLYPVICQIRSGECYLFWSSSKK   GSKDKEAJQAYSESLMTSAPKGSVLQFKWHYAQYV   LLALGCVLLLYPVICQIRSGECYLFWSSSKK   GSKDKEAJQAYSESLMTSAPKGSVLQFKWHYAQYV   LLALGCVLLLYPVICQIRSGECYLFWSSSKK   GSKDKEAJQAYSESLMTSAPKGSVLQFK   GSKDKEAJQAYSESLMTSAPKGSVLQFK   GSKDKEAJQAYSESLMTSAPKGSVLQFK   GSKDKEAJQAYSESLMTSAPKGSVLQFK   GSKDKEAJQAYSESLMTSAPKGSVLQFK   GFLLLSLVSSSLVSLSLCPPLTQA   FFLLLSLVSSSLVSLSLCPPLTQA   FFLLLSUSSSLVSLSLCPPLTQA   FFLLLSUSSSLVSLSLCPPLTQA   FFLLLSUSSSLVSLSLCPPLTQA   FFLLLSUSSSLVSLSLCPPLTQA   FFLLTTRITELQRRPTWTPDQYLRGGLCAYSG   QAGVVRSSQDLSCDFCNDVLARAKYLKRHG   FFLLTTRITELQRRPTWTPDQYLRGGLCAYSG   QAGVVRSSQDLSCDFCNDVLARAKYLKRHG   FFLLTTRITELQRRPTWTPDQYLRGGLCAYSG   QAGVVRSSQDLSCDFCNDVLARAKYLKRHG   GAGVVRSSQDLSCDFCNDVLARAKYLKRHG   GAGVVRSQDLJARGSSAAARADL   HVYKKNGVGVSVGDLJARGSSAARADL   HVYKKNGVGVSVGDLJARGSSAARADL   HVYKKNGVGVSVGDLJARGSSAARADL   HVYKKNGVGVSVGVDGLJARGSSAAGGKKKALIVG   HCMGFGMMTFRFDSNVVLIEDMGNFVGTR   KTPITSLKRGGSSYSVLJANGFVGVSDLJARGSSAGGKKKALIVG   HCMGFGMMTFRFDSNVVLIEDMGNFVGTR   KTPITSLKRGGSSVSVLJANGFVGVSDLJARGSAGGSTFTBDT   GAGVAFINSSBLGGSSTAGGSSTFTBDT   GAGVAFINSSBLGGSSTAGGSSTAGGAGATVG   VAGSGAGIGTVFGSLIGYARNFSLKQQLFSY   ALIGFALSEAMGLCCMVAPLLITAM   GAGVAFGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	1	1		1			SRIHL VDK WNGLSKVDFWHSDQCNMINGTS
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1034 2384 A 8597 640 164 VITSCIIPFAFGLGVRASERLAEIDMPYLLKYQ PMMQTIGQKYCMDAVIAGVLSRKSPGDKIL VNMGDRTSMVQDPGSQAPTSWISESQVFQTT EVLTTRITELQRRPFTWTPDQYLRGGLCAYSG GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F  1035 2385 A 8603 936 204 AMASTLEYSPPLRRLVGPAAGFSRAARADL SWDPMAFFTGLWGPFICVSRVLSHHCFSTTG SLSAIQKMTRVRVVDNSALGNSPYHRAPRCI HVYKKNGVGKVGDQILLAIKGGKKALIVG HCMFGPRMTPKFDSNNVVLIEDNGNPVGTRI KTPIFTSLRKREGEYSKVLAIAQNPV TQYLQPRSPECKMFACAKLACTPSLIRAGSR VAYRPISASVLSPSARTIGEGSTYPNGQANG VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIGYARNPSLKQLFSY ALGFALSEAMGLFCLMVAFLLIFAM SPGPSLPESAESLDGSQEDKRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVONISWQRRKDLINNPLFIMDGISPTDI CQGLGDCWLLAAIGSLTTCPKLLYRVYPRG QSFKKNYAGIFHFQIWQFGGWNIVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNILRILRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGREWNIAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHFGTFWTNPCFKISLPEGDPEDDAEGNV VVCCTLVALMGKNWRHARQQGAQLQTIGFVL LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSELFTNSREVSSQLRLPPGEYTIIDSTFEPHRADFL LRVFTERHESSEWELDEVNYAEQLQEEKVSED DMDQOPHLFKIVAGGKEISVTEQAPLINR MAIKFKSFKKGFGLDACRCMINLMDKDGSG KLGLLEFKLIWKKLKKWMDIFRECDQDHSGT LNSYEMRUVIEKAGGKLNNKVMQVLVARYA DDDLIDDFDSFEISCFLKLKTMFTEFT.TMDPKNT	1033	2383	A	8292	393	101	FCLLLSLVSSSLVSLSLCPPLTQA
PMMQTIGQKYCMDPAVIAGVLSRKSPGDKIL VNMGDRTSMVODPGSQAPTSWISSQVFOTT EVLTTRITELQRRFPTWTPDQYLRGGLCAYSG GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F  1035 2385 A 8603 936 204 AMASTLEYSPSPLRRLVGPAAGFSRAARADL SWDPMAFFTGLWGPFTCVSRVLSHHCFSTTG SLSAJQKMTVRVYVDNSALGNSPYHRAPRCI HVYKKNGVGKVGDQILLAHKGQKKKALIVG HCMFGPRMTPRFDSNNVVLEDNORPVGTRI KTPIPTSLRKREGEYSKVLAIAQNPV  1036 2386 A 8606 1 562 PTRAHSFDLCCSPCRRRLIGREAGEEPTSPV TQYLQPRSPEECKHACAKLACTPSLRAGSR VAYRPISASVLSRPEASRTGEGSTVFNGAQNG VSQLJQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIGVYARNPSLKQQLFSV AILGFALSEAMGLFCLMVAFLILFAM  1037 2387 A 8615 2 2364 SPGPSLPESAESLDGSGEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSLGFKDLG PNSKNVQNISWGRKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSEVTSDSELES MTDKMLVGHAYSVTGLQDVHYRGKMETLI RVRNPWGREWNGAWSDSAREWEEVASDIQ MQDLLKTEDGEF WMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHBGTFWINPCFKISLPEGDDPEDDAEGNV VCCTCLVALMGKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFIL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQOPHLHFKIVAGGEKGREGVYELQRLINR MAIKFKSFKTKGFGLDACRCMINIMDKDGSS KLGLLEFKILWKKLKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKMQVLVARYA DDDLIIDFDSFISTECFT LLKYMFTFFTLTMDFKNT						100	VITSCHPEAEGI GVRASERI AEIDMPYLLKYO
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SLSAIQKMTRVRVVDNSALGRSPYHRAPRCI HVYKKNOVGKVGDQILLAIKGQKKKALIVG HCMPGPRMTPRTDSNNVVLIEDINGNPVGTRI KTPIPTSLRKREGEYSKVLAIAQNFV TOYLQPRSPEECKMFACAKLACTPSLIRAGSR VAYRPISASVLSRPEASRTGEGGTVFNGAQNG VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM  1037 2387 A 8615 2 2364 SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINISRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWGFGQWVNVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGA WSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHIPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGPSEI FTNSRE VSSQLRLPPGEYIIBSTFEPHRDADFL LRVFTEKHSESWELDEVNYAGQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDOSGS KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMLFRESCELLKIMFTFFLTMDFKNT	1035	2383	A	8003	750	1	SWDPMAFFTGLWGPFTCVSRVLSHHCFSTTG
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GGATDGGGETDVIYSLIRRREPLEYVINIVPCV   LISGLVILLAYPLPAQAGGGCKTVSINVILAQUI   VELFILAQKIPETSLSVPLIGRELIFVMVVATLI   VANCVIVLINVQQRTPTISAPERLIFVLIEL   LPRLLGSPPPPEAPRAASPPRASSVCILLRAE   ELILKKPRSELVFEGQRIRQGTWTAAFCOSL   GAAAPEVRCOVDANFVAESTRODEATGE   VSDWYRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDFLYPACIOP   ALAYFNRVPDFTSSACATSSSGGCN   GAYFNRVPDFTSSACATSSTSGASSSGGCN   NSSGGGGRTGFQISVYSGIPBQTVQVIQQ   ALHROPSTAAQVIQQMYAAQQQHLMLOTTA   ALQQHLSSAQLAQVIQQMYAQQQHLMLOTTA   ALQQHLSSAQLAQSSSINLAAQQQASLYSNRQGST   SGSNVSAQAPAQVIQQMYAQQQHLMLOTTA   ALQQHLSSAQLAQSSSINLAAQQASLYSNRQGST   SGSNVSAQAPAQSSSINLAAAQQQAFTPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILALKPTPGGSQPLPTPA   QAFALAQUILTRIQTGFAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAGCIPTQPV   PSILAKPTPAAAAAGCIPTQPV   PSILAKPTPAAAAAGCIPTQPV   PSILAKPTPAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				1	1	ļ	KTINKIDIDTEAYTENGEWAIDFCPGVIRRHH
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BELLIKKPRSELVFEGQRIRGGTWTAAFCQSL   GAAPPEVRCCVDAVNFVAESTRDQEATGE   VSDWVRMGNALDNICFWAALVLFSVGSSLF    LGAYFNRVPDLPYAPCIQP    PGRERFGGGGARRFQGILFALLPSERPDCATI   QAMENELPVPHTSSSACATSSTGASSSSGGN   NSSGGSRPTGFGISVYSGFPDQTVQVIQQ   ALHRQPSTAAQYLQQMYAAQQABLMLQTA   ALQQQHLSSAQLQSLAAVQQASLVSNRQGST    SGSNVSAQAPAQSSSNLAASPAAAQLLNRA   QSVNSAAASGIAQQAVLLGNTSSPALTASQA   QMYLRAQMLIFFTAATVAYQPELGTGSPAR   PPTPAQVQNLTLRTQQTPAAAASGPTPTQPVI   PSLALKPTPGGSQPLTTAYQQECTGGSPAR   PPTPAQVQNLTLRTQQTPAAAASGPTPTQPVI   PSLALKPTPGGSQCLSTGMAPNLKGRPKKKPCF    RRDSFSGVLDSNNNSDGKAVAKVKCEARSA   LTKPKNNHNCKKVSNEEKPKVAIGEECRADE    QAFLVALYKYMKERTPEREPTLGFKQNLW    TMFQAAQKLGGYETITAROWKHIYDELGG    NPGSTSAATCTRRHYERLILPYERFIKGEEDK    LPIKPRRQENSSCENENKTKVSGTKRIKHEID    KSKKEKENAPKPQDAAEVSSEQEKEQETLISK    KSPEPLPAADMKKKEGYQEFSAKPLASRVT    PEKDNETDQGSNSEKVAEAGEKGPTPIPS    PLAPEKDSALVPOASKQPLTSPSALVDSKQES    KLCCFTESPESPCPGASFPRLPHHTGHRWQTR    MRRRMTNCPPWQTILFTAP    TMFQAAQKLGGYETTTAROWKHIYDELGG    KSPEPLPAADMKKKEGYQEFSAKPLASRVT    PEKDNETDQGSNSEKVAEAGEKGPTPIPS    PLAPKDSALVDSKQES    KLCCFTESPESPCPGASFPRLPHHTGHRWQTR    MRRRMTNCPPWQTILFTAP    GIKARITQRALDYGVQAGMKMEQMLKEKK   LPPILSGSESLEFLKVDYVNYNFSNIKISAFSP    NTSLAFVPGYGIKALTNGTANISTDWGFESI   LFVLYNSFAEPMERPILLNEMLCPILASEVI   ALNANLSTLEVLIKDNYTLLDYSILSSPETTE    NYLDLNLKGVPYPLENLTDPPSPYPFVLPER    SNSMLYIGIAEYFFKSASFAHFTAGVNVNTLS    TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM    VRIMATEPPIINLQPGNITLDIPSSIMMLTQFK    NSTVETIVSMDFVASSSVGLVLGQRLVCSLS    LNRFRLALPESNRSNEVLREFRLSSILHFGVL   PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGE    LLISTDLKYETSKSQCPSFHVWEGLNLISRQW    PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGE    LLISTDLKYETSKSQCPSFHVWEGLNLISRQW    PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGE    LLISTDLKYETSKSQCPSFHVWEGLNLISRQW    PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGE    LLISTDLKYETSKSQCPSFHVWEGLNLISRQW    ARRIBRTRESKAAVSQDNVPALQPGKKKKLI	1				j		I DDI I GSPPPPFAPRAASPPRRASSVGLLLRAE
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SGSNVSAQAPAGSSSINI.AASPAAAQLLNRA QSVNSAAASGIAQQAVLLGNTSSPALTASQA QMYLRAQMLIFTPTATVATVQPELGTGSPAR PPTPAQVQNI.TLRTQOTPAAAASGPTPTQPVI PSLALKPTPGGSQPLPTPA  1040 2390 A 8645 98 1388 ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSF HEHRHQSGRCLSTGMAPNI.KGRPKKKPCPC RRDSFSGVKDSNNNSDGKAVAKVKCEARSA LTKPKNNHNCKKVSNEEKPKVAIGEECRADE QAFLVALYKYMKERKTPIERIPYLGFKQINLV TMPQAAQKLSGYETITARQWKHIYDELGG NPGSTSAATCTRRTYERLILPYERFIKGEEDK. LPPIKPRKQENSSQENENKTXVSGTKRIKHEIL KSKKEKENAPKPQDAAEVSSEQEKEQETLISK KSIPEPLPAADMKKKIEGYQEFSAKPLASRVT PEKDNETDQGSNSEKVAEEAGEKGPTPPLPS, PLAPEKDSALVPGASKQPLTSPSALVDSKQES KLCCFTESPESEPQEASFPRLPHHTGHRWQTR MRRRMTNCPPWQITLPTAP MRRRMTNCPPWQITLPTAP GIKARITQRALDYGVQAGMKMEQMLKEKK LPDLSGGSSLEFLKVDYNYNNFSNIKISAFSPP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPILASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS. TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS. LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANKLQGGFPLPNPHKFLFVNSDIEVLEGG LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP			1				ALHROPSTAAQYLQQMTAAQQQHLMLQTA
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KSKKEKENAPKPQDAAEVSSEQEKEQETLISG KSIPEPLPAADMKKKIEGYQEFSAKPLASRVI PEKDNETDQGSNSEKVAEEAGEKGPTPPLPSA PLAPEKDSALVPGASKQPLTSPSALVDSKQES KLCCFTESPESEPQEASFPRLPHHTGHRWQTR MRRMTNCPPWQITLPTAP  LLQEMCTKTIPVLWGCFLLWNLYVSSSQTTYI GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFI LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLI		1		-			LPPIKPRKQENSSQENENKTKVSGTKRIKHEIP
KSIPEPLPAADMKKKIEGYQEFSAKPLASRVE PEKDNETDQGSNSEK VAEEAGEKGPTPPLPSA PLAPEKDSALVPGASKQPTSPSALVDSKQES KLCCFTESPESEPQEASFPRLPHHTGHRWQTR MRRMTNCPPWQITLPTAP LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIVI GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPILASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLI				1		1	KSKKEKENAPKPODAAEVSSEQEKEQETLISQ
PEKDNETDQGSNSEKVAEEAGEKGPTPPLPSAPEKDSALVPGASKQPLTSPSALVDSKQES KLCCFTESPESEPQEASFPRLPHHTGHRWQTR MRRRMTNCPPWQITLPTAP  LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYI GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGGRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLI	İ		1	}	1	1	KSIPEPLPAADMKKKIEGYQEFSAKPLASRVD
PLAPEKDSALVPGASKQPLTSPSALVDSKQES KLCCFTESPESEPQEASFPRLPHHTGHR WQTR MRRRMTNCPPWQITLPTAP  LQEMCTKTIPVLWGCFLLWNLYVSSSQTIYI GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLI			-				PEKDNETDOGSNSEKVAEEAGEKGPTPPLPSA
KLCCFTESPESEPQEASFPRLPHHTGHRWQTR MRRRMTNCPPWQITLPTAP  1041 2391 A 8646 113 1492 LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYI GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSODNVPALQPGKKKKLI			1	1	1		PLAPEKDSALVPGASKQPLTSPSALVDSKQES
MRRRMTNCPPWQITLPTAP  1041 2391 A 8646 113 1492 LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYI GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPILASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLI	1	1		1			KLCCFTESPESEPOEASFPRLPHHTGHRWOTR
1041 2391 A 8646 113 1492 LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYM GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVM ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGV PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP			1		1		
GIKARITQRALDYGVQAGMKMIEQMLKEKK LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLI	L				<del>                                      </del>	1402	LL OFMCTKTIPVI WGCFLLWNLYVSSSOTIYP
LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLI	1041	2391	A	8646	113	1492	CIL ADITOR AL DAGACA CARRAMETONI KEKK
NTSLAFVPGVGIKALTNHGTANISTDWGFESI LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLI			1	1			OLIVANI TAVATO LO L'AVOLUTATIONI L'ATECATO
LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVI ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQFFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLI							LEDING A CANCACATA A LANGUAGA COLLANDO COLLANDO CANCACATA A LANGUAGA CANCACATA CANCACA
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NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLI	1		1		1		LEVLYNSFAERMENPILKNUNEMLUTHASEVA
SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLF	1			1	1	İ	ALNANUSTLEVETKIDNYTELDYSLISSPETTE
TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLF			1	1	1		NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER
VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLF		1					SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS
NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLF		1		1			TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM
NSTVETIVSMDFVASTSVGLVILGQRLVCSLS LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLF		1					VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK
LNRFRLALPESNRSNIEVLRFENILSSILHFGVI PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP ARRIARTRESKAAVSQDNVPALQPGKKKKLF	1	1			1		NSTVETIVSMDFVASTSVGLVILGQRLVCSLS
PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLF					1		LNRFRLALPESNRSNIEVLRFENILSSILHFGVL
LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLE							PLANAKLOOGFPLPNPHKFLFVNSDIEVLEGF
RGKSAP  RGKSAP  ARRIARTRESKAAVSQDNVPALQPGKKKKLI	1				1		LLISTDLKYETSSKOOPSFHVWEGLNLISROW
ARRIARTRESKAAVSQDNVPALQPGKKKKLI			1				
1042 2392 A 8672 538 170 ARCHARTACIACH SECRET SECRE				<del></del>	<del> </del>	120	ARRIARTRESKAAVSODNVPALOPGKKKKLR
LOURANN NI I KU	1042	2392	Α	8672	538	170	I GGKKKKEKERI PKEFKKOLMYSPSNFKKM
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PCT/US01/03800

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SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
-pas	uence	i	09/496 914	ng to first	acid residue	O=Ghitamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	•	/=possible nucleotide deletion, \=possible
		}		sequence		nucleotide insertion
	<del> </del>					TSLAGNTVQCLNKLKYVIYSAQYPAYGNITT
		1		<u> </u>		LDMITSTDHVLEQDFWICFTFYSVKERQI GLKTRAPATPTFQREVLGPAKQDMQRRCPRI
1043	2393	A	8688	359	17	GLKTRAPATPTFQREVLOFARQDMQRCFRG
				Į		HHADTLGDRGGLQGDHSELLQWQKRILRTE
						GEPSPKYISKNIFPICSYITGFL
	<u> </u>	<del>  </del>	0710	292	1490	GTVKTSVATPITAGHSCSSGGVLQVKSPATQS
1044	2394	Α	8718	292	1450	GFKFTSKMEDFNMESDSFEDFWKGEDLSNYS
			[			YSSTLPPFLLDAAPCEPESLEINKYFVVIIYAL
					İ	VFLLSLLGNSLVMLVILYSRVGRSVTDVYLL
		}	1	1		NLALADLLFALTLPIWAASKVNGWIFGTFLC
{		1				KVVSLLKEVNFYSGILLLACISVDRYLAIVHA
		1				TRTLTQKRYLVKFICLSIWGLSLLLALPVLLFR RTVYSSNVSPACYEDMGNNTANWRMLLRIL
	}	1	1			POSFGFIVPLLIMLFCYGFTLRTLFKAHMGQK
1						HRAMRVIFAVVLIFLLCWLPYNLVLLADTLM
			1			RTOVIOETCERRNHIDRALDATEILGILHSCLN
		1	-			PLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDS
1					}	RPSFVGSSSGHTSTTL
1045	2395	A	8724	254	3184	FRANLAITVANRRGAQGGKMHTCCPPVTLEQ
1043	2373	1 ''	"-"			DLHRKMHSWMLQTLAFAVTSLVLSCAETIDY
ļ	j	1			1	YGEICDNACPCEEKDGILTVSCENRGIISLSEIS
		1				PPRFPIYHLLLSGNLLNRLYPNEFVNYTGASIL HLGSNVIQDIETGAFHGLRGLRRLHLNNNKL
				1		ELLRDDTFLGLENLEYLQVDYNYISVIEPNAF
)		1			}	GKLHLLQVLILNDNLLSSLPNNLFRFVPLTHL
						DLRGNRLKLLPYVGLLOHMDKVVELQLEEN
	1		Į		1	PWNCSCELISLKDWLDSISYSALVGDVVCETP
		ł			1	FRIHGRDLDEVSKOELCPRRLISDYEMRPQTP
			ļ	1		LSTTGYLHTTPASVNSVATSSSAVYKPPLKPP
						KGTRQPNKPRVRPTSRQPSKDLGYSNYGPSIA
		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	·			YQTKSPVPLECPTACSCNLQISDLGLNVNCQE RKIESIAELQPKPYNPKKMYLTENYIAVVRRT
		1	1	}		DLLEATGLDLLHLGNNRISMIQDRAFGDLTN
		1		1		LRRLYLNGNRIERLSPELFYGLQSLQYLFLQY
-		İ				NI IREIOSGTFDPVPNLOLLFLNNNLLQAMPS
		1		}		GVFSGLTLLRLNLRSNHFTSLPVSGVLDQLKS
		ļ		Į		LIOIDLHDNPWDCTCDIVGMKLWVEQLKVG
				i		VLVDEVICKAPKKFAETDMRSIKSELLCPDYS
}		1				DVVVSTPTPSSIQVPARTSAVTPAVRLNSTGA
				1		PASLGAGGGASSVPLSVLILSLLLVFIMSVFVA
						AGLFVLVMKRRKKNQSDHTSTNNSDVSSFN MQYSVYGGGGGTGGHPHAHVHHRGPALPK
1						VKTPAGHVYEYIPHPLGHMCKNPIYRSREGN
1		-		1		SVEDVKDLHELKVTYSSNHHLQQQQQPPPPP
1				1		OOPOOOPPPOLOLOPGEEERRESHHLRSPAYS
1				1	1	VSTIEPREDLLSPVQDADRFYRGILEPDKHCST
1		1		1		TPAGNSLPEYPKFPCSPAAYTFSPNYDLRRPH
1		[				QYLHPGAGDSRLREPVLYSPPSAVFVEPNRNE
						YLELKAKLNVEPDYLEVLEKQTTFSQF
1046	2396	A	8736	28	452	SPSAAGGLAWVSLALGSGSRGRDHSGSGVGT
1.0.0				}	1	AMAGALVRKAADYVRSKDFRDYLMSTHFW
						GPVANWGLPIAAINDMKKSPEIISGRMTFALC
1		- [				CYSLTFMRFAYKVQPRNWLLFACHATNEVA QLIQGGRLIKHEMTKTASA
L				1		ALPGTPQQTVTLNTDGKVKSFTSPHSNPNLPP
1047	2397	A	8741	673	924	AKFFTSLQSLNWSSHLPPSPATESVGKRGNAK
	1					PPTTK LLHSSPLWNFFAOOL
\- <u></u> -		<del></del>	0717	+2	5054	PEVTKPSLSQPTAASPIGSSPSPPVNGGNNAKR
1048	2398	A	8747	3	1 3034	1

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	Į.		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ		residue of	sequence	/-possible nucleotide deletion, \-possible
				peptide		nucleotide insertion
		ļ	ļ	sequence	<del> </del>	VAVPNGQPPSAARYMPREVPPRFRCQQDHK
	1				1	VILKRGOPPPPSCMLLGGGAGPPPCTAPGAN
	1		į.		Į.	PNNAQVTGALLQSESGTAPDSTLGGAAASNY
					1	ANSTWGSGASSNNGTSPNPIHIWDKVIVDGS
		1	1			DMEEWPCIASKDTESSSENTTDNNSASNPGSE
		-	1	ł	ł	KSTLPGSTTSNKGKGSQCQSASSGNECNLGV
						WKSDPKAKSVOSSNSTTENNNGLGNWRNVS
		1	ł		1	GODRIGPGSGFSNFNPNSNPSAWPALVQEGTS
	İ	1			Ì	RKGALETDNSNSSAOVSTVGQTSREQQSKME
	1	1			1	NAGVNFVVSGREQAQIHNTDGPKNGNTNSL
	-					NLSSPNPMENKGMPFGMGLGNTSRSTDAPSQ
i			1			STGDRKTGSVGSWGAARGPSGTDTVSGQSNS
		1	}			GNNGNNGKEREDSWKGASVQKSTGSKNDS
	1					WDNNNRSTGGSWNFGPQDSNDNKWGEGNK
	{					MTSGVSQGEWKQPTGSDELKIGEWSGPNQPN
		1				SSTGAWDNQKGHPLLENQGNAQAPCWGRSS
						SSTGSEVEGQSTGSNHKAGSSDSHNSGRRSY RPTHPDCQAVLQTLLSRTDLDPRVLSNTGWG
						QTQIKQDTVWDIEEVPRPEGKSDKGTEGWES
						AATQTKNSGGWGDAPSQSNQMKSGWGELS
1			1			ASTEWKDPKNTGGWNDYKNNNSSNWGGGR
						PDEKTPSSWNENPSKDQGWGGGRQPNQGWS
Į.		ļ	-	l.		SGKNGWGEEVDQTKNSNWESSASKPVSGWG
		İ	ļ			EGGONEIGTWGNGGNASLASKGGWEDCKRS.
		-			}	PAWNETGROPNSWNKQHQQQQPPQQPPPPQ
1		- [	- }	ì		PEASGSWGGPPPPPPGNVRPSNSSWSSGPQPA
İ	i					TPKDEEPSGWEEPSPQSISRKMDIDDGTSAWG
1				1		DPNSYNYKNVNLWDKNSQGGPAPREPNLPTP
				}		MTSKSASDSKSMQDGWGESDGPVTGARHPS
1			Į			WEEEEDGGVWNTTGSQGSASSHNSASWGQG
1				1		GKKQMKCSLKGGNNDSWMNPLAKQFSNMG
		1			1	LLSQTEDNPSSKMDLSVGSLSDKKFDVDKRA
		-		1		MNLGDFNDIMRKDRSGFRPPNSKDMGTTDS
		Ì			]	GPYFEKGGSHGLFGNSTAQSRGLHTPVQPLN SSPSLRAQVPPQFISPQVSASMLKQFPNSGLSP
1	İ	- 1	Ì			GLFNVGPQLSPQQIAMLSQLPQIPQFQLACQL
,		ļ			}	LLQQQQQQLLQNQRKISQAVRQQQEQQLA
		j		· I		RMVSALQQQQQQQQRQPGMKHSPSHPVGPK
				1		PHLDNMVPNALNVGLPDLQTKGPIPGYGSGF
				1		SSGGMDYGMVGGKEAGTESRFKQWTSMME
1						GLPSVATOEANMHKNGAIVAPGKTRGGSPY
1			1		{	NOFDIIPGDTLGGHTGPAGDSWLPAKSPPTNK
1			1			IGSKSSNASWPPEFOPGVPWKGIQNIDPESDP
				1	1	VVTPGSVLGGTATSPIVDTDHOLLRDNTTGS
j						NSSLNTSLPSPGAWPYSASDNSFTNVHSTSAK
					1	FPDYKSTWSPDPIGHNPTHLSNKMWKNHISS
				1		RNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRG
	1					WGTODSRLASASTWSDGGSVRPSYWLVLHN
İ	1		1	1		LTPQIDGSTLRTICMQHGPLLTFHLNLTQGTA
						LIRYSTKQEAAKAQTALHMCVLGNTTILAEF
1		1		}		ATDDEVSRFLAQAQPPTPAATPSAPAAGWQS
			1	1		LETGONOSDPVGPALNLFGGSTGLGQWSSSA
	1	1				GGSSGADLAGASLWGPPNYSSSLWGVPTVED
						PHRMGSPAPLLPGDLLGGGSDSI
1049	2399	-	8748	200	1387	VPWKRQDEQLSLQVETLYLDSPAVIHLLSPTF
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						ELTKLLLCAFSLLVGWQAWPQGPPPWRQAA PFALSALLYGANNNLVTYLQRYMDPSTYQVL

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amino acid residue of peptide residue of peptide sequence peptide sequence	, -	uence		I .			O=Glutamine, R=Arginine, S=Serine,
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MPLHITIGLILLILYCLISGI.SSVYTELLY  ROPLALQNIPLTFOYLINI,GIHAGGGS GILEGFSGWAALVVLSQALMGLIMSASVILRQLY FFILATILLIGLAMRLYYGSR  WYSSMGFEELEQVGGFGPOLRNVALLA RVLPLHFILLPILAQVABRCALPGAPYOA  NTILGERQSRGELEDEPATYPCSQGWYY NTILGERQSRGELEDEPATYPCSQGWYY SEFSSTIATESQWDLYCESQGLINRAASTFF GVLVGAVARGYLSDRFRRILLIAVAVST LGLASAASVSYVMFATTLIFCARLMS PVCEDSFSQEAVSKVAAGGRVVRRFSYLLIAVAVST LGLASAASVSYVMFATTLIFCARLMS PVCEDSFSQEAVSKVAAGGRVVRRFSYLLIAVAVST LGLASAASVSTVMFATTLIFCARLMS PVCEDSFSQEAVSKVAAGGRVVRRFSYLLIAVAVST GRRLIAGTALLAGTIRLIFCARLMS PVCEDSFSQEAVSKVAAGGRVVRRFSYLLIALD RTFRLRHISLCCVVVWFGVNFSYTGLSLD GLGLNYYQTQLLFGA VELPSKLLVYLSSDMSS TVLAVMGKAFSEAAFTTAYLFTSELYPT QTGMGLTALVGRLGSSLAPHTV QTGMGLTAPHTV QTGMGLTAPH					·	}	MAAGACYAAGGLOVPGNTLPSPPPAAAASP
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GILEGFSGWAALVVLSQALMGLLMSAVLERQLT GSSTRI-FVVSCSLVVVAVLSAVLERQLT FFI-ATILIGI AMRILYYGSR  WVSSMGFEBLLEQVGGFGPGLRNVALIA RVLLPLHFILPIFLAVPABRCALPOAPS HQDV-WLEAHLPREPDGTLSSCLRFAYPQA NTTI-GERGSKGELEDEATVPCSQGWEYI SEFSSTIATESQWDL-VCEQKGLNRAASTIFI GVLVGAVAFGYLSDFGFRRAILVAY-VST LGLASAASVSYVMFAITRTLTGSALAGFTI MPLELEWLDVEHRITVAGVLSSTFWTGGVI LALVGYLIRDWRWLLLAVTLPCAPGILSU VPESARWLLTQOHVECHARTULAGALNO PVCEDSFSQEAVSKVAAGERVVRRPSYVGLSLD GLGLNYVQTQLLFGAVELPSKLLVVLSSTFWTGGVI LALVGYLIRDWRWLLLAVTLPCAPGILSU VPESARWLLTQOHVECHARTULAGALNO PVCEDSFSQEAVSKVAAGERVVRRPSYVGLSLD GLGLNYVQTQLLFGAVELPSKLLVVLSSTFWTGGVI LALVGYLIRDWRWLLLAVTLPCAPGILSU VPESARWLLTQOHVECHARTULAGALDGVW GRRLTQAGTLAGTALLIPSTRELYPTVV QTGMGLTALVGAVELPSKLLVVLSSTFWTGGVI LALVGNCASESAASTLAVLFTSELYPTVV QTGMGLTALVGAVELPSKLLVSDMKS GRRLTQAGTLAGTALLIPSTRQAQLFE QDVERKSAFTSLGEEMPMKQVQN LFKLTYGGGALLAGTALLIPSTRQAPG GRRTAGAVARSLEDELGCPLCQLDCDGSREQLIA YQHTAAVVSAKSYMCPVCGRALSSPGSC HLULSDNCAAVKSLLEQCCPLCQLDCGSREQLIA YQHTAAVVSAKSYMCPVCGRALSSPGSC HLULSDNCAAVKSLLEQCTPSVKKWAA QNEPLEVRLQRLEEERTAKKSRRDNETTEI VRRNDREAKRLORMGETDEGRARLGGE EAMBLKRANFTPEKRQABLIRREEARIK LEKMDMMLRAQFGGDPSAMLAAENN QLPVSGVELDSQLLGKMAFEEQNSSSLH LEKMDMMLRAQFGGDPSAMLAAENN QLPVSGVELDSQLLGKMAFEEQNSSSLH ROBLAGMAVHALGER FENDMANVAMAYGG ASHGKMWHEELHREVSVSKLKVFFADAM VFYSSGVSNLSGGRAVSPGLGCSTFGR ASLV-VPTTRRSGGFSCTASVAAMAYTISGY HGSKHRARAPPPPPLDDTSGGYSSGFSCTASVAAMAYTISGY HGSKHRARAPPPPPLDDTSGGYSSGFSCTASVAAMAYTISGY PATGADVAFSVSHLLGDFMANVAMAYGG ASHGKMWHEELHREVSVSKLKVFFADAM VFTSSSVNSSAYTIMGKOK YSNEGDLIKH FEDINFHVMLSAAHVLLGGEREDP VLMCAGALVXANSLIGGCKMNNVNVVTI NELNKLKTADHDVQGGFHRAVAKKREMEDELR FEDINFHVMLSSAHVYLLLIGGAEKPTVCS  1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAFGM PEDINFHVMLSSAHVYLLLIGGAEKPTVCS  1054 2404 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAFGM PEDINFHVMLSSAHVYLLLIGGAEKPTVCS  1055 2405 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAFGM PEDINFHVMLSSAHVYLLHKGENIEDP VLMCCAHLVKANSIGGCKMNNVNVVTIVI NELNKLKTADHDVQGGFHRAKKREEMBER SSLMKVPNMSSNODONDSDEFM  1055 2406 A 8768 2 712 RPPRVWYPSGLAGAEKPTVCS							ORLPLALONLFLYTFGVLLNLGLHAGGGSGP
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1050   2400   A   8758   3   1660   WYSSMGFEELLEQVGGGFQLRNVALLA   WYSSMGFEELLEQVGGGFQLRNVALLA   WYSSMGFEELLEQVGGGFQLRNVALLA   WYLSHLELPFLAVPAHRCALPGAPAN   HQDVWLEAHLPREPDGTLSCLRFAYPOA   NTTLGEERQSRGELDEPATVPCSQGWEYI   SEFSSTIATESQWDLVCEQKGINRAASTFF   GVLVGAVAFGYLSDRFGRRRLLVAYVST   LGLASAASVSYWHFAITRIT.TGSALAGFII   WPLELEWLDVEHRTVAGGUISSTFWTGGW   LALVGYLRDWRWLLLAVTLPCAPGLISLV   VPESARWLLQGHVKEAHSYLLHCARLN   PVCEDSFSQEAVSKVAAGERVVRRSYLD   GLGLNVYQTQLLFGAVELPSKLLVYLSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSVR   GRRLTQAGTLLGTALAFGTILLVSLVSLV   GRRTTSLAGTLSTAG	ł	Ì	-		1		GSSITRLFVVSCSLVVNAVLSAVLLRLQLTAA
1050   2400   A   8758   3   1660   WVSSMGFEELLEQVGGFGFQLRVALLA RVLILHFILLPITLAAVPARCALPGAPAN RVLILHFILIPITLAAVPARCALPGAPAN RVLILHFILIPITLAAVPARCALPGAPAN RVLILHFILIPITLAAVPARCALPGAPAN RVLILHFILIPITLAAVPARCALPGAPAN NTTLGEROSGGELEDFATVPCSQGWEY! SEPSSTIATESQWDLVCEQKGLNRAASTFF GVLVGAVAFGYLSDRFGRRELLLVAYVST LGLSASAXSVYMFAITRITGSALAGFTII MPLELEWLDVEHRTVAGVLSSIFYWTGWT LALVGYLIRDWRWLLLAVTLPCAPGILSU VPESARWILLTQGHYKEAHRYLLLVAAVYST LGLSASAXSVYMFAITRITGSALAGFTII MPLELEWLDVEHRTVAGVLSSIFYWTGWT LALVGYLIRDWRWLLLAVTLFOR GRILTQAGTLLGTALAFGTRILLVSSDMSS TVLAVMGKAFSEAAPTTALTSELYPTV QTGMGLTALVGRUGGSLAPLAALLDGWW LPKLTYGGILALAGTILLFETRQAQLPE QTGMUNTALVGRUGGSLAPLAALLDGWW LPKLTYGGILALAGTRILLVSSDMSS TVLAVMGKAFSEAAPTTAQALPE QTGMUNTALVGRUGGSLAPLAALLDGWW LPKLTYGGILALAGTRILLVSSDMSS TVLAVMGKAFSEAAPTTAQALPE QTGMUNTALVGRUGGSLAPLAALLDGWW LPKLTYGGILALAGGTRILLVSSDMSS TVLAVMGKAFSEAAPTTAQALPE QALVENGWEY LEENGGVVVKEKELENTEQPVGGRAVSHET GRINSSPILLELQCPLCQCLCQLDCGSRGCLIA YQHTAAVXASSYMCPVGGRALSSPOSLC HLIHSEDGRSNCAVGARFTSHATTNSEK EVIDAMESLTYTHREGPVGGRAVSHET GRINSSPILLICQCPLCQCLCCGRACHESPOSLC HLIHSEDGRSNCAVGARFTSHATTNSEK EVIDAMESLTYTHREGPVGGRAVENDET VAGNET GRINSPILL GACHEVATA QUEVE GREGOVVAKELENTEQPVGGRAVSSCHILLTSSEK EVIDAMESLTYTHREGPVGGRAVENDET VAGNET GRINSPILLGQCPLCQCPLCQCDCSRGCLIA SPOSLC HLIHSEDGRSNCAVGARFTSHATTNSEK EVIDAMESLTYTHEGPVGGRAVAGAN QUEVSGVEKELENTEQPVGGRAVSSCHILTSSEK EVIDAMESLTYTHEGPVGGRAVEN GARTINSEK EVIDAMESLTYTHEGPVGGRAVEN GARTINSEK EVIDAMESLTYTHEGPVGGRAVEN GARTINSEK EVIDAMESLTYTHEGPVGGRAVEN GARTINSEK EVIDAMESL GARTINGT GARTI	ł	Ì			ĺ		FFLATLLIGLAMRLYYGSR
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HQDVWLEAHLPREPDGTLSSCLRFAYPQA NTTLGERGSRGELEDFAYPCSQGWEY) SEFSSTIATESQWDLVCEQKGLNRAASTFF GVLVGAVAFGVLSDRFARELLVAYVST LGLASAASVSYVMFAITRITTGSALAGFTI MPLELEWLDVHRITVAGVLSSTFWTGGW LALVGYLIRDWRWLLLAVTLFCAPGILSLV VPESARWLLTQGHVKEAHRYLLLCARLNC PVCEDSFSQEAVSKVAAGERVVRRSYLDJ RTPRLRHISLCCVVVWFGVNFSYYGLSDN GLGLNVYOTQLLFGAVBLSVALGERVLYLSVR GRRLTQAGTLLGTALAFGTRLLVSSDMKS TVLAVMGKAFSEAAPTTAYLFTSELYPTV) OTGMGLTALVGRLGGSLAPLAALLDGVW LPKLTYGGIALLAGGTALLJOVW LPKLTYGGIALLAGGTALLDGVW LPKLTYGGIALLAGGTALLDGVW LPKLTYGGIALLAGGTALLDGVW LPKLTYGGIALLAGGTALLDGVW LPKLTYGGIALLAGGTALLDGVW LPKLTYGGIALLAGGTALLDGVW LPKLTYGGIALLAGGTALLFTRQAQCE GREDGGVVKYEKLENTEQPVGGNEVVEHH TGNLNSDPLLELCQCPLCQLDCGSRGLIA YQHTAAVVSAKSYMCPVGGRALSSPGSLC HLIHSEDGRSNCAVCGARFTSHATNSEK EVLNMESLFTVHNEGFSSAGCKDLASPGSV AGILLVCNNCAAVRKLLEAQTFSVKWAAI QNEPLEVFU.GREERETAKKSRRDNETPEL VRRMDREAKRLQRMQETDEGRARRLGR EAMKLKRANETPEKRGARLIREREKARLK LEKNDMMLRAQFGQDFSAMAALAAENN QLPVSGVELDSQLLGKMAFEGONSSUH LEKNDMMLRAQFGQDFSAMAALAAENN QLPVSGVELDSQLLGKMAFEGONSSUH HENDBMRRAGFGGGRSAMAVHSOY GRANGADWYKELHREVSKIKYFFAVO VYAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYTPTMAFITYVLLAGMALGG RFSSEVLGLGASTALVWVMEVLALLLGL ATVRSDLSTFHLLAYSGVKYVMMLSVLT LFGSDGYVALAWTSSALMYFIVRSLRTA GPDSMGGPVRQRIQLYLTLGAAAFQPLU VLTHILVR LTHI	1050	2400	A	8/38	] 3	1000	RVLLPLHFLLPIFLAAVPAHRCALPGAPANFS
NTTLGEERQSRGELEDFATVPSQGWEYN SERSTIATESQWDLVCEQKGLNRAASTFF GVLVGAVAFGYLSDRFGRRELLLVAYVST LGLASAASVSVVMFRITLTGSALAGFTII MPLELEWLDVEHRTVAGVLSSTFWTGGVN LALVGYLIRDWRWLLLAVTLFCAPGILSLV VPESARWLLTQGHVKEAHRYLLHCARING PVCEDSFSQEAVSKVAAGERVYLRFSYLGLD GIGLNYVQTQLLFGALAGFTILVSSDMSS TYLAVMGKAFSEAFTTAVLFTSELYPTV QTGMGLTALVGRLGSSLAPLAALLDGVW LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLPETRQAQLPE VQHTAAVVSSAFSGDEEETTQDEVSSI EEDGGVVKVEKELENTEQPVGGREVVEH TONLNDSLLELCQFQLQLCGSREQLIA YQHTAAVVSSAFSGDEEETTQDEVSSI HLLHISEDQRSNCAVGARTSIAHTNNSEK EVLNMESLFTVHNEGPSSAEGKDIAFSPWA QNEPLEVELQRLEERETAKKSRRNETPEI VRRMRDREAKRLQRMQETDEGPSRCAKAL QNEPLEVELQRLEERETAKKSRRNETPEI VRRMRDREAKRLQRMQETDEGRARLQR EVLNMESLFTVHNGEPSSAEGKDIAFSPWA QNEPLEVELQRLEERETAKKSRRNETPEI VRRMRDREAKRLQRMQETDEGRARLQR EVLNMESLFTVHNGEPSSAEGKDIAFSPWA QNEPLEVELQRLEERETAKKSRRNETPEI VRRMRDREAKRLQRMGETDEGRARLQR EVLNMESLFTVHNGEPSSAEGKDIAFSPWA QNEPLEVELQRLEERETAKKSRRNETPEI VRRMRDREAKRLQRMGETDEGRARLQR ASLVFVFTRRSSGFSGTASVAAMAYHSQV ASHGKMALAGEM QNEPLEVELQRLEERETAKKRL EKMDMMLRAAGFGQDFSAMAYHAGV ASHGKARAAPPEPIPDDTSGGVSSQPG PATGADVAFSVHILLGDPMANVAMAYGS ASHGKDMYHKELHRFYVSKLKYFFAVD YVAKKLGLLVFPYTHQNLAGMALGIG ATVRSDLSTFHILAYSGYKYVGMILSVLT LFGSDGYVYALAWTSSAIMYFIVRSLTTA GFDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RFSTEVLICASTALVWVMEVLALLIGG ATVRSDLSTFHILAYSGYKYVGMILSVLT LFGSDGYVYALAWTSSAIMYFIVRSLTTA GFDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR VFSLTATAMDUSQGGCKMNNVNVYT SNLKKTADMUSQGGGGFMKREKERMKKREMDELR NSLKKAQIGEMKKREKEMKKREMDELR SSLMKVENMSSNQDGRDSDEFM SEATTLAGDNSCWYERSGUGAAKKPETVCS SSLMKVENMSSNQDGRDSDEFM	İ		1	1		·	HODVWLEAHLPREPDGTLSSCLRFAYPQALP
SEFSTIATESQWDLVCEQKGINRASITEF GVLVGQAAFGYLSDRFGRRRLILVAYVST LGLASAASVSYVMFAITRIT.TGSALAGFTII MPELEWLDVEHRIVAGVLSSTFWTGGW LALVGYLIRDWRWLLIAVTLPCAPGILSLV VPESARWLLTQGHVKEAHRYLHCARLM PVCEDSFOGAVSKVAAGERVVRRPSYLDI RTFRLRHISLCCVVWFGVNFSYGLSLDW GLGLNWYQTQLLFGAVELPSKLLVYLSVR GRRLTQAGTLLGTALAFGTRLLVSSDMKS TVLAVMGKAFSEAFTTAYLFTSLYTVI QTGMGLTALVGRLGGSLAPLAALLDGVW LPKLTYGGIALLAAGTALLLPETRQAQLFE QDVERKSAPTSLQEEEMPMKQVQN ERTPVAVSSAPSGDSEGDEETTQDEVSS EDDGGVKVEKELENTEQPVGGNEVVEHI TONLNSDPLLELCQCPLCQLDCGSREQLIA YQHTAAVVSAKSYMCPVCGRALSSPGSLG HLLHIBSDQRSNCAVCGARFTSHATRNSEK EVLNMESLPTVHNEGPSSAEGKDIAFSPPV AGGLLVCNNCAAYRKILBAQTPSVRKWAI QNEPLEVELQRLERERTAKKSRRDNETPEI VRRMRDREAKRLQRGDEDGARRLOR EAMRLKRANETPEKRQARLREREAKRLK LEKMDMMLRAQFQQDPSKKULASRANAMAYHSGY HGSKHRARAAPDPPLFDDTSGGYSQPGG PATGADVAFSVNHLLAGFTGVSSCHAG SLYVPYTRRSGSFGRSGGLGRYPGRG ASLVFVPTRRSGSFGRSGGLGRYPGRG ASLVFVPTRRSGSFGRSGGLGRYPGRG ROPLANDLYIPTMAHTTYVLLAGMALGIG RFSFEVLGLCASTALVWVMEVLALLIGI ATVRSDLSTFHLLAYGGVKYVGMLSVLT LFGSDGYYVALAWTSSALMYFIVRSLRTA GFDSMGGPVPRQRLQLYTLLAGAAFQPLI NOTHELV ROPLANDLYPTMAHTTYVLLAGMALGIG RFSFEVLGLCASTALVWVMEVLALLIGI ATVRSDLSTFHLLAYGGVKYVGMLSVLT LFGSDGYYVALAWTSSALMYFIVRSLRTA GFDSMGGPVPRQRLQLYTLLAGAAFQPLI NUTFHLV RSCHAGGGGRKRAFFRAGGM VFTSSSVNSSAYTTYMGKDKYVENEDLIKH PEDIWFHVDKLSSAHVYLRLHKGENIEDJP VLMDCAHLVKANSIQGCKMNNVNVVYT SNLKKTADMDVGGGFRRQEVLKHKGENIEDJP VLMDCAHLVKANSIQGCKMNNVNVVYT NSLKKTADMDVGGGFRRQEVGLKRKCREMKKREMDELR SSLMKVENNSSNODGNDSDEFM							NTTLGEEROSRGELEDEPATVPCSQGWEYDH
GVLVGAVAFGYLSDRFGRRRLLLAVYNST LGLASAASVSVYMFAITRTLTGSALAGFTI MPLELEWLDVEHRTVAGVLSTFWTGGW LALVGYLIRDWRWLLLAVTLPCAPGILSLV VPESARWLLTQGHVKEAHRYLLHCARLM PVCEDSFSQEAVSKVAAGERVYLFSYLGLSDL GLGLNVYQTQLLFGAVELPSKLLVYLSVR GRRLTQAGTLLGTALAFGTRLLVSSDMKS TVLAVMGKAFSEAAFTTAYLFTSELYPTVI QTGMGLTALVGRLGGSLAFLAALDGVW LPKLTYGGIALLAAGTALLLPETRQAQLFE QDVERKSAPTSLQEEEMFMKQVQN LPKLTYGGIALLAAGTALLLPETRQAQLFE QDVERKSAPTSLQEEEMFMKQVQN EERTPVANSSAFSGOSDEETTTQDEVSSI EEDGGVVKVEKELENTEQPVGGNEVVEH TGNLNSDPLLELQCPLCQLDCGSREQLIA VQHTAAVVSAKSYMCPVCGRALSSPGSL HLLHISEDQRSNCAVCGARTTSHATNISEK EVLNMES.PTVTHREGDSEGKDLATSPFV AGILLVCNNCAAYRKLLBAQTFSVRKWAL QNEPLEVRLQRLERERTAKKSRRDNETFEI VRRMRDREAKRLQRMQETDEORARRLOR EAMRLKRANETFEKRQARLIRERAKRLK LEKMDMMLRAQFGQDFSAMAALAAEMN QLPVSGVELDSQLLGKMAFEGGLGRYPGRG ASLVFVPTRRSGGGRVARPGGLGRYPGRG ASLVFVPTRRSGGGRVARPGGLGRYPGRG ASLVFVPTRRSGGGSTASVAAMAYHSGY HGSKHEARAAPDPPPLFDDTSGYSSQPG PATGADVAFSVNHLLGDFMANVAMAYG ASHGKOMVHKELHEFVSVSKLKYFAVO YVAKKLGLLVFPTVHONWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSFEVLGLCASTALVWVVMEVLALLICI ATVRSDLSTFFILLAYSGYKYVOMILSVLT LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVFRQRLQLYLTLGAMAAFQFLI WLTFHLVR  1053 2403 A 8768 2 712 RPPRWYPELRELSAAAPRWSHRTAPGIM YFISSVNSSAYTIYMKGMXYENEDLIKH PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIGCKMNNVNVYTY SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAARERCDREI NEKAQIQEMKKREKEEMKKREMDELR SSLMKVENNSSNODGNDSDEFM					]	1	SEFSSTIATESOWDLVCEQKGLNRAASTFFFA
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MPLELEWLDVERRTVAGVLSSTFWTGGISLS  LALVGYLRDWRWLLAVTLPCAPGILSLY VPESARWLLTOGHVKEAHRYLLHCARLN PVCEDSFSQEAVSKVAAGERVVRRPSYLDI RTPRILRHISLCCVVVWFGVIFSYYGLSLDY GRALTOQATLLGTALAFGTRLLVSSDMKS GRALTOQATLLGTALAFGTRLLVSSDMKS TVLAVMGKAFSEAAFTTAYLFTSELYPTVI QTOMGLTALVGLGGSLAPLAALDGVW LPKLTYGGIALLAAGTALLPETRQAQLPE QDVERKSAPTSLQEEMPMKQVQN  1051 2401 A 8759 515 1625 ERIPTVAVSSAPSGEGDEETTQDEVSSI EEDGGVVKVEKELENTEQPVGGNEVVEHI TGNLNSDPLELCQPLCQLDCGSRGCLIA YQHTAAVVSAKSYMCPVCGRALSSPGSLG HLLHISEDQRSNCAVCGARTSHATTNSEK EVLNMESLPTVHRSSSAEKGNLAFSPPV AGILLVCNNCAAYEKLLEAQTPSVRKWAN QNEPLEPVLQRLERETAKKSRRDNETPEI VRRMCDREAKRLORMQETDEQRARLOR EAMRLKRANETPERQAALREREAKRLK LERMDMLRAQFQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEQNSSSLH LERMDMLRAQFQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEQNSSSLH LERMDMLRAQFQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEQNSSSLH VSMKHARAAADPPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD VVAKKLGLLVPYTHQNNEVGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD VVAKKLGLLVPYTHQNNEVGYSSQPG PATGADVAFSVNHLLGDFMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD VVAKKLGLLVPYTHQNNEVGYSRDAFL RQDLNAPDLYTPTMAFITYULLGAAAFQPLI WLTFHLVR RQDLNAPDLYTPTMAFITYULLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGI ATVRSDLSTHFILAYSGYKYVGMILSVLTV LFGSDGYVALAWTSSALMYFIVRSLRTA GPDSMGGPVRQRLQLYLTLGAAAFQPLII WLTFHLVR RGSDGYVALAWTSSALMYFIVRSLRTA GPDSMGGPVRQRLQLYLTLGAAAFQPLII WLTFHLVR RFRVWTYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSATYTYMGKKYENEDLIKH PEDIWFHVDKLSSAHVYLLRHKGENIEDIP VLMDCAHLVKANSIQGCKMNVNVYTY SNLKKTADMDVGQIGFHRQKDVKIVTVEI VNEILNRLEKTKVERFPDLAAEKECRDEI NEKKAQQQEMKKREKEEMKKKREMDELR SSLMKVENNSSNQDGNDSDEFM PEATTL ACDNCWERSSI GACKFTVCS							LGLASAASVSYVMFAITRTLTGSALAGFTIIV
VPESARWILITOGHYKEAHRYLHICARYL PVEGDSPSOGAVSKAGERVVRPSYLDI GIGLNYYQTQILIFGAVELPSKLLVYLSVR GRRLTQAGTILIGTALAFGTRILIVSSDMKS TVLAVMGKAFSEAAFTTAJFTSELYPTVI QTGMGITALVGRIGGSLAPLAALIDGVW LPKLTYGGIALIAAGTALLIPSTROAQLEE QDVERKSAPTSLQEEMPMKQVON  1051 2401 A 8759 515 1625 EEDGGVVKVEKELENTEQPVGGNEVVEH EEDGGVVKVEKELENTEQPVGGNEVVEH TGNLNSPPLELELQCPLCQLDCGSREQLIA YQHTAAVVSARSYMCPVCGRALSSPGSLG HILHISEDQRSNCAVCGARFTSHATTNSEK EVLNMESLPTVHNEGPSSAEGKDIAFSPPV AGILLVCNNCAAYRKLLEAQTPSVRKWN QNEPLEVRLQRLERTTAKSKRINETPEI VRRMDRFAKRLQRMGETDEQRARRLOR EAMRLKRANETPEKQARLIREREAKRLK LEKMDMMLRAQFGQDFSAMAALAAEMN QLPVSCVELDSQLLGKMAFEQNSSLM LEKMDMMLRAQFGQDFSAMAALAAEMN QLPVSCVELDSQLLGKMAFEQNSSLM LEKMDMMLRAQFGQDFSAMAALAAEMN QLPVSCVELDSQLLGKMAFEQNSSLM SALGKDMYHKELHRPVSVSKLKYFFAVD YVAKKLGLLVPYTHQNWEVQYSSQPG PATGADVAFSVNHLGDPMANVAMAYGS ASHGKDMYHKELHRPVSVSKLKYFFAVD YVAKKLGLLVPYTHQNWEVQYSSQPG RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLIGI ATVRSDLSTHILLAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVRQRLQLYLTLGAAAPQPLI WLTFHLVR 1053 2403 A 8768 2 712 RPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSATYTYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHYVLKHKGENIEDIP VLMDCAHLVKANSIQGCKMMNVNVYT SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKCRDRE VNEILNRLEKTKVERFPDLAAEKCRDRE VNEILNRLEKTKVERFPDLAAEKCRDRE VNEILNRLEKTKVERFPDLAAEKCRDRE SSLMKVENNSNODGNDSDEFM						ŀ	MPLELEWLDVEHRTVAGVLSSTFWTGGVML
PVCEDSFSQEAVSKVAAGERVVKPSYTGLSLDV RTPRIRHISLCCVVVWGGVNFSYYGLSLDV GLGLNVYQTQLLFGAVELPSKLLVYLSVR GRRLTQAGTLLGTALAFGTRLLVSSDMKS TVLAVMGKAFSEAAFTTAYLFTSELYPTVI QTGMGLTALVGRLGGSLAPLAALLDGVW LPKLTYGGIALAGTALLPFTRQAQLFE QDVERKSAPTSLQEEEMPMKQVQN  1051 2401 A 8759 515 1625 EIRTPVAVSSAFSGDSEGEETTQDEVSSI EEDGGVVKVVEKELENTEQPVGGNEVVEHL TGNLNSDPLLELCQCPLCQLDCGSREQLIA YQHTAAVVSAKSYMCPVCGGARLSSPGSLC HLLHSEDQRSNCAVCGARPTSHATFNSEK EVLNMESLPTVHNEGPSSAEGKDIAFSPV AGILLVCNNCAYKLLEAQTPSVRKWAI QNEPLEVRLQRLERERTAKKSRRDNETPEI VRRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREARALK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSOLLGKMAFEEQNSSLH LEKMDMMLRAQFGGDPSAMAALAAEMN QLPVSGVELDSOLLGKMAFEEQNSSLH HGSKHRARAAPDPPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVO' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSFEVLGLCASTALVWVVWEVLALLIGI ATVRSDLSTFHLLAYSGYKYVGMILSVLT- LFGSDGYYVALAWTSSALMYFIVYRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLI VLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDLP VLMDCAHLVKANSIQGCKMNNVNVYYTI SNLKKTADMDVQQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDEI NEKKAQIQEMKKREKEEMKKREMDELFS SLMKVENMSSNODGNDSDEFM		}	ļ		Į.		LALVGYLIRDWRWLLLAVTLPCAPGILSLWW
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TGNLNSDPLLELCQCPLCQLDCGSREQLIA YQHTAAVVSAKSYMCPVCGRALSSPGSLG HLLIHSEDQRSNCAVCGARFTSHATFNSEK EVLNMESLPTVHNEGPSSAEGKDIAFSPPV AGILLVCNNCAAYRKLLEAQTPSVRKWAI QNEPLEVRLQRLERERTAKKSRRDNETPEI VRRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH LEKMDMMLRAQFGGGRVARPGGLGRYPGGG ASLVFVPTRRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPLFDDTSGGYSSQPGG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RPSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGGKMNNVNVYYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1051	2401	A	8759	515	1625	EIRTPVAVSSAPSGDSEGDEEET IQDEVSSATS
YQHTAAVVSAKSYMCPVGRALSSPGSLO HILIHSEDQRSNCAVCGARFTSHATFNSEK EVLNMESLPTVINEGPSSAEGKDIAFSPPV AGILLVCNNCAAYRKLLEAQTPSVRKWAI QNEPLEVRLQRLERERTAKKSRRDNETPEI VRRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH HGHGRGDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITTYVLLAGMALGIG RFSFEVLGLCASTALVWVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSYLTI LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNVNVYYTI SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFFDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM		1	1	Ì	1		EEDGGVVKVEKELENIEQFVGGVEVVLILLV
HLLIHSEDQRSNCAVCGARFTSHATFNSEK EVLNMESLPTVHNEGPSSAEGKDIAFSPPV AGILLVCNNCAAYRKLLEAQTPSVRKWAI QNEPLEVRLQRLERERTAKKSRRDNETPEI VRRMRDREAKRLQRMQETDEQRARRLQS EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEQNSSSLH RHGHGRDRRGGGRVARPGGLGRYPFGR ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTG LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTTYMGKDKYENEDLIRHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1				1		IGNENSUPLLELCYCFLCQLDCGSAEQLIFATY
EVLNMESLPTVHNEGPSSAEGKDIAFSPPV AGILL VCNNCAAYRKLLEAQTPSVRKWAI QNEPLEVRLQRLERERTAKKSRRDNETPEI VRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH RHGHGGRDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRRSGPSGTASVAAMAYHSGY PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRPVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL' RQDLNAPDLYIPTMAFITYVLLAGMALIGI RFSPEVLGLCASTALVWVVMEVLALLIGI ATVRSDLSTFHLLAYSGYKYVGMILSVLTG LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVRQRLQLYLTLGAAAFQPLII WLTFHLVR  1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVYYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENNSSNQDGNDSDEFM							THE HIGEDODENCA VCGARETSHATENSEKLP
AGILL VCNNCAAYRKLLEAQTPSVRKWAI QNEPLEVRLQRLERERTAKKSRRDNETPER VRRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSKLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSVAGMA QLPVSGVELDSQLLGKMAFEGGGRVARPGGLGRYPGRG ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLIGL ATVRSDLSTFHLLAYSGYKYVGMLSVLT' LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR PEDIWFHVDKLSSAHYYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVYTT SNLKKTADMDVGGIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM  TOTAL TERMINISTORY  RGRINGWESSENSIGACKFIVGS							HILLIASEDORSNEAV COALD TOTAL THOUSEN
QNEPLEVRLQRLERERTAKKSRRDNETPER VRRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH RHGHGGRDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVWMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTG LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVYTT SNLKKTADMDVGGIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENNSSNQDGNDSDEFM		1	1				ACT L VCNNCA AVRKI LEAOTPSVRKWALRR
VRRMRDREAKRLQRMQETDEQRARRLQR EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH RHGHGGRDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPGG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLT LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDK YENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM							ONTED! EVEL ORLERERTAKKSRRDNETPEERE
EAMRLKRANETPEKRQARLIREREAKRLK LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH RHGHGGRDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLT LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDIP VLMDCAHLVKANSIQGCKMNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNSDEFM		i					UDB MR DREAKRLORMOET DEORARRLORDR
LEKMDMMLRAQFGQDPSAMAALAAEMN QLPVSGVELDSQLLGKMAFEEQNSSSLH  1052 2402 A 8763 1106 70 RHGHGRDRRGGGRVARPGGLGRYPGRO ASLVFVPTRRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPGO PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVDY YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIO RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHILAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM							FAMRI KRANETPEKROARLIREREAKRLKRR
QLPVSGVELDSQLLGKMAFEEQNSSSLH  RHGHGGRDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPGG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTT SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1	1	1				LEKMDMMLRAOFGODPSAMAALAAEMNFF
1052 2402 A 8763 1106 70 RHGHGGRDRRGGGRVARPGGLGRYPGRG ASLVFVPTRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPGG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGI ATVRSDLSTFHLLAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTT SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM							OLPVSGVELDSOLLGKMAFEEQNSSSLH
ASLVFVPTRRRSGPSGTASVAAMAYHSGY HGSKHRARAAPDPPPLFDDTSGGYSSQPGG PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTG LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM  DEATTLAGRNSCWVESRCSLGACKPTVCS	1000	10400	<del> </del>	0762	1106	70	RHGHGGRDRRGGGRVARPGGLGRYPGRGAA
HGSKHRARAAPDPPPLFDDTSGGYSSQFGGPATGADVAFSVNHLLGDPMANVAMAYGSASHGKDMVHKELHRFVSVSKLKYFFAVDYVAKKLGLLVFPYTHQNWEVQYSRDAPLRQDLNAPDLYIPTMAFITYVLLAGMALGIGATVRSDLSTFHLLAYSGYKYVGMILSVLTVLFGSDGYYVALAWTSSALMYFIVRSLRTAGPDSMGGPVPRQRLQLYLTLGAAAFQPLIIWLTFHLVR  1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAPGIMYFTSSSVNSSAYTIYMGKDKYENEDLIKHGPEDIWFHVDKLSSAHVYLRLHKGENIEDIPVLMDCAHLVKANSIQGCKMNNVNVVYTISNLKKTADMDVGQIGFHRQKDVKIVTVEKVNEILNRLEKTKVERFPDLAAEKECRDRENNEKKAQIQEMKKREKEEMKKKREMDELRSSLMKVENMSSNQDGNDSDEFM	1052	2402	A	8/03	1100	'	ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA
PATGADVAFSVNHLLGDPMANVAMAYGS ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALLVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTL LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFFDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM							HGSKHRARAAPDPPPLFDDTSGGYSSQPGGY
ASHGKDMVHKELHRFVSVSKLKYFFAVD' YVAKKLGLLVFPYTHQNWEVQYSRDAPL' RQDLNAPDLYIPTMAFITYVLLAGMALGIG RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTG LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFFDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM					1		PATGADVAFSVNHLLGDPMANVAMAYGSSI
YVAKKLGLLVFPYTHQNWEVQYSRDAPL RQDLNAPDLYIPTMAFITYVLLAGMALGIC RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHC PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM			}				ASHGKDMVHKELHRFVSVSKLKYFFAVDTA
RQDLNAPDLYIPTMAFITYVLLAGMALGIC RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM							YVAKKLGLLVFPYTHQNWEVQYSRDAPLPP
RFSPEVLGLCASTALVWVVMEVLALLLGL ATVRSDLSTFHLLAYSGYKYVGMILSVLTV LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM					1		RODLNAPDLYIPTMAFITYVLLAGMALGIQK
ATVRSDLSTFHLLAYSGYKYVGMILSVLTG LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDK YENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM PEATTLACPNSCWVESRCSLGACKPTVCS		1		ļ	1		RESPEVLGLCASTALVWVVMEVLALLLGLYL
LFGSDGYYVALAWTSSALMYFIVRSLRTA GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDK YENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM PEATTLACPNSCWVESRCSLGACKPTVCS		ł					ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL
GPDSMGGPVPRQRLQLYLTLGAAAFQPLII WLTFHLVR  712 RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDK YENEDLIKHG PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVEE VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1	1				]	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
WLTFHLVR  RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTE SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDRER NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM			1				GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY
1053 2403 A 8768 2 712 RPPRVWYPELRELSAAAPRWSHRTAPGIM YFTSSSVNSSAYTIYMGKDKYENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREK NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM			1				WLTFHLVR
YFTSSVNSSAYTIYMGKDKYENEDLIKHO PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVEH VNEILNRLEKTKVERFPDLAAEKECRDREH NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1000	2402	+	9760	+2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVF
PEDIWFHVDKLSSAHVYLRLHKGENIEDIP VLMDCAHLVKANSIQGCKMNNVNVVYTI SNLKKTADMDVGQIGFHRQKDVKIVTVEH VNEILNRLEKTKVERFPDLAAEKECRDREH NEKKAQIQEMKKREKEEMKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1053	2403	A	6/00	-	1	YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW
VLMDCAHLVKANSIQGCKMNNVNVVYTT SNLKKTADMDVGQIGFHRQKDVKIVTVEK VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1		İ		-		PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE
SNLKKTADMDVGQIGFHRQKDVKIVTVER VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM				1			VLMDCAHLVKANSIQGCKMNNVNVVYTPW
VNEILNRLEKTKVERFPDLAAEKECRDREI NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM							SNLKKTADMDVGQIGFHRQKDVKIVTVEKK
NEKKAQIQEMKKREKEEMKKKREMDELR SSLMKVENMSSNQDGNDSDEFM	1			1	1		VNEILNRLEKTKVERFPDLAAEKECRDREER
SSLMKVENMSSNQDGNDSDEFM  PEATULACENSCWVESECSLGACKETVCS		1		1			NEKKAQIQEMKKREKEEMKKKREMDELRSY
DEATH ACRNSOWVESRCSI GACKPTVCS	]	1		- [			SSLMKVENMSSNQDGNDSDEFM
TINGE TANK TA 18760 1344 1527 I KEATTLACKING WY TOKOSEGACIGITY OF	1054	2404	+	8769	344	527	REATTLACENSCWVFSRCSLGACKPTVCSMP
1054 2404 A 8769 344 SLSRQGSQTLCLRLAEYCMESVDSQRLLLS	1034	2404	^	0/03	344		SLSRQGSQTLCLRLAEYCMESVDSQRLLLS

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucl <b>e</b> otide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		j	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	İ	Ì	ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	· '	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
1055	2405	A	8770	430	1104	QQESPAAGAARMNCKEGTDSSCGCRGNDEK
1033	1103	''				KMLKCVVVGDGAVGKTCLLMSYANDAFPEE
		Ì		ļ		YVPTVFDHYAVTVTVGGKQHLLGLYDTAGQ
		1				EDYNQLRPLSYPNTDVFLICFSVVNPASYHNV
				1	}	QEEWVPELKDCMPHVPYVLIGTQIDLRDDPK
			1	1	Ì	TLARLLYMKEKPLTYEHGVKLAKAIGAQCYL ECSALTQKGLKAVFDEAILTIFHPKKKKKRCS
			l	1		ECSALTQKGLKAVFDEALLTIFTH KKKKKKKK
		l				EGHSCCSII
1056	2406	A	8773	261	332	NPRIQLSGNSCCAGSCRVWLSEQ PAGIRHEQARGADRMGKCRGLRTARKLRSH
1057	2407	A	8778	3	477	RRDQKWHDKQYKKAHLGTALKANPFGGAS
						HAKGIVLEKVGVEAKQPNSAIRKCVRVQLIK
	1		1			NGKKITAFVPNDGCLNFIEENDEVLVAGFGR
		1		}	1	KGHAVGDIPGVRFKVVKVANVSLLALYKGK
Ì		1	1	}	l	KERPRS
		J		\	881	PGLSQEPSGSMETVVIVAIGVLATIFLASFAAL
1058	2408	Α	8808	171	001	VI VCRORYCRPRDLLORYDSKPIVDLIGAME
1		1	l			TOSEPSELELDDVVITNPHIEAILENEDWIEDA
		1	1			SGLMSHCIAILKICHTLTEKLVAMTMGSGAK
1					1	MKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
1						DPKLLDARTTALLLSVSHLVLVTRNACHLTG
			1	1		GLDWIDQSLSAAEEHLEVLREAALASEPDKG
i		-	j	,		LPGPEGFLQEQSAI
1059	2409	A	8809	246	757	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWC
1033	2405	1				EGPRMLSWCPFYKVLLLVQTAIYSVVGYASY
		i				LVWKDLGGGLGWPLALPLGLYAVQLTISWT VLVLFFTVHNPGLALLHLLLLYGLVVSTALI
ļ		1	1	1	•	WHPINKLAALLLLPYLAWLTVTSALTYHLWR
Ì			1			DSLCPVHQPQPTEKSD
		1			1201	PKLSVYPLQSHHCLSEPFQSLVCCLA
1060	2410	A	8810	304	381 848	SCKTENLLEMWWFQQGLSFLPSALVIWTSAA
1061	2411	Α	8820	1673	040	FIESVITAVTI.HHIDPALPYISDTGTVAPEKCLF
İ		i i				GAMINIAAVLCIATIYVRYKQVHALSPEENVI
		1		1		IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA
	İ		i		İ	HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH
		}	1			GKOVFWIRLLLVIWCGVSALSMLTCSSVLHS
1	1			1		GNFGTDLEQKLHWNPEDKGYVLHMITTAAE
					-	WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL
1		1				TLYDTAPCPINNERTRLLSRDI
1062	2412	- A	8824	1	763	GGAPPASVPARESPVSGAQGSSRTRGHKRAA
1002	2712	'`		1		GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA
1	ļ		1	1		YSLAPATPEVKVACSEDVDLPCTAPWDPQVP
		i		1		YTVSWVKLLEGGEERMETPQEDHLRGQHYH
				}		QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET
		1	1	ì		FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI
		- 1				FRKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT
		l		1		
}	1					ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE
1063	2413	A	8826	147	627	HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT
		- 1		1		AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ
	Ī		1			KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH
Ì					İ	CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL
					ļ	
Ì					1960	TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE
1064	2414	A	8835	2982	1869	LNKQVSELSQLYKEAQAELEDYRKRKSLEDV
İ					1	TAEYIHKAEHEKLMQLTNVSRAKAEDALSE
		1		L.	1	1/11/14/14/14/14/14/14/14/14/14/14/14/14
l l	ŀ		- 1	ł		MKSOYSKVLNELTOLKOLVDAQKENSVSITE
						MKSQYSKVLNELTQLKQLVDAQKENSVSITE HLQVITTLRTAAKEMEEKISNLKEHLASKEVE

PCT/US01/03800

						(A-Alamina C-Cycleina
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ì				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
		Į	ŀ	sequence		nucleotide insertion
			<del> </del>	sequence		VAKLEKOLLEEKAAMTDAMVPRSSYEKLQS
	'			1		SLESEVSVLASKLKESVKEKEKVHSEVVQIRS
		1	1			FVSOVKREKENIOTLLKSKEQEVNELLQKFQ
					1	QAQEELAEMKRYSESSSKLEEDKDKKINEMS
				ļ	}	KEVTKLKEALNSLSQLSYSTSSSKRQSQQLEA
	·	ł	į.			LQQQVKQLQNQLAECKKQHQEVISVYRMHL
	1	1		1		LYAVQGQMDEDVQKVLKQILTMCKNQSQK
		1	ı	(		K PROPERTY P
1065	2415	A	8841	3	663	AAATAASLSPRGCRLRTPSSDVGPSRAPPPSA
1005	21.15		1	1		APLPTGRAQMSPSGRLCLLTIVGLILPTRGQTL
•	1				)	KDTTSSSSADATIMDIQVPTRAPDAVYTELQP
	1	1				TSPTPTWPADETPQPQTQTQQLEGTDGPLVT
						DPETHKSTKAAHPTDDTTTLSERPSPSTDVQT DPQTLKPSGFHEDDPFFYDEHTLRKRGLLVA
	1					AVLFITGIILTSGKCRQLSRLCRNHCR
		1			10004	FVGEQEGGCEAGAGRGAQTYPGEAGERWFG
1066	2416	A	8853	3806	2204	RRRRGRVVSRKKMSLKSERRGIHVDQSDLL
			1	}		CKKGCGYYGNPAWQGFCSKCWREEYHKAR
	1	1		1		QKQIQEDWELAERLQREEEEAFASSQSSQGA
	1			1		OSLTESKFEEKKTNEKTRKVTTVKKFFSASSR
ļ	1					VGSKKEIOEAKAPSPSINROTSIETDRVSKEFIE
ļ		ļ	}	1		FLKTFHKTGOEIYKOTKLFLEGMHYKRDLSIE
1				}		EOSECAODFYHNVAERMQTRGKVPPERVEKI
			1			MDOJEKYIMTRLYKYVFCPETTDDEKKULAI
	1			1	ļ	QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV
1	-	İ		1	ĺ	KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI
		Ì		1	Ì	KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI
					}	QYITRECNESRLMTGEDGYYFTNLCCAVAFIE
1	1		j	j	1	KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES WSPDACLGVKQMYKNLDLLSQLNERQERIM
1				Ĭ		NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI
			1			KPPNQPLAAIDSENVENDKLPPPLQPQVYAG
İ	İ	l				SNMREVGCGWLVPVIPAFWEAEVGGSLEARS
1067	2417	Α	8855	1372	1513	LROAWATKQDPISKKK
				<del></del>	1602	PCRPGMECNSMISVHCNL
1068	2418	A	8856	1530	1583	PCRPGMECNSMISVHCNL
1069	2419	Α	8857	1530	1583	PYPQGGYPQGPYPQGGYPQGP
1070	2420	A	8866	293	1675	YPOSPFPPNPYGOPOVFPGQDPDSPQHGNYQ
						EEGPPSYYDNODFPATNWDDKSIRQAFIRKVF
		}		1		LVLTLOLSVTLSTVSVFTFVAEVKGFVRENV
1				1		WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL
}		1				VALSVLTASLSYMVGMIASFYNTEAVIMAVG
					ì	TITAVCETVVIESMOTRYDETSCMGVLLVSM
	}	i	1	1		VVI.FIFAILCIFIRNRILEIVYASLGALLFTCFLA
1						VDTOLLLGNKOLSLSPEEYVFAALNLYTDIINI
}		1		1	1	FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP
				1		WHGSASCTSPLSCPQAQPREKDASLQPSCMY
					1	TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC
		Ì	1			HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ
1		}		1		EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS
			]		1	GDMRSGGLIPVLSPE
	2421	$-\frac{1}{A}$	8868	2	358	ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH
1021	1 2461	1	5505	_		DDKMGSNTFFKRNDCRYVMISCKADMAYDN
1071	1		1	1	ĺ	VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII
1071			ŧ	į.	1	
1071						LNGEKLKVFPVRSGT*QGCSVWP
	2422	A	8870	33	658	LNGEKLKVFPVRSGT*QGCSVWP  MESVLSKYEDOITIFTDYLEEYPDTDELVWIL
1071	2422	A	8870	33	658	LNGEKLKVFPVRSGT*QGCSVWP  MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKOHLLKTEKSKLLSDISARLWFTYRRKFSPI
	2422	A	8870	33	658	LNGEKLKVFPVRSGT*QGCSVWP  MESVLSKYEDOITIFTDYLEEYPDTDELVWIL

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	001.55	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uchoc		į.		arnino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion \=possible
				peptide		/=possible nucleonde deletion, \-possible
		}		sequence		nucleotide insertion  CYSIHQMAQMGVGEGKSIGEWVLGPNTVAQ
						GV*KNLA/LFDEW/NSLGLVYVSM/DNPSGSIA
		l				RFPKKLCRVLPL\SADTAGLTGP
		İ				DFSV*GDVDIEVTCPICLQLLTEPLSLNCGLRL
1073	2423	A	8879	146	412	*QVCITA*IKESVIISGG*SSSPVCHTTFQPANL
			1			RTSRYLPT*SIKSLGPDEPQEG
		1				HLQGRSIRTLQLTGENEKNCEVSERIRRSGPW
1074	2424	A	8884	67	435	KEISFGDYICHTFQGDCWADRSPLHEAAAHG
		-				RLLALKTLIAQGVNVNLWTL/DRVSSLHEACL
	1					*GPVACAKPYWKMVPRHGGTVTGPPLLMV
						RSGDRNGLTHQLGGLSQGSRNQSYRSRSRSR
1075	2425	A	8896	1294	248	SRERPSAPRGIPFASASSSVYYGSYSRPYGSDK
		1				PWPSLLDKEREESLRQKRLSERERIGELGAPE
				1		VWGLSPKNPEPDSDEHTPVEDEEPKKSTTSAS
		}	1			TSEEEKKKKSSRSKERSKKRRKKKSSKRKHK
		1		İ		KYSEDSDSDSDSETDSSDEDNKRRAKKAKKK
						EKKKHRSKKYKKKRSKKSRKESSDSSSKES
				}		QEEFLENPWKDRTKAEEPSDLIGPEAPKTLTS
						QDDKPLNYGHALLPGEGAAMAEYVKAGKRI
		1	1			PRRGEIGLTR*RNCHHLNAQVM**VVSRHRR
	1	- {	1	İ		MEAVRTAKREPESTVLMRREPLHPFNPRRET
i		ļ		1		KERE
				146	789	GDSTEAFKEPAFDERTGKGRRLPRAGEFHG*E
1076	2426	Α	8899	140	103	*APGPGPRSFOVSRKMPEE\PPGARKHPFSGKS
l						FYLDLPAGKNLOFLTGAIQQLGGVIEGFLSKE
			1		1	VSYTVSSRREVKAESSGKSHRGCPSPSPSEVR
	}	1	1			VETSAMVDPKGSHPRPSRKPVDSVPLSRGKE
İ						LLQKAIRNQK**CTVQQLSHCRLY\GEKTTAK
				1		RSQREHVQQQSQEHGKWPDLKGPR
1077	2427	A	8901	352	3	AKIGAYKYIQELWRKKQSDVMHFLLRVRCW
10//	12421			}	1	QYPALHRAGTEWQLSALHRAPRSTQPDKAC
j		-				RLGYKAKQGYIIYRICVRRGGWKCPVPKAVT
ŀ						\YGKPVHHGVN*LKFAQSLQSVAEEQ
1078	2428	A	8905	536	781	ACPAENREVPEMAAGQAPHAGPGAGPGQPA PALPFAATPGSRGQALCRGGRRRQHLHGPLH
1		1		İ		RP*QAAPALHAGCQLAPHPPT
	İ					NLIWKLCVTERRLVILDNYDLASE/YEANKYI
1079	2429	A	8912	121	376 ·	CNRIIQFKPGQDKYFTLGLPTGSTPL*CYPKLI
				<b>\</b>		EYNKNGHLSFKYVKTFSMDEY
		i _			1.500	SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG
1080	2430	A	8920	381	1788	GHSLFSCEPITLRMCQDLPYNTTFMPNLLNHY
					1	DOQTAALAMEPFHPMVNLDCSRDFRPFLCAL
	1	ļ	i			YAPICMEYGRVTLPCRRLCQRAYSECSKLME
		]		}	ļ	MFGVPWPEDMECSRFPDCDEPYPRLVDLNLA
		[	1			GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY
				1		SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS
	}		1	1		TICL SATLETEVTELIDVTRERYPERPIKCYAV
				1		WHMMVSLIFF\IGFLLEDRVACNA\SIPAQYKA
		1				STVTOGSHNKACTMLFMILYFFTMAGSVWW
		-				VILTITWFLAAVPKWGSEAIEKKALLFHASA
1		1	1	1		WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD
		1				VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR
		- 1		1		VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL
		1				VVIGCYFYEOAYRGIWETTWIQERC
					420	EFRTKMSTGPDVKATVGDISSDGNLNVAQEE
1081	2431	Α	8922	56	420	CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG
1						TLANEVE\CSVRHGLALILQLCNFSIYTQQMN
		1	1			I SIAIPAMVNNTAPPSOPNASTERPST
					1	, ~~~ ~~ · · · · · · · · · · · · · · · ·
1082	2432	A	8923	355	1079	PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV

SEQ ID	
Docation   Docation	line,
	•
1083   2433   A   8948   28   385   1   2434   A   8950   156   318   HYPPNTDIENSENNKOW GY*E   HMGQLGYFIQCWWECKELISHW 1TH STOPLEN HAVE HAVE HAVE HAVE HAVE HAVE HAVE HAVE	ine,
Amino acid residue of peptide sequence	
residue of	ın,
Peptide sequence	on,
	ole
Square   GPFSKEDQYDVKAPAMFNIRNTG  QGTQIASDGLKGLLFEVSLADLQN   FKLITEDVQDKNCLTNFYGMDLTG   EKWSTMIEAHVDVKITDGYFFHL   HNNQILKTSYA*HQOS/RQIQKKM QTNDLKEVVNKLIPDNIGKDTEKV DVFIRKYVKMLEPNGFERMELRGG   CHAPTER   CHA	
QGTQIASDGLKGLLFEVSLADLO   FKLITEDVQDKNCLTNFYGMDLTG    EKWSTMIEAHVDVKTTDGYFFHL    HNNQILKTSYA*HQQSRQIQKKM    QTTNDLKEVVNKLIPDNIGKDTEKV    DVFIRKVKMLENPGFERMELRGG    DVFIRKVKMLENPGFERMELRGG    LTWPQPHIPSCPAMSEETLQSKLAW    WGAVQGSRAMSDLLLLLDLTLL    AGYSQLAGVAVSAGSPPIRYKFI    GWLLTÆSCSISPKLCSIAVH*DNP-    GWLLTÆSCSISPKLCSIAVH*DNP-    GWLLTÆSCSISPKLCSIAVH*DNP-    HYPINTDTIENSENNKCW*GY*E*    WGGKRVQPFWKRVWQKRTLNLR    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWWECKRLISFNWI    HMGQLGYFIQCWCCKCCWCCWCCCWCCWCCWCCWCCWCCWCCWCCWCCWC	C/TLVART
FKLITEDVQDKNCLTNFYGMDLTC   EKWSTMIEAHVDVKTTDGYFFHL   HNNQILKTSYA*HQQSRQIQKKM   QTMDLKEVVNKLIPDNIGKDTEKV   DVFIRKVKMLENPGFERMELRGG   DVFIRKVKMLENPGFERMELRGG   LTWPQPHIPSCPAMSEETLQSKLAL   WGAVQGSRAMSDLLLLLDLTLL   AGYSGQLAGVAVSAGSPPIRYKFI   GWLLTZESCSISPKLCSIAVH*DNPA   GWLLTZESCSISPKLCSIAVH*DNPA   GWLLTZESCSISPKLCSIAVH*DNPA   GWLLTZESCSISPKLCSIAVH*DNPA   GWLLTZESCSISPKLCSIAVH*DNPA   GWLLTZESCSISPKLCSIAVH*DNPA   GWLLTZESCSISPKLCSIAVH*DNPA   GWGKRVQPFWKRVWQKRILNLE   WGKRVQPFWKRVWQKRILNLE   WGKRVQPFWKRVWQKRILNLE   WGKRVQPFWKRVWQKRILNLE   WTIYTSYDTAIPIS/GI/YPKRMSSKC   MFILAPFTATIKGKQLTCPLVEERI   HKYYIKVKNIA*VTITHTWTVNLN   YSHKYY   WTIYTSYDTAIPIS/GI/YPKRMSSKC   MFILAPFTATIKGKQLTCPLVEERI   HKYYIKVKNIA*VTITHTWTVNLN   YSHKYY   WTIYTSYDTAIPIS/GI/YPKRMSKC   WPGARGCSARLHRCTPAWTT   WTIYTSYDTAIPIS/GI/YPKRMSKC   WFGARGCSARLHRCTPAWTT   WTIYTSYDTAIPIS/GI/YPKRMSKC   WFGARGCSARLHRCTPAWTT   WTIYTSYDTAIPIS/GI/YPKRMSKC   WFGARGCSARLHRCTPAWTT   WTIYTSYDTAIPIS/GI/YPKRMSKC   WFGARGCSARLHRCTPAWTT   WTIYTSYDTAIPIS/GI/YPKRMSKC   WFGARGCSARLHRCTPAWTT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNQKIT   WTIYTSYDTAIPIS/GI/YPKRNGKIT   WTIYTSYDTAIPIS/G	DEVAFRK
EKWSTMEAHDVKTDGYFFH   HNNQILKTSYA*HQQS/RQIQKKM    QTNDLKEVVNKLIPDNIGKDTEKV     DVFIRKVKMI_ENPGFERMELRGG     LTWPQPHIPSCPAMSEETLQSKLA.     WGAVQGSRAMSDLLLLLDLTLL     AGYSQQLAGVAVSAGSPPIRYKFI     GWLLT/ESCSISPK1_CSIAVH*DNP_    GWLLT/ESCSISPK1_CSIAVH*DNP_    GWLLT/ESCSISPK1_CSIAVH*DNP_    GWLLT/ESCSISPK1_CSIAVH*DNP_    GWLLT/ESCSISPK1_CSIAVH*DNP_    GWLLT/ESCSISPK1_CSIAVH*DNP_    GWLLT/ESCSISPK1_CSIAVH*DNP_    WGGRVQPFWKRVWQKRILNIR     HYPINTDTIENSENNKCW*GY*EV     WGGRVQPFWKRVWQKRILNIR     HMGQLGYFIQCWWECKRLISPWI     "TIYTSYDTAPIS/GI/YPKRMSSKC     MFILAPFTATIKGKQLTCPLVEER     HKYYIKVKRN1_*VTITHTWVNLN     YSHKYY     NFKKYT     1086   2436   A 8962   868   1026   H*KILQVGRAQRAHXSRL*SQLLR     NPGARGCSEARLHRCTPAWTT     LHVKHLGHFQLVFSEVICHCILMP     **ersvCafhvCiotyvCLQVYACK     FVSVYGGGLCTCVCMDYICVC     FVSVYGGGLCTCVCMDYICVC     FVSVYGGGLCTCVCMDYICVC     VSKENKHMSIA*STKKHDKLD/LIK     KYTUKRIKHPTOLEKMLRNHLSI     YKDLSKLNRRKTE/S*/VKKWVKL     VISMENKHKKIFSTS     1089   2439   A 8991   60   329   MALTPESPSFOLAATGSVPEP     NSWDSPTEPSSLEDLEATGTIGTI     GVEDNAYTLEVNSYMRAVGIM     GGYPGGTQSVFLTGVLVSSVFUP     NSWDSPTEPSSLEDLEATGTIGTI     GGYPGGTQSVFLTGVLVSSVFUP     ULAALFIIVQYWKQSKDHYI     LIALALFIIVQYWKQSKDHYI     LIALALFIIVQYWKQSKDHYI     TIO90   2440   A 8997   97   456   YPLPVCSYLSGPRGEHWNSLGGK     LVSSRFKISKVIVVGDLSVGKTCL     AELGRVGPSLARWAGSRSQHLVF     FDKNYKAPIGADFEMERFEVLGIF     FDKNYKAPIGADFE	DKICSMV
HNNQLKTSYA*HQQSRQIQKKM  QTNDLKEVVNKLIPDNIGKDTEKV DVFIRKVVMLENPGFERMELRGG	FCVGFTKK
1083   2433   A   8948   28   385	MEIMT*EV
1083	CPIYPLH
1083	GSSS
WGAVQGSRAMSDLLLLLLLTLTL	AAKKKLP
AGYSGQLAGVAVSAGSPPIRYKF    GWLLTZESCSISPKLCSIAVH*DNPZ    GWLLTZESCSISPKLCSIAVH*DNPZ    GWLLTZESCSISPKLCSIAVH*DNPZ    GWLLTZESCSISPKLCSIAVH*DNPZ    GWLLTZESCSISPKLCSIAVH*DNPZ    GWLLTZESCSISPKLCSIAVH*DNPZ    GWLLTZESCSISPKLCSIAVH*DNPZ    HYTPINTDTIENSENNKCW*GY*PE*   WGGKRVQPFWKRVWQKRTLNLR    HMGQLGYFIQCWWECKRLISFWI    *TIYTSYDTAPIS/GIYPKRMSSKC    HMGQLGYFIQCWWECKRLISFWI    *TIYTSYDTAPIS/GIYPKRMSSKC    HMGQLGYFIQCWWECKRLISFWI    *TIYTSYDTAPIS/GIYPKRMSSKC    HMGQLGYFIQCWWECKRLISFWI    *TIYTSYDTAPIS/GIYPKRMSKC    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HMGQLGYFIQCWWECKRLISFWI    HKYYKKRNL*VTITHTWWNLN     YSHKYY     **ERSVCAFHVCIQTYVCLQVYACN     **ERSVCAFHVCIQTYCLQVYACN     **ERSVCAFHVCIQTYCHAPITCHIPH     **ERSVCAFHVCIQTYCHAPIT     **ERSVCAFHVCIQTYCHAPIT     **ERSVCAFHVCIQTYCHAPIT     **ERSVCAFHVCIQTYCHAPIT     **ERSVCAFHVCIQTYCHAPIT     **ERSVCAFHVCIQTYCHAPIT     **ERSVCAFHVEIQTICCHAPIT     **ERSVCAFHVEIQTICCHAPIT     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFWILTET     **ERSVCAFW	LLLMLLGF
1084	HVEPYGET
1084	\WF
1084	VGLIHHW
1085	V
1083	CTI*OSPAK
MFILAPFTATIKGKQLTCPLVEERI	HOETCAR
HKYYIKVKRNL*VTITH\TWVNLN	DY\MWYS
1086	ILMFEILW
1086	
NPGARGCSEARLHRCTPAWTT	RLRHESHL
1087	
1087	VS*ELQRL
1088   2438   A   8989   394   404   N*KWILHVNVRIQSIFF/IKRNQK/II   KKFLDMMSNA*STKKHDKLD/LIK   KYTVKRIKHPTDLEKMLRNHI.SE   YKDLSKLNRRKTE/S*/VKKWVKE   VISMENKHKKIFSTS   MALTPESPSSFPGLAATGSSVPEPF   NSSWDSPTEPSSLEDLEATGTIGTI   GVEDNAYTLEVNSRYMRAVGIM*   GVEDNAYTLEVNSRYMRAVGIM*   GVEDNAYTLEVNSRYMRAVGIM*   GGYPGGTQSVFLTGVLVSSVFYNI   LLIAALFIIVQYWKQSKDHYI   GGYPGGTQSVFLTGVLVSSVFYNI   LLIAALFIIVQYWKQSKDHYI   1091   2441   A   8997   97   456   YPLPVCSYLSGPRGEHWNSLGGK   LVSSRFKISKVIVVGDLSVGKTCL   AELGRVGPSLARWAGSRSQHLVP   FDKNYKAPIGADFEMERFEVLGIP   FDKNYKAPIGADFEMERFEVLGIP   SSFIKRHILIFEDDWHQTTCCHHPI   FHIFYVSVQNSISPSLSVSSSHPDRI	<b>ACVYYICM</b>
1088	VQEFL
KKFLDMMSNA*STKKHDKLD/LIKKYTVKRIKIHPTDLEKMLRNHLSLYKDLSKLNRRKTE/S*/VKKWVKLYSMENKHKKIFSTS	NSHELKLD
KYTVKRIKIHPTDLEKMLRNHLSE	FKT/LCSA
YKDLSKLNRRKTE/S*/VKKWVKE VISMENKHKKIFSTS   NALTPESPSSFPGLAATGSSVPEPF NSSWDSPTEPSSLEDLEATGTIGTI GVEDNAYTLEVNSRYMRAVGIM* I090   2440   A   8996   2   351   SNITITLT*MKKYDNTFCW*GCGQ WQESKFIQAFWSKIQQYLA*ISHI GGYPGGTQSVFLTGVLVSSVFYN LLIAALFIIVQYWKQSKDHYI 1091   2441   A   8997   97   456   YPLPVCSYLSGPRGEHWNSLGGK LVSSRFKISKVIVVGDLSVGKTCL AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP I092   2442   A   8999   548   811   SSFIKRHILIFEDDWHQTTCCHHPI FHIFYVSVQNSISPSLSVSSSHPDRI	)KD*YS/GV
VISMENKHKKIFSTS   VISMENKHKKIFSTS   MALTPESPSSFPGLAATGSSVPEPF   NSSWDSPTEPSSLEDLEATGTIGTI   GVEDNAYTLEVNSRYMRAVGIM*   SNITITLT*MKKYDNTFCW*GCGC   WQESKFIQAFWSKIQQYLA*ISHI   GGYPGGTQSVFLTGVLVSSVFYN   LLIAALFIIVQYWKQSKDHYI   LLIAALFIIVQYWKQSKDHYI   VSSFKISKVIVVGDLSVGKTCL   AELGRVGPSLARWAGSRSQHLVP   FDKNYKAPIGADFEMERFEVLGIP   FDKNYKAPIGADFEMERFEVLGIP   SSFIKRHILIFEDDWHQTTCCHHPI   FHIFYVSVQNSISPSLSVSSSHPDRI	LSRYFIKE
1089 2439 A 8991 60 329 MALTPESPSSFPGLAATGSSVPEPF NSSWDSPTEPSSLEDLEATGTIGTI GVEDNAYTLEVNSRYMRAVGIM 1090 2440 A 8996 2 351 SNITITLT*MKKYDNTFCW*GCGC WQESKFIQAFWSKIQQYLA*ISIHI GGYPGGTQSVFLTGVLVSSVFYN LLIAALFIIVQYWKQSKDHYI 1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGK LVSSRFKISKVIVVGDLSVGKTCL AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP FDKNYKAPIGADFEMERFEVLGIP SSFIKRHILIFEDDWHQTTCCHHPI FHIFYVSVQNSISPSLSVSSSHPDRI	
NSSWDSPTEPSSLEDLEATGTIGTIGVEDNAYTLEVNSRYMRAVGIM*   1090	GGPNATL
GVEDNAYTLEVNSRYMRAVGIM*   1090	LSDMGVV
1090   2440   A   8996   2   351   SNITITLT*MKKYDNTFCW*GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	HL
WQESKFIQAFWSKIQQYLA*ISIHI GGYPGGTQSVFLTGVLVSSVFYNI LLIAALFIIVQYWKQSKDHYI  1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGK LVSSRFKISKVIVVGQDLSVGKTCLI AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP FDKNYKAPIGADFEMERFEVLGIP SSFIKRHILIFEDDWHQTTCCHHPI FHIFYVSVQNSISPSLSVSSSHPDRI	IG/T/LIYC
GGYPGGTQSVFLTGVLVSSVFYNLLLAALFIIVQYWKQSKDHYI  1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGK LVSSRFKISKVIVVGDLSVGKTCL AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP FDKNYKAPIGADFEMERFEVLGIP SSFIKRHILIFEDDWHQTTCCHHPP FHIFYVSVQNSISPSLSVSSSHPDRI	LFDPAFLFL
LLIAALFIIVQYWKQSKDHYI	MKMLHTR
1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGK LVSSRFKISKVIVVGDLSVGKTCL AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP FDKNYKAPIGADFEMERFEVLGIP FDKNYKAPIGADFEMERFEVLGIP FHIFYVSVQNSISPSLSVSSSHPDRI	
LVSSRFKISKVIVVGDLSVGKTCLI AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP FDKNYKAPIGADFEMERFEVLGIP FHIFYVSVQNSISPSLSVSSSHPDRI	SSCPLPLPT
AELGRVGPSLARWAGSRSQHLVP FDKNYKAPIGADFEMERFEVLGIP 1092 2442 A 8999 548 811 SSFIKRHILIFEDDWHQTTCCHHPI FHIFYVSVQNSISPSLSVSSSHPDRI	INR*GGAG
1092 2442 A 8999 548 811 SSFIKRHILIFEDDWHQTTCCHHPH FHIFYVSVQNSISPSLSVSSSHPDRI	SQ\VCKDS
FHIFYVSVONSISPSLSVSSSHPDRI	'F
FHIFYVSVONSISPSLSVSSSHPDRI	IHP\F*RCQ
, , , , , , , , , , , , , , , , , , ,	PDHEVHQH
RAAHHHQHGQGPLGHGLVARVG	
2745 ALLGLOOPAOSLILSRSSVMGVRO	3LQGFVGS
TCPHICTVVNFKELAEHHRSKYPO	CIPTIVVD
AMCCLRYWYTPESWICGGQWRE	YFSALRDF
VKTFTAAGIKLIFFFDGMVEQDKI	DEWVKRR
I.KNNREISRIFHYIKSHKEQPGRNI	VIFFIPSGLA
VFTRFALKTLGOETLCSLQEADY	EVASYGLQ
HNCLGILGEDTDYLIYDTCPYFSIS	SELCLESLD
TVMLCREKLCESLGLCVADLPLL	ACLLGNDII
PEGMFESFRYKCLSSYTSVKENFI	KKGNIILA
VSDHISKVLYLYQGEKKLEEILPL	/VTKQSSFL
*RNGIISFTRT/INLHGFSKNPKV**	LWTNK*YP
RVOTPNPGKKFPCVOMLNPGKKI	PCVQALNP
GEKFPCIHI/PEPROEVPTCSDPEPR	<i><b>QEVPTCTG</b></i>
PFSRREVPMCSDPEPROEVPMCTO	GPEPRQEVP
MCTGPEAROEVPMCTDSEPRQEV	
ROFVPMYTGSEPROEVPMYTGPE	PMCTDSEP
TGPESRQEVLIRTDPESRQEIMCTO	PMCTDSEP SRQEVPMY

					T 10 1 1 1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence	İ	[	914	ng to first	acid residue	Q=Glutamine, K=Arginine, S=Serille,
	1	Į		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	{	1	1	peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		<del>                                     </del>				PICTOPISKQEDSMCTHAEINQKLPVATDFEFK
	1	1				LEALMCTNPEIKQEDPTNVGPEVKQQVTMVS
	ł	1	1			DTEILKVARTHHVQAESYLVYNIMSSGEIECS
	ļ	1	ŀ			NTLEDELDQALPSQAFIYRPIRQRVYSLLLED
		i				CQDVTSTCLAVKEWFVYPGNPLRHPDLVRPL
	-	1	1	1	1	QMTIPGGTPSLKILWLNQEPEIQVRRLDTLLA
	1	i	1			CFNLSSSREELQAVESPFQALCCLLIYLFVQV
	Ì	1			<b>b</b>	DTLCLEDLHAFIAQALCLQGKSTSQLVNLQP
	İ	1		[		DYINPRAVOLGSLLVRGLTTLVLVNSACGFP
						WKTSDFMPWNVFDGKLFHQKYLQSEKGYA
		1	1			VEVL/CRTK*ISAHQIPQPEGSRLQGLHEGEQT
		1				HHWPSPLGLTPRREVGKTGLQLPQDGLWV
1004	2444	+A-	9021	97	834	AREACRAKTDFPGRRFRLWPSCCCRVIVGAE
1094	2444	A	9021	31	1 057	T*H\MAEPVSPLKHFVLAKKAITAIFDQLLEFV
		-				TEGSHFVEATYKNPELDRIATEDDLVEMQGY
		1				KDKLSIIGEVLSRRHMKVAFFGRTSSGKSSVI
	}	1				NAMLWDKVLPSGIGHITNCFLSVEGTDGDKA
						YLMTEGSDEKKSVKTVNQLAHALHMDKDLK
		1	1	1		AGCLVRVFWPKAKCALLRDDLVLVDGPGTD
			1			VTTELDSWIDKFCTKSSTREITNSGSDT
400.5	246	<del> </del>	9022	1	537	LVLNSRVEDFVPPEGAGRTLPFALRPLAACW
1095	2445	Α	9022	1 1	337	LLHRRARRSSALCPRPRSWGVSGGEGAGARE
		1			i	P*ITSSSCCLSAA/SHLSIQSPNMAGARRIRPQ
		)		1	1	LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF
						DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV
		1				FAYGQT\GAGKTYTMGTGFD
	1000	<del>-   -  </del>	9029	1	285	FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL
1096	2446	A	9029	1 1	265	GQHSETPSLKKK\LAGYSGMCL*SQVLRRLRQ
l	ĺ	į.	1			EDCLSPGGGNCRES*SCPYTPAWITERDPV
				716	357	ARSTGFWGEILWCGFLKRSLALSPRVKCSGAI
1097	2447	Α	9032	/10	337	LAHCNFRHAGFPPLSCLSLPNRWEYRRPPARP
ļ			ļ			GKFFLVFLVETGFQC/G*DGLDLLTSRSACLG
}		l	İ			LPKCWDYRREPAASIIFQTTFFINSK
		<del>-  </del>	0020	230	652	KVVVMSCEDINISGSFYRNKLKYLAFLCKRTS
1098	2448	Α	9038	230	652	TNPSQGPYHLWVPSHIFWQTTCGRLPHKTKQ
			1			G*AALDHLKVFDRIPLPYDKKKQMAVSATLE
1		1	j	1		VVRPKP*RKFAYLGHWAQKVDWKYQAMTA
				į		TMGEKRKVYYQKICYQKK
			1	105	202	IIFYSHQQCMRV/WQGCGDIETLIHCW*E*KII
1099	2449	A	9043	185	372	HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP
1						RKIKTCPQNSCTSMLINAIHNDQKWKKINI
				1.50	604	ROSLALSPRLECSGTISAHCRLCPLVFTPLSCL
1100	2450	A	9045	763	584	SLTSSWDYRRPPPHPANFLYFK*RRGF
						LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL
1101	2451	A	9050	275	2	FLLFEMESLPVA/RVECSGTISAHCNLCLPGSS
-		1		[		POPAGAGANA GITTO ACRUTOL II EUA C
1		1		_		DSPASAS*VAGITDMCRYTQLILFHAS
1102	2452	A	9053	449	1224	KTSMFWKFDLHSSSHIDTLLEREDVTLKELM
		-1				DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF
		İ	1			N*EEPPQDMDEKIRYKYPNISCELLTSDVSQM
1	i		ļ	1		NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF
1			1			SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG
1				1		TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ
						RNL*HST*NVMDISKYVNLHWGLNKSHSLL*
						LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS
1			1	1		SLV
1103	2453	$+_{A}$	9058	403	3	GLHVYDFQVYREHILTLNVKKCSVSFWGLRE
1103	2433	^	7030	'03	1	WLYLOMYEIIKSPRFPIIKMTDITKCW*GC\GA
	ı		1	1	1	THE PROPERTY OF THE PROPERTY O
	i	i	- (			AGMONH/CM/MCANAGKI MEMO-1 ITTVTOI
						AGMQI/H/CW\WCVNVGKFWEMS*YYLLKLSI ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA

			1.000	D - P - P	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	055N 09/496	сопеspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide		/=possible nucleotide deletion, \=possible
		1		sequence	Ì	nucleotide insertion
		<del> </del>	<del>                                     </del>		1	APFVLAVNC
1104	2454	A	9064	75	393	KWLFSSLNITGRGDIIGHLKWLDCR\NCSSFPI
1104	1.5.7	1			I	KRNROTHSTESNKLKAGHSFGYN*LIH*NS\V
		1				KTDCGCGANSKGVVVVMKV\KTAQQKQTTS
				1	<u></u>	YMQIGTTKNSRAT
1105	2455	A	9065	366	778	DLLILRNLAFPELKRRNCISRFYLAYHLHKIYS
						RSILLCNNCSGFYILSL*QYDVFFFNYFFFRDR
}						AWPCCPGWSAAWLTTVILAHYRRPGLERSCC
		1			ļ	LSLSSSWDHRRVPPCPANF*/YFSMGFTAFPRL
1						VLNS*TQGI
1106	2456	A	9083	673	816	ESGSLIH*WWENKPAQPLWWEI*QHVQKLPT
1	l					HFPCDPAIPLLGICPED
1107	2457	A	9086	580	18	KPSSGSFIRAIYIFLSTAHVPALFSVLVRTKLT*
		1		1		AFSQSSVLWAHKQQKTSLSLVIR/ERLQIKTA
				1		VRENFLPIRLAKILKLDNVKCWQG/SGSNMSL I/HCWWEYNVIHIIWNSVTFPRKVEHVYITYA
		1			1	PEISVR*IHGGLPTLVHQETHTSVFRGAPSVIP
		1				ETR\CRPTKESINKLLHIYTMEHYGDENK
	10:55	<del>   </del>	10003	540	1	GGNDCSVTPTTEPGRKEIT*KRKF*EKTDRLP
1108	2458	Α	9093	540	1	GA/PPSRTPPTPYPCPHGDRLLPPSRPLPAGPA
	<b>f</b> '					SAFPPAERSRGHRRASL*RARWSAAVPRRSA
		1	1	1	1	GSASEPVQSRWLRLPVGSDSPPAVPVRVCPAP
1				1		DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG
						ORPPPPSGDSLSPPGCCRY
1109	2459	A	9099	1255	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL
1109	2433	1	1000	1 .2	1	GAVAHSCNPSTLVGRGGRITRGQELR
1110	2460	A	9103	242	70	EEOFFFFAVGMFP*VDFLAPASGELWDRLRLT
1110	2400	1		-	1	CSRPFTRHQSFGLAFLRVCSSLDSLDDSVVGP
						SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS
						LLRKQRNKRMAIP
1111	2461	A	9110	189	121	SFLSVRLECNGAIMAHCALPLPG
1112	2462	A	9113	100	910	RRRGGGSRPRRTPVPAPGPGPSFGMDVRFYP
			1		İ	AAAGDPASLDFAQCLGYYGYSKFGNNNNYM
		1		1		NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT
				1	]	PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT
1	1	ľ	1	•	1	POFPPOSLDLPSITISRNLVEQDGVLHSSGLHM
		1				DOSHTOVSOYRODPSLIMR\PSST*PDAARSG
						VMPPAQLTTINQSQLSAQLGLNLGGASMPHT SPSPPASKSATPSPSSSINEEDADEANRAIGEK
			1		1	RAAPDSGKKPKTPKK
	<u> </u>		0122	2452	3051	FLRPSFALVPQAGVQWCALSWLQPPSPRFK*F
1113	2463	A	9120	3452	1005	SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH
						VGOAGHEPLTSGDPPASASQSAGITGVSHQA
		Ì				WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS
			ľ	1	[	LLKCWDY
1111	3454	1	9122	152	377	NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS
1114	2464	A	9122	1 32	3''	SLHP*PPG\SSDPPAPPS*VLGITGQRYHACLII
1		)	1	}		YLYVOTVPORV
1115	2465	A	9124	553	981	QRPLLRQQLGSWPTCRSLEGDLASPW**RLPG
1115	2465	A	7124	333	701	SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM
						TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE
i		1				WRLQHKGRGRGDLHLPDHHLSVPSSADHPA
						OOPSOFNGRNLYFLPLFR
1116	2466	$+$ $\overline{A}$	9135	48	410	SASHEPAEHDGGADSLSASQPPRPAGRPAGA
1110	2400	1	7133	1	1	OHVHVPPWTDVLAGQDRRAPTAGDGAPWP
		1	-			APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ
	1	1	1	1	1	THE ADVIAGE DATE OF THE CONTRACT AND A DECEMBER OF A
ĺ					1	PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA
						GAGGP*GSPAGRACGAAGCRPRPPRPAASSA *NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS

SEQ   D   SED   Met   SEQ   Do of hold in peptide contide seq.   SEQ   Do of hold in peptide contide seq.   SEQ   Do of hold in mucleotide location   SEQ						<del>, ,</del>	Amino acid sequence (A=Alanine C=Cysteine,
NO of mel- entide onlide sq. uence unnee    No. of mel- entide onlide sq. uence unnee   No. of mel- sq. uence   No. of mel- sq	SEO ID	SEQ ID	Met		l .	l	Amino acid sequence (A=Alainie C-Cysteine,
United   Section   Secti		NO: of	hod	ID NO:			D=Aspartic Acid, E=Glutamic Acid,
enice uence		peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
uence uence 9144 of the first amino acid residue of peptide sequence peptide sequenc			Į.	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
uence   914   ng to first a minion scild of peptide residue of peptide residue of peptide sequence   7-  Thirrobnine, V-Valine, W-Trytophan, Y-Tyrosine, X-Unkanown, Y-Stop todon, Y-Sto			١.	09/496	correspondi		M=Methionine, N=Asparagine, P=Proline,
minio acid residue of sequence   foreign   f	1 '		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	uemee	j	ļ	ļ		of peptide	T=Threonine, V=Valine, W=Tryptophan,
Peptide   Pept	Ì		Ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ł				/=possible nucleotide deletion, \=possible
CPARTSVQGGTWTC*APAGRAGLGGWEAD		1			1		nucleotide insertion
RESAPPSCAGS*PDA**GAEPWGAGSRSWG**   1117   2467   A   9141   380   939   SKGMWAECLG/PRIPRICPIC/COPHWKSDCP TCPGAVPRAPGITLPQGSLTDS*PDULSLVAGE**   1118   118			<del> </del>	<del> </del>	Sequence		CPARTSVOGGTWTC*APAGRPAGLGGWEAE
1117	1		1		1		RESAPPSCSAGS*DAD*GAEPWGAGSRSWGS
TCFGAVPRAPGITLPGGSLTDSFPDLLSLVARE	L	<u> </u>	<u> </u>		200	020	KSGHWAKECI OPRIPPRPCPICVGPHWKSDCP
1118	1117	2467	A	9141	380	939	TCDGAVDRAPGTI POGSI TDSFPDLLSLVAED
NTEATHSTLPSFQGPVSLASITVVGIDQASAE   LKTPQ1.WCQLGQYSTM-HTV-IPTCPVPLLG   CII.TKLSAFLTIPRLQPHLIAALSPSS   GII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAALSPSS   CII.TKLSAFLTIPRLQPHLIAAVILQEKARILLPPAES   ERGEGGHCPAEAPLPPPPQVCLAKIPLLIKLP   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNKLNFIKKVRQLASWEKETQIA   CIV.TKLSTNSTSSVSAHSRDAGRESLRSDVFSGSFIR SNFSISDDSYPRKECGADLEFSHNSRDQVIG   SKNSCENSTREKECLEK   CSRDYDVDHIGEADSVLRGGSQVQARGRAL   NIVDQEGSLLGKGETQQLLTARGQVGKLVTIL   RIV.TKLSTNVTIKKIPTVNRTIFKTQGTNQQKNTSPD   VIT.GTNPGTEDIOPPTQKEIQLDLKNLRIPRR   KMSFDIJDKSDVFSRFGIEJKWAGFHTIKDDIK   FSQLFOTLFELETTCAKMLASKECHAVETQD   CSSWSQCYSFGIEJKFPDKYVMRQDRLLKSVTP   LLMACNAYELSVKMKTLSNPLDLALALETTN   SLCRKSLALLGOTISLASSTREKELEK   CSRDYDVDHIGEADSVLRGGSQVQARGRAL   NIVDQEGSLLGKGTQQLLTARGQVGKLVTIL   RIV.TKLSTNPLDLALALETTN   SLCRKSLALLGOTISLASSTREKELEK   CSRDYDVDHIGEADSVLRGSQVGKENTALLDKG   CAV.TKLNCFFEIJEPTDKYVMRQLDRLLAKSVTP   LLMACNAYELSVKMKTLSNPLDLALALETTN   SLCRKSLALLGOTISLASSTREVAKVTUGSQVGKRGSQVGLVTHVVNTJENSKRYKYKKL   KLAEMQRMSENI-RGADOKTTSADCAVRMIL   YSRAVRNLKKKLIPMQRRGIAAQGUAG   WKARRATTOTQTLLFLRAGGLKGHAQAGA   CSRCSTSTADGLPGSENSTENSKLSKNENDPDPL   WFILDQNSSSAFFYYKKVYELCSSICTSSTB   NLHTGGGDTTGSQESPYDLMEGBAEFEDEP   PREALESSEWDAPPEDEDEDIOGEAPAPO   GAGKSEGSTPADGLPGBAABDDLAGAPALSQ   ASSGTCPTRKRSSKSKLVKVPLCRSICTSSTB   NLHTGGGDTTGSQESPYDLMGRAGAPGCVATICNQTTVKCSPVV   FNRCKFCRAGCCPTV KCSQPVSWF   FNRCKFCRAGCCPTV KCSQPVSWF   FNRKEFCAPLQNSRISSCSTVCMFKYCLCSPICTSTB   NHTGGGDTTGSCESPYDLAGAPALSQ   ASSGTCPTRKRSSKSKLVKVPLCEPSICTSTB   FNRKGECRAGCCPTV KCSQPVSWF   FNRKGECRAGCCPTV KCSQPVSWF   FNRKGECRAGCCPTV KCSQPVSWF   FNRKGECRAGCCPT KCCGFT CORTICATOR   CGAGGGCVATIVNQPFROCLQCFDSTHIT   SKRQW*   MYDRSPLITSV			į.	ļ		J	*CCLAAGEAGWTITEL WVTI TVEGKSVP/CI
LKTPQLWCQLGQYSSMHYFLVJPTCPYLLG*   GILTKLSAFLTPRIQPHLLALASPSS	1	ļ	1	1			ATTENTION DEPOCATION ASSTRAIGHTON SKP
Till8   2468   A   9154   471   2   AAGGVVVEVTSHLYLCTISDAGLRLLFPAES   ERGEGCHCPAEAPLPPRPOYCLAKIPILIKLD   ERKILDPYLTOHKINSKQLKYLSVARAKTQ   LVEGNIGVALQNTELKGH*INGFLDTIPEAQE   TKEKTINKLNFIKVKRQLAEWEKTQIA   TKEKTINKLNFIKVKRQLAEWEKTQIA   ACPRILARRRRKVESKRRRGWLRARWSRGQ   NNMAARRITQETFDAVLQEKAKRYHMDAG   EAVSETLQFKAQDLLRAVPRSKERMYDDVHS   GRYSLSGSVAHSRDAGRESLRSDVTSGPSFR   SNPSISDDSYRKECGRDLEFSHNSRDQVIG   RRKLGHPRSQDWKFALRGSWEQDFGHPVSQ   ESSWSQEYSFGSAVLGDFGSSFLEKKECLEK   ESRDYDVDHPGEADSVLRGGSQVQARGRAL   NIVDQEGISLLGKGFTQGLLTGDLKNLRIPRR   KMSPDIDKSDVFSRRGGEIKWAGFHTIKDDIK   FSQLFQTLFFELTETCAKMLASFKCSLKPER   DFCFFTIKFLKHSALKTRRVDNETIAMLLDKG   AVKTKNCFFEIINFPDKYMBLQDRLLKSVTPL   LIMACNAYELSVEMKTLSSVPLDALALALETTN   SLCRKSLALLGQTFSLASSFRQEKLI*AVGLQ   DIAPSPAAFPREDSTLFGRSTUDLVKRVEGOS   ASSISTANTED   STREET	Į	ļ		ļ			NIEATHSTEPSPOOL COVERNATIVE VIDTORVEL G.
Titis	1	ļ	1	1		1	LK IPOL WCQLGQ I SPINH I FLAT SPEC
ERGEGHCPAEAPLPPRPQYCLAKPPLRKLY ERGKILDPJYLOHTKINKSQIKYLSVYAKTITQ LVEGNIGVNI, QNITELKQH*INGFLIDTTPEAQE TKEKITNILNFIKKVKKQICALAWEKIFQIA  1119 2469 A 9155 2 3187 ACPRLARRRRVRSLRRRRGWLRARWSRGQ NNMAARRITQETEDAVLQEKARKYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVGSFGFSFS SSNPSISDDSYTRKEGGRDLEFSHSNSRDQVIG HIKLGHFRSQDWKFALRGSWEQDGHHVSQ ESSWSQSYSFGPSAVLGDFGSSRLEKECLEK ESRDYDVDHPGEADSVARGGSWQARGRAL NIVDQEGSLIGKGFTGGLITAKGGVGKLVTL RNVSTKKIPTVNRIPKTQGTNQIGKNTFSPD VTLGTINGTEDIOFPFIGKPTGLIAKNLARPR KMSFDIIDKSDVFSSFGFBEILK WAGPHTKDDIK FSQLFQTLFELETELCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIIKFPDKYIMRLQDALKSVTP LLMACNAVELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQSKLAVGLQ DIAFSPAAFPNEDSTLFGGEVTDHLKAWLVS SGCPLQVKKAPPEPMREEKMPPTKEIQAK APSSLSDAVPQADHRWVGTIDQLVKRVIEGS LSPKERITLIKEDPAYWFLSDENSLEVKYYKL KLAEMORMSENLRGADVARML YSRAVRNLKKLLPWORRGLLAGQULRG WKARRAYTGTOTLLFLRAPGLKHIGGOAPG LSQAKPSLPDRNDAAKDCPPPVGPSPQDPSL EASGPSKPAGVDISEAFGTSSPCFSADIDMAT METABKLARFVAQVOFELGFSIENSTDNPDL WFLHDQNSSAFKYRKKVFELCPSADIDMAT METABKLARFVAQVOFELGFSIENSTDNPDL WFLHDQNSSAFKYRKKVFELCPSTSPH NLHTGGGDTTGSQESPYDLMEGGAFEPDEPP PREABLESSPVMPEEDEDDEDGEGGEFAPAG GAGKSEGSTPAGLFGGEAFADDLAGAPALSQ ASSGTCFPRKRISKSLKVGMPAPKVCLIQE PREGEPPETYTASSTVLGEGFLISTSHTANDFL WFLHDQNSSAFKYRKKVFELCPSTSPH NLHTGGGDTTGSQESPYDLMEGGAFEPDEPP PREABLESSPVMPEEDEDDEDGEGGEAFAPG GAGKSEGSTPAGLFGGEAFADDLAGAPALSQ ASSGTCFPRKRISKSLKVGMPAPKVCLIQE PREGEPPETYTASSTVLGEGFLISTSHTANDFL*EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGMFILLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGMFILLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGMFILLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGGFLLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGGFLLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGGFLLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG G*GGWLA*VREFETSLGGFLLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG FG*GGWLA*VREFETSLGGFLLISTNLAF**EK VCSHITDSLKFIGKGWVGMVTHACNFGTLG FG*GGWLA*VREFETSLGGFLLISTNLAF**EK VCSHITDSLK	į		1	1			GILTKLSAFLTIPKLQPHLIAALSPSS
ERGEGGHCPAEATLPPROTYCLSAVRAKTIO ERGKIKLDPYLTOHTKINKSKORYLSAVRAKTIO LVEGNIGVNLQNITELKQH*INGFLIDTIPEAQE TKEKTINKLINFKKVKRKQLAEWEKIFQIA ACPRI.ARRRRVSLERRRGWLRARWSRGQ NNMAARRITOETIDAVLQEKARWSHADASG EAVSETLQFKAQULLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLBSDVFSOPSFR SSNYSISDDSYFRKECGROLEFSHSNSRDQVIG HIKKLGHFRSQDWKFALRGSWQDYGHRVACH HIKLGHFRSQDWKFALRGSWQDYGHRVACH HIKLGHFRSQDWKFALRGSWQDYGHRVACH HIKLGHFRSQDWKFALRGSWQDYGHRVACH HIVDQGGSLLGKGETQGLITAKGGVGKLVTL RNVSTKKIFTVNRITPKTQGTNQIGKNTESPD VTLGTNPGTEDIOFFIGKPLGLLAKAGGVGKLVTL RNVSTKKIFTVNRITPKTQGTNQIGKNTESPD VTLGTNPGTEDIOFFIGKPLGLLKNALPRR KMSFDIDDKSDVFSRFGEILK WAGFFITKDDIK FSQLFQTLFLEITETCAKASFKCSLKFEHR DFCFFTIKFLKHSALKTPRVDNETHMLLDKG AVKTRNCFFEIKFPDLYMIRLODRLLKSVTP LLMACNAY FELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQSKLAVCLQ DIAPSPAAPNEDSTLFGGEVTDHLKAWLVS SGCPLQVKKAEPEPMREEKKMPTKFEIQAX AFSSLSDAVPQRADHRWVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEVKYYKL KLAEMQRMSENLRGADQKFTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAGQLRG WKARRATTGTOTLLFLARPGLKHIGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPOTSSPCPSADIDNSL MKARRATTGTOTLLFLARPGLKHIGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPOTSSPCPSADIDNSL MKARRATTGTOTLLFLARPGLKHIGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPOTSSPCPSADIDNSL MKARRATTGTOTLLFLARPGLKHIGRQAPG ASSGTCFPRKRISKSLKVGMIPAPKRVCLIQE PREALESPEVMPEEDEDDEDEGGEAPAPG GAGKSGGSTPADGLPGEGGAFEDDEP PREALESPEVMPEEDEDDEDEGGEAPAPG GAGKSGGSTPADGLPGEAAEDDLAGAPALSQ ASSGTCFPRKRISKSLKVGMIPAPKRVCLIQE PREACPPGTVASSTVLGWWAVRYRRDRW HTNPKEFCAPLONVSRHSCFTVV VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTVV VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTVV VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTVV VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTGVT VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTDVT VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTGVT VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTGVT VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTDVT VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCTFTCH VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCTFTCH VICHIUS WAVRNDRW HTNPKEFCAPLONVSRHSCFTCHTVOTTCHTTCHTTCHTTTTTTTTTTTTTTTTTTTTTT	1118	2468	A	9154	471	2	AAGQVVVEVTSHLYLCIISDAAGLRLLPPAES
LVEGNIGVNLQNTELKQH*INGFLQTPQAE   TKEKTINKLNFKKVRKQLAEWEKIFQIA   THE	1110	2.00	1				ERGEGGHCPAEAPLPPRPQYCLAKHPLLRKLP
TIKEKTNKLNFIKKVKRQLAEWEKFQLA  A 9155 2 3187 ACPRI-ARRRRVNSIRERRGWURARWSRGO NNMAARRITOETEPJAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SNPSISDDSYFRKEGRDLEFSHNSRDQVIG HRKLGHFRSQDWKFALAGSWEQDFGHFVSQ ESSWSQEYSGPSAVLGDFGSSRLJEKECLEK ESRDYDVDHPGEADSVLRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTLAKGGVGVGLVTL RNVSTKLFTVNRITPKTQGTNQIQKNTTSPD VTLGTNPGTEDIOFPIQKEPLGLDLKNLRJPRR KMSFDIDKSDVFSRFGIEIK WAGPHTKDDIK FSQLFQTLFELETEICAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEIPKINDLLDKG AVKTKNCFEIKEFDEXYMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCKSLSLALGGTTSLASSFRQEKIL-*AVGLQ DIAPSPAAFPNFEDSTLFGREYDDILKAWLVS SGCPLQVKKAFPEPMREEBKMPFTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYSL KLAEMQRMSENLRGADQCFTSADCAVRAML YSRAVRNLKKKLLIPWQRRGLLRAQGLKGI WKARRATTGTQTLLTLARGIKHHGRQAPG LSQAKFSLPDRNDAAKDCPPDPVGSPQDPSL EASGPSIKPAGVDISEAPDTSSPCPSADIDMKT METABKLARFVAQVGPEIGOFSIENSTDNPDL WFLHDONSSARKFYRKVELCPSICTSSPH NLHTGGGDTTGSQESPVDLMEGBAFEDEPP PREAELESPEVMPEEDEDDEDGEEAPAPG GAGKSEGSTPAGLPGGAAEDDLAGAPALSQ ASSGTCFPKRRISKSLKVGMPBAFKRVCLIQE PKGECPPPEGTVASSTVLGWWAVRVRRDRW HFNYKEFCAPLONVSRHSCFPVV  1120 2470 A 9163 124 207 PPRACENFPRACPCPPT*KCSQPVSWPC  1121 2471 A 9166 272 523 PMSSLQGCFYTFKCIIFKGIFLLISNLIAF**EK V/CSHITDSLKFIGKGWVGMVTHACNTGTLG G*GGWLA*VREFETSLGMM  1122 2472 C 9170 442 236 MNRRRPLRPADCHSGMRGTENGACSEGESQI  1123 2473 A 9171 10 423 MVDRSPLLTSVIJFYLAIGAAIFFSVLEEPHIWKE AKKNYYTOKLHLLKEPPCLGQEGLDKILEVV SDAAGQGVATIGNTNNWNWPNAMARATA VTITTIGYGRVANASKTEGGELGCIPTOETHIT FSKRQN*  1122 4473 A 9171 10 423 MVDRSPLLTSVIJFYLAIGAAIFFSVLEEPHIWKE AKKNYYTOKLHLLKEPPCLGQEGLDKILEVV SDAAGQGVATIGNTNNWNWPNAMARATA VTITTIGYGRVANASKTEGGELFCGFYGLEGVFFC				1	1		EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ
TIKEKTNKLNFIKKVKRQLAEWEKFQLA  A 9155 2 3187 ACPRI-ARRRRVNSIRERRGWURARWSRGO NNMAARRITOETEPJAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SNPSISDDSYFRKEGRDLEFSHNSRDQVIG HRKLGHFRSQDWKFALAGSWEQDFGHFVSQ ESSWSQEYSGPSAVLGDFGSSRLJEKECLEK ESRDYDVDHPGEADSVLRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTLAKGGVGVGLVTL RNVSTKLFTVNRITPKTQGTNQIQKNTTSPD VTLGTNPGTEDIOFPIQKEPLGLDLKNLRJPRR KMSFDIDKSDVFSRFGIEIK WAGPHTKDDIK FSQLFQTLFELETEICAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEIPKINDLLDKG AVKTKNCFEIKEFDEXYMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCKSLSLALGGTTSLASSFRQEKIL-*AVGLQ DIAPSPAAFPNFEDSTLFGREYDDILKAWLVS SGCPLQVKKAFPEPMREEBKMPFTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYSL KLAEMQRMSENLRGADQCFTSADCAVRAML YSRAVRNLKKKLLIPWQRRGLLRAQGLKGI WKARRATTGTQTLLTLARGIKHHGRQAPG LSQAKFSLPDRNDAAKDCPPDPVGSPQDPSL EASGPSIKPAGVDISEAPDTSSPCPSADIDMKT METABKLARFVAQVGPEIGOFSIENSTDNPDL WFLHDONSSARKFYRKVELCPSICTSSPH NLHTGGGDTTGSQESPVDLMEGBAFEDEPP PREAELESPEVMPEEDEDDEDGEEAPAPG GAGKSEGSTPAGLPGGAAEDDLAGAPALSQ ASSGTCFPKRRISKSLKVGMPBAFKRVCLIQE PKGECPPPEGTVASSTVLGWWAVRVRRDRW HFNYKEFCAPLONVSRHSCFPVV  1120 2470 A 9163 124 207 PPRACENFPRACPCPPT*KCSQPVSWPC  1121 2471 A 9166 272 523 PMSSLQGCFYTFKCIIFKGIFLLISNLIAF**EK V/CSHITDSLKFIGKGWVGMVTHACNTGTLG G*GGWLA*VREFETSLGMM  1122 2472 C 9170 442 236 MNRRRPLRPADCHSGMRGTENGACSEGESQI  1123 2473 A 9171 10 423 MVDRSPLLTSVIJFYLAIGAAIFFSVLEEPHIWKE AKKNYYTOKLHLLKEPPCLGQEGLDKILEVV SDAAGQGVATIGNTNNWNWPNAMARATA VTITTIGYGRVANASKTEGGELGCIPTOETHIT FSKRQN*  1122 4473 A 9171 10 423 MVDRSPLLTSVIJFYLAIGAAIFFSVLEEPHIWKE AKKNYYTOKLHLLKEPPCLGQEGLDKILEVV SDAAGQGVATIGNTNNWNWPNAMARATA VTITTIGYGRVANASKTEGGELFCGFYGLEGVFFC	1	1	1	1		1	LVEGNIGVNLQNTELKQH*INGFLDTTPEAQE
1119   2469   A   9155   2   3187	1		1				TKEKTNKLNFIKKVKRQLAEWEKIFQIA
NNMAARRITIGETFDAVLQEKARYHMDASG EAVESTLDFKAQDILRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHFVSQ ESSWSQEYSFGPSAVLGDFGSSSLIEKECLEK ESRDYDVDHIPGEADSVLRGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLITAKGGSQVQARGRAL NIVDQEGSLLGKGETQGSQVARGRAL NIVDQEGSLLGKGETQGSQVARGRAL NIVDQEGSLLGKGETQGSQVARGRAL SSQLAPSTAFTAGESTLGREVIDHLKSVTP LLMACNAYELSVKMKTLSPELDALALETIN SLCRSSLALLGQTFSLASSFRQEKIL*AVGLQ DIASPAAFPNFEDSILGKSVFILGKSVTP LLMACNAYELSVKMKTLSPELDALALETIN SLCRSSLALLGQTFSLASSFRQEKIL*AVGLQ DIASPAAFPNFEDSILGREVIDHLKAWLVS SGCPLQVKKAFPEPMREEKMIPTKPELQAK APSSLSDAVPQRADHTSLGSVTPLICKSVTP LLMACNAYELSVKMKTLSPELDALALETIN SLCRSSLALLGQTFSLASSFRQEKIL*AVGLQ SGCPLQVKKAFPEPMREEKMIPTKPELQAK APSSLSDAVPGRADHTSLGSVTPLICKSVTPLICKSVTP LLMACNAYELSVKMKTLSVPLDLALALETIN SLCRSSLALLGQTFSLASSFRQEKIL*AVGLQ SGCPLQVKKAFPEPMREEKMIPTKPELQAK APSSLSDAVPGRADHTSLGSVTPTY SGCPLAVKTTSSPTPLACK NAVARTICATION SCCPLAVATION SGCPLQVKKAFPEPMREEKMIPTKPELQAK APSSLSDAVPGRADHTSLGSVTPTY SGCPLAVATION SGCPLQVKKAFPEPMREEKMIPTKPELQAK APSSLSDAVPGRADHTSLGSVTPTY SGCPLAVATION SGCPLQVKKAFPEPMREEKMIPTKPELQAK APSSLSDAVPGRADHTSLGSVTPTY SGCPLAVATION SGC	1110	2460	<del> </del>	0155	2	3187	ACPRLARRRRRVRSLRRRRGWLRARWSRGQ
EAVSETLOFKAQDLLRAVPRSARMYDDVHS DGRYSLGSGVAHSRDAGRESLRSDYSGYPSFS SORYSIGSDASYPREGEGRDLEFSHSSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSO ESSWSQCYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHFGEADSV/LRGGSQVQARGRAL NIVDGEGSLLGKEGFGLTAKGGVGKLVTL RNVSTKKIPTVNRITFKTQGTNOJGKNTFSPD VTLGTMPGTEDJQPPJGKPLGLDLKNLRIPRR KMSFDIDKSDVFSRFGIEIK WAGPHTIKDDIK FSQLFQTLFLETETCAKMLASFKCSLKPFEHR DPCFFTIKFLKHSALKTPRVDHELLANLLDKG AVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTP LLMACKAYELSVKMATSPLDLALALETTN SLCRSLALLGGTFSLASSFRQEKIL*AVGLQ DIASPAAFINFEDSTLFGREVIDHLKAWLVS SGCPLQVKKAPEPMREEEKMIPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWHLSDENSLEVKYYKL KLAEMQRMSENLRGADQKPTFSADCAVRAML YSRAVBNLKKKLLPWQRRGGLRAQGLRG WKARRATTGTOTLLFLRAFGLKHHGRQAPA LSQAKPSLPDRNDAKDCPPDVVGPSQDPS LSQAKPSLPRNDAKDCPPDVGPSQDPS LSQAKPSLPRNDAKDCPPDVGPSQDPS LSQAKPSLPRNDAKDCPPDVGPSQDPS LSQAKPSLPRNDAKDCPPDVGPSQDPS LSQAKPSLPRNDAKDCPPDVGPSQDPS NH.HTGGGDTTGSQESPVDLMEGAEFEDEPP PREABLESPEWMPEEDEDDEDGGEAPAPG GAGKSEGSTPADGLPGEAAEDDLAGAPALSQ ASSGTCFPRKRISSSLXVQMPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HTNPKEFCAPLQNNSRHSCPTV  1120 2470 A 9163 124 207 PPRACEBEPEDEDDEDGGEAPAPG GAGKSGSTPADGLPGEAAEDDLAGAPALSQ ASSGTCFPTKRISSSLXVQMPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HTNPKEFCAPLQNNSRHSCPTVV  1120 2471 A 9166 272 523 PMSSLQGCFYTFKCIIFKGIFLLISNILAF**eK V/CSHITDSLKFIRGWOMVTHACNPGTLG G*GGWL**VREFETSLGNM  1122 2472 C 9170 442 236 MNRRRFLRFADCHSGMRGTENGACSEGSQOI HCGAGGGGVQLVHVNQPEROCLQFDSTHIT FSKRQN*  1123 2473 A 9171 10 423 MVDRSPLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYTQKHLLKEFPCLGGGGLDKLLEVV SDAAGGGVAITGNQTTNNNWNWNAMIPAAT VITTIGYGNVASKTIPGGRLFCGFYGLEFGYPC	11119	2409	A	2177	1	3107	NNMAARRITOETFDAVLQEKAKRYHMDASG
DGRYSLGSSVAHSRDAGRESLRSDVYSGSFSF SSNPSIDDSYTRECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSVLRAGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITYQGTNQIQKNTPSPD VTI.GTNPGTEDIQFPIQKIPLGIDLKNLRLPRR KMSPDIIDKSDVFSRFGEILK WAGPHTIKDDIK FSQLPQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTRYVDNEFLNMLLDKG AVKTKNCFFEIRKFDKYMMLQDRLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGGFLASSFRQEKL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAEPEPMREEEMIPPTKPEIQAK APSSLDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERITLIKEDPAYWFLDSENSLEYKYYKL KLAEMQRMSENLAGOKPTSADCAYRAML YSRAVRNLKKKLLPWQRRGLLRAQGLRGW WKARRAVITGTQLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAQTISSPCPSADIDMKT METAEKLARFVAQPELGPSIENSTDNPDL WFILHDQNSSAFKFYRKKVFELCPSICFTSSPH NILHTGGGDTTGSQESPVDLMEGEAFFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP PREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGKSEGSTPADGLPGGAAEFDDEPP FREAELESFEVMPEEDEDDEDOGEEAPAPG GAGGGVGVAVVAVVVAVVAVVAVATATTTGAATAVATTTGAAATAVATTTGAAATAVATTTGAAATAVATTTGAAAATAVATTTGAAAATAVATTTGAAAATAVATTTGAAAATAVATTTGAAAATAVATTTGAAAATAVATTTGAAAATAVATTTGAAAAATAVATTTGAAAAAAAA	1	-	1				EAVSETLOFKAQDLLRAVPRSRAEMYDDVHS
SSNPSISDDSYFRECGRUEFSHSNSRDQVIG HRKLGHPRSQDWKFALRGSWEQDFGHPVSC ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSVLRRGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGYGVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGYGVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGYGVARGRAL NIVDQEGSLLGKGETQGLLTAKGGYGVARGRAL NIVDQEGSLLGKGGTQGLLTAKGGYGKLYTL RNYSTKKIPTVNRITPKTQGTDQIQKINTPSPD VTI.GTIPPGTEDJOFCKPLGLDLKNLRLPRR KMSFDIDKSDVFSRFGIEIK WAGFHTIKDDIK FSQLFQTILFELETETCAKMLASFKCSLKPEIR DFCFFTIKFLKHSALKTRVDNEFLINMLDKG AVKTKNCFFEIKFDKYNKLQDRLLKSVTP LLMACNAYELSVKMKTLSPNDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAPREEEKMIPFKPEIQAK APSSLSDAVPQRADHRVVGTDQLVKRVIEGS LSPKERTILKEDPAYWFLSDENSLEVKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGGLRAQGLRG WKARRANTTGTGTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVOPSPODPSL EASGPSPRPAGVBERGLTSSPCPSADIDMKT METAEKLARFVAQVGPEIEQFSIENSTDNPDL WFLHIDQNSSAFKFYRKKVFLCFSICFTSSPH NLHTGGGDTTGSGESPVDLMEGGAFFEDEPP PRRAELESPEVMPEEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGGAEPEDDEPP PRRAELESPEVMPEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGAAEDDLAGAPALSQ ASSGTCFPRKRISSKSLKVOMIPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV  1120 2470 A 9163 124 207 PPRACRECPRACPCPPT*KCSQPVSWPC  1121 2471 A 9166 272 523 PMSSLQGCFYTFKCIIFKGIFLLISNLIAF**EK VICKHITDSLKFIRGGWVGMVTHACNPGTLG G*GGWIA*VREFETSLGNM  1122 2472 C 9170 442 236 MNRRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGGGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*  1123 2473 A 9171 10 423 MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTOKLHLLKEFPCLGGGGLDKILEVV SDAAGGGGVAUTGNCHYNNWPNAMIFAAT VITTIGYGNVASKTFGGRLFCGFYGLFGVPFLGGFFCF	1		1				DGRVSLSGSVAHSRDAGRESLRSDVFSGPSFR
HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPALQFDGSRLEKECLEK ESRDYDVDHPGEADSV/LRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVQKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD VTLGTNPGTEDIQFPIQKIPGLDLKNLRLPRR KMSFDIDKSDVFSPGIELIK WAGFHTKDDIK FSQLFQTLFELETECAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIRKFDKYNMRLQDRLLKSVTP LLMACNAYELSVKMKTLLSSFRQEKLK"AVGLQ DIAPSPAAFPNFEDSTLFGRSYIDHLKAWLVS SGCPLQVKKAEPEPMREEEKMPPTKPEIQAK APSSLSDAVPQRAADHRVVGTIDQLVKRVTEGS LSPKERITLIKEDPAYWELSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAQGLRG WKARRATTGTOTLLFLRAPGIKHHGRQAPG LSQAKFSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARFVAQPETEGPSTENSTDNPDL WFLHDQNSSAFKFYRKKVFELCPSICFTSSPH NLHTGGGDTTGSGSPVDLMEGGAEFEDEPP PREAFLESPEVMPEEDEDDEDGGEEAPAPG GAGKSEGSTFADGLPGEAAEDDLAGPALSQ ASSGTCFPRKRISSKLKVGMPAPKRVCLIGE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV  1120 2470 A 9163 124 207 PPRACRPCPTASCTLASSTLAGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV PKGCCPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV PKGCCPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLGNVSRHSCFPV  1121 2471 A 9166 2772 523 PMSSLQGCFYTFKCIIKFGIFLLISNILAF*EK VCSHITDSLKFTGKGWVGMVTHACNPGTLG G*GGWIA*VREFETSLGNM  1122 2472 C 9170 442 236 MNRRFLRFADCHSGMRGTENGACSEGESQI HCGAGGGGVQLVHVVNQPENGCLQFPSTHIT FSKRQN*  1123 2473 A 9171 10 423 MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGGGGLDKILEVV SDAAGGGVALTGNQTFRNNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFLGFFYGLFG	1			1			SSNPSISDDSYFRKECGRDLEFSHSNSRDOVIG
ESSWSQEYSFGPSAVLGGFGSSNLERECLEK   ESRDYDVDHFGADSVVLRGGSQVQARGRAL   NIVDQEGSLLGKGETQGLLTAKGGVQKLVTL   RNVSTKKIPTVNRIPKTGOTNQIQKNTPSPD   VTLGTNPGTEDIQFPJQKPJGLDLKNLRLPRR   KMSFDIDDKSDVPSRFGIEIK WAGFHTIKDDIK   FSQLFQTILFELETETCAKMLASFKCSLKPEHR   DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG   AVKTKNCFFEIIKPFDKYMRLOPRLKSVTP   LLMACNAYELSVKMKTLSNPLDLALALETTN   SLCRKSLALLGQTFSLASSRQEKIL*AVGLQ   DIAPSPAAFPNFEDSTLFGREYDHLKAVUV   SGCHQVKKAPFEPNREDEKMIPPTKPEIQAK   APSSLSDAVPQRADHRVGTIDQLVKRVIEGS   LSPKERTLLKEDPAYWFLSDENSLEYKYYKL   KLAEMQRMSENLRGADQKPTSADCAVRAML   YSRAVRNLKKKLLPWQRRGLLRAQGLRG   WKARRATTGTULFLRAPGLKHGRQAPG   LSQAKPSLPDRNDAAKDCPPDVGPSQDPSN   EASGPSKPAGVDISEAPQTSSPCPSADIDMKT   METAEKLARFVAQVGPEEQFSENSTONPDL   WFLHIPQNSSAFKFYRKKVFELCPSICFTSSPH   NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP   PREAELESSPSWPEEDDEDDGEDGEEAPAPG   GAGKSEGSTPADGLPGEAAFDDLAGAPALSQ   ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE   PKGECPPVGTVASSTVLGWWAVRVRDRWR   HFNPKEFCAPLQNVSRHSCFPVV   PMSSLQGCFYTFKCISQPVSWPC   PMSSLQGCFYTFKCISGRWGMVGMVTHACNPGTLG   G*GGWIA*VREFETSLGMM   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**  1122 2472 C 9170 442 236   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFADCLISGMRGTENGACSEGESQI   HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT   FSKRQN**   MNRRFLRFAGGRLFCGGGLDKILEVV   SDAAGQGVAITGNQTTNNWNPNAMIFAAT   VITTIGYGNVASKTFGGRLFCGGFGLGKILEVPRC	1				1		HRKI GHERSODWKFALRGSWEODFGHPVSO
ESRDYDVPHFGEADSVLRGGSQVQARGRAL   NIVDQGGSLLQKGETQGLLTAKGGVGKLVTL   RIVSTKKIPTVNRITPKTQGTNQIQKNTPSPD     VTLGTNPGTEDIQFPIQKPLGLDLKNIRLPRR     KMSFDIJMSSDVFSRFGIEJIKWAGFHTIKDDIK     FSQLFQTLFELETETCAKMLASFKCSLKPEHR     DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG     AVKTKNCFFEIIKPFDKYIMRLQRALLKSVTP     LLMACNAYELSVKMKTLSNPLDLALALETTN     SLCRKSLALL GSTELASSFRQEKIL*AVGLQ     DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS     SGCPLQVKKABPEPMREBEKMIPTKPEIQAK     APSSLDAVPQRADHRVVGTIDQLVKRVIEGS     LSPKERTLLKEDPAYWFLSDENSLEYKYYKL     KLAEMQRMSENLRGADQKPTSADCAVRAML     YSRAVRNLKKKLPWQRRGLLRAQGURG      WKARRAITGTQTLLFLRAPGLKHHGRQAPG     LSQAKPSLPDRAAKDCPPDPYGPSPQDPS     LSQAFSLPDRAAKDCPPDPYGPSPQDPS     LSQAFSLPDRAAKDCPPDPYGPSPQDPS     LSQAFSLPDRAAKDCPPDPYGPSPQDPS     LPHDQNSSAFKPYRKKVFELCPSICFTSSPH     NLHTGGGDTTGSQESPVDLMEGEAFEDEPP     PREAELESPEVMPEEEDEDDEDGGEAPAPG     GAGKSEGSTPAGELGEAAEDDLAGAPALSQ     ASSGTCFPRRRISSKSL KVGMIPAPKRVCLIQE     PKGECPPVGTVASSTVLGWWAVRVRDWR     HTNKEFCAPLQNVSRHSCFPVV     PFRACRFCPRACFCPPT*KCSQFVSWPC     PMSSLQGCFYTASSTVLGWWAVRVRDWR     HTNKEFCAPLQNVSRHSCFPVV     PMSSLQGCFYTEKCIPKGFELLISNLIAF*EK     VICSHITDSLKFIGKGWVGMVTHACNPGTLG     G*GGWLA*VREFETSLGMM     MTNRRFLRFADCHISGMRGTENGACSEGESQI     HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT     FSKRQN**     1123   2473   A 9171   10   423   MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE     AKKNYYTQKLHLLKEFPCLGGGGLDKILEVV     SDAAGQQVAITGNQTTNNWNPNAMIFAAT     VITTIGYGNVASKTFGGRLFCGFYGLFGVPFC							ESSWSORVSEGPSAVI GDEGSSRIJEKECLEK
NIJDQEGSLLGKETQGLITAKGGVGKLVTL   RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD   VTLGTNPGTEDIQFPIQKIPLGDLKNLRLPRR   KMSPDIIDKSDVPSRFGIEIK WAGFHTIKDDIK   FQQLFQILFELFTETCAKMLASFKCSLKPEHR   DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG   AVKTKNCFFEIIKPFDKYMRLOPRLKSVTP   LLMACNAYELSVKMKTLSNPLDLALALETTN   SLCRKSLALLGQTFSLASSFRQEKL*AVGLQ   DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS   SGCPLQVKKAEPEPMREEKKMPPTKPEIQAK   APSSLSDAVPQRADIRVGTIDQLVRRVIEGS   LSPKERITLKEDPAY WFLSDENSLEYKYYKL   KLAEMQRMSEINLRGADQKPTSADCAVRAML   YSRAVRNLKKKLLPWQRRGLLRAQGURG    WKARRAITTGTDLFLRAPQLKHHGRQAPG   LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL   EASGPSPKPAGVDISEAPQTSSCPSADIDMKT   METARKLARPVAQVGPEIEQFSIENSTDNPDL   WFLHDQNSSAFKFYRKKVFELCPSICFTISPH   NLHTGGGDTTGSQESPVDLMEGEAEPDEPP   PREAFLESPEVMPEEEDEDDEDGGEAPAPG   GAGKSEGSTPADGLPGEAAEDDLAGAPALSQ   ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE   PKGECPPVGTVASSTVLGWWAVRVRDWR   HFNPKEFCAPLQNVSRHSGFPVV   HFNPKEFCAPLQNVSRHSGFPVV   PFRACTRYCKSQPVSWPC   PFRACTRYCKSQPVSWPC   PFRACTRYCKSQPVSWPC    1120	1		1	1			ESD WOOLD GEAD SWILL REGSOVOARGRAL
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VTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRR KMSFDIIDKSDVFSRFGEIIK WAGGHTIKDDIK FSQLFQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFEBIKPFDKYJIMRLQDRLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DLAPSPAAFPNFEDSTLFGRESTVDHLKAWLVS SGCPLQVKKAEPEPMREEKMIPPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLP\WQRRGLLRAQGLRG\ WKARRANTTCTQTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARTVAQVGPEIEQFSIENSTDNPDL WFLHDQNSSAFKFYKKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP PREAELESFEVMPEEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGEAAFDDLAGAPALSQ ASSGTCFPRKRISSKSLKVGMPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV PPRACPPTT*KCSQPVSWPC PMSSLQGCFYTFKCIIFKGIFLLISNLIAF**EK V/CSHITDSLKFIGKGWVGMVTHACNPGTLG G*GGWIA*VRFETSLGNM MNRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN**  1123 2473 A 9171 10 423 MVDRSFLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKLILEVV SDAAGQGVAITRONWFNAMIPAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVFCC	i		ì	-		İ	NIVDQEGSCLGKGETQGCDTAKGGVGKLYTD
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1122 2472 C 9170 442 236 MNRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*  1123 2473 A 9171 10 423 MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC					1	1	
HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*  1123 2473 A 9171 10 423 MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC			1		<u> </u>		
HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*  1123 2473 A 9171 10 423 MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC	1122	2472	C	9170	442	236	MNKKKI LKPADCHOUMKU I ENUACOEUEOQI
1123 2473 A 9171 10 423 MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC	]		1			1	
AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC				İ			FSKRQN*
AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC	1177	2472	ΙΔ	9171	10	423	MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE
SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC	1123	24/3	^	71/1	1.0		AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV
VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC	1		i				SDAAGOGVAITGNQTFNNWNWPNAMIFAAT
							VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC
ELAMATOMIO							
					ــــــــــــــــــــــــــــــــــــــ		DI WHAT DOES I C

			T-=-	T 11.4.4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in USSN	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		Ì		peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
1124	2474	A	9173	3	374	GPSPSLLVLLPQEPGGTGTPVRAGAGAGMWL
1124	27/7	1	****			WEDQGGLLGPFSFLMLMLLLETRNPVNACLL
			1		1	TGSLFVLLGVFSFEPVPSCRALQELKPRDRISA
	1			ļ		IAHRGGRHDPPENTLGAIR/QGS**WSNRR
1125	2475	A	9179	704	188	ESSSGLLFQCFQGIHVQKLTLQARPTLFSWWL
1123	1	'-		ĺ		CSKPPKETGELENAESGGDGGRRGGKQDNV
		1			1	AWWRRM\QKG\DFPWDDEDFPQSGPFGGQA
		1	i			LPMGFFYLYFRDPGREITWKHFVQYYLARGL
		1	1		ì	VDRLEVVNKQSVRVIPAPGTSSEVRGEFKAE
			ŀ			YCRHKFISCKNVVFYFFQ
1126	2476	A	9183	153	233	MEYMAESTDRSPGHILCCECGVPISPN  MEYMAESTDRSPGHILCCECGVPISPN
1127	2477	Α	9185	1	321	LTGQLGSILLRVFSKSRAGLGARKLKAYRTM
		İ	1	-	1	EYMAESTDRSPGHILCCECGVPISPNPAQY\CV ACLRSSFHIYHCIPKLFIHPFSKTSSSAFITPSHY
		1				
		İ		<u> </u>	<del></del>	LTFFSTIS   VLKFLLLQTMDEQSQGMQGPPVPQFQPQKAL
1128	2478	Α	9186	183	847	RPDMGYNTLANFRIEKKIGRGQ\FSEVYRAAC
		-		1		LVLDGVPVALKKVQIFDLMDAKARADCIKEID
İ						LLKQLNHPNVIKYYASFIEDNELNIVLELADA
	.	1		1		GDLSRMIKHFKKQKRLIPERTVWKYFVQLCS
			-			ALEHMHSRRVMHRDIKPANVFITATGVVKLG
		ľ	Ì	1		DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHD
1	}			1		NG
1100	2479	A	9190	1	370	GTSWKIPSAAVSESSPNGAAYASGLPCGVRG
1129	24/9	A	7130	1.	"	PPWAGLALLPSPTLMALLRRPTVSSDLDNIDT
į	İ	-		1	j	RATTIKIRVVATITRARIEDMRHSATALTRPD
į	İ	1	ĺ	1	1	ATTAQIPKLPVTTVCNRRANPGIPPSVL
1130	2480	A	9194	131	487	AYLKRLPVPESITGFARLTVSEWLRLLPFLGV
1130	2.00				\	LALLGYLAVRPFLPKKKQQKDSLINLKIQKEN
1		1			Ì	PKVVNEINIEDLCLTKAAYCRCWRSKTFPAC
Ì	Ì					DGSHNKHNELTGDNVGPLILKKKE
1131	2481	A	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE
					}	PLAFLRALELLFAIFAFATCGGYSGGLRLSVD CVNKTESNLSIDIAFAYPFRLHQVIFEGPTCE
1				i		GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL
L				<del></del>	1052	AATGVYIFFQNKY GGGRAGAGSRDMGSTDSKLNFRKAVIQLTTK
1132	2482	A	9206	1	852	TQPVEATDDAFWDQFWADTATSVQDVFALV
				1	1	PAAEIRAVREESPSNLATLCYKAVEKLVQGA
					1	ESGCHSEKEKQIVLNCSRLLTRVLPYIFEDPD
1		ļ ,	İ	1	1	WRGFFWSTVPGAGRGGQGEEDDEHARPLAE
1		Ì		1		SLLLAIADLLFCPDFTVQSHRRSTVDSAEDVH
	1	1				SLDSCEYIWEAGVGFAHSPQPNYIHDMNRME
						LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS
1		1		}		FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY
	1					NHLY
L	- I - I	<del></del>	0200	1165	1463	GPRARVOGESGADIVKEMALGSMYLVLTLIV
1133	2483	A	9208	1103	1405	AKVLRGAEPCCGPLKNRVLRPCPLP/VPLPPP
		1		1	ĺ	HPQPSRGNPVGCLPTYKVVYKLLSWPLHSNS
		Į.		1		NVYFIV
113:	2404		9210	66	1586	MAGAGPKRRALSAPVAEEKEEAREKIMAAK
1134	2484	Α	9210	00	1550	RADGAAPAGEGEGVTLQGNITLLKGVAVIVV
	1					AIMGSGIFVTPTGVLKEAGSPGLALVVWAAC
Ì		1	i			GVFSIVGALCYAELGTTISKSGGDYAYMLDV
				1		
						YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL
						YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL
						YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL LKPLFPTCPVPEEAAKLVACLCVLLLTAVNC YSVKAATRVODAFAAAKLLALALIILLGFVQI
						YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
ucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
eq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ience			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ì	1	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						IVTLVYVLTNLAYFTTLSTEQMLSSEAVAVDE
	ĺ		-	1		GNYHLGVMSWIIPVFVGLSCFGSVNGSLFTSS
						RLFFVGSREGHLPSILSMIHPQLLTPVPSLVFT CVMTLFYAFSKDIFSVINFFSFFNWLCVALAII
						GMIWLRHRKPELERPIKVNLALPVFFILACLF
		1		1		LIAVSFWKTTPWSVASDFTIILSGLPVYFFGV
				ĺ		WWKNKPKWAPPGHLSPRPSCVRSSCMVVPQ
		1			<u> </u>	RDRLPPAYFCRPVVCVVTALDVG\SPESQEM
1135	2485	Α	9216	40	410	DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV
	ĺ					MQETLRNLASIGEKWKDQNIEDQYKNPRNNI
				1		RSLLGERVDENTEENHCGETSSQIPDDTLNK
	_	<u> </u>	J			RRRRSRYRRCSRFPRPGPLAVSMPHAFKPG
1136	2486	Α	9223	3	983	DLVFAKMKGYPHWPARIDDIADGAVKPPPN
		1		1		KYPIFFFGTHETAFLGPKDLFPYDKCKDKYGI
		1				PNKRKGFNEGLWEIQNNPHASYSAPPPVSSSI
		Ì			}	SEAPEANPADGSDADEDDEG\RGVMAVTAV
						ATAASDRMESDSDSDKSSDNSGLKRKTPALK
	ŀ		İ			MSVSKRARKASSDLDQASVSPSEEENSESSSI
			1	1		SEKTSDQDFTPEKKAAVRAPRRGPLGGRKKI
		]	1	1		APSASDSDSKADSDGAKPEPVAMARSASSSS
		}	ŀ			SSSSSDSDVSVKKPPRGRKPAEKPLPKPRGR
	1	Y				PKPERPPSSSSSD
	0.407	+A	9229	21	239	LFPRLECRDPVTVNCTLNLPGSKNAPTTASQ
1137	2487	A	9229	21	233	GSTWNYRGGLPHPTNFFVKTGFRCSQAGLK
						RGSREPPAWA
1138	2488	A	9231	1664	2	TRSVGVNTCEVGVVTEPECLGPCEPGTSVNL
1138	2488	I A	7231	1004	-	EGIVWHETEEGVLVVNVTWRNKTYVGTLLI
	İ			Ì		CTKHDWAPPRFCESPTSDLEMRGGRGRGKR
		1				ARSAAAAPGSEASFTESRGLQNKNRGGANG
			1			GRRGSLNASGRRTPPNCAAEDIKASPSSTNK
				1		KNKPPMELDLNSSSEDNKPGKRVRTNSRSTP
		ì				TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK
					1	YKHINGLRYHQAHAHLDPENKLEFEPDSEDI
		1				ISDCEEGLSNVALECSEPSTSVSAYDQLKAPA
	1	]				SPGAGNPPGTPKGKRELMSNGPGSIIGAKAG
	ł	ì				NSGKKKGLNNELNNLPVISNMTAALDSCSA
		- 1			1	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK
		1				ANNCKTDKN\PSKLKSARPIAPAPAPTPPQLL
	}	1	Į.			IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPP KPIQPKPTIMGEPITVNPALVSLKDKKKKKKK
	İ			1		KLKDKEGKETGSPKMDAKLGKLEDSKGASH
		1	ļ			DLPGHFLKDHLNKNEGLANGLSESQESRMA
						IKAEADKVYTFTDNAPSPSIGS
	1				<del></del>	TRRGQPWRRRAAAAGILPGREAAACLPSC/A
1139	2489	A	9234	207	443	VTAAVSGLLVGYELGIISGALLQIKTLLALSC
						HEQEMGVSSLVIGALL
				<del> </del>	338	MAQGNNYGQTSNGVADESPNMLVYRKV
1140	2490	Α	9238	248	328	FVEAAVKMLGSLVLRRKALAPRLLLRLLRS
1141	2491	A	9242	2	535	TLRGHGGASGRNVTTGSLGEPQWLRVATGO
		1				RPGTSPALFSGRGAATGGRQGGRFDTKCLA
			1			ATWGRLPGPEETLPGQDSWNGVPSRAGLGN
						WPWAAALVVHCYSKSPSNKDAALLEAARA
						WMQEVSRNRCALLHSAAVQEYGYGN
}						HLCFWFFVGLFLPEQQIMLFATLLRMAQGC
1142	2492	A	9245	157	466	FALGNDFLNITTKAQA/TKEKLDKLDFIKIKT
1						CTSMDAIEKTEPLTKWTKAFVSHVSYKRLL
		1				
			1			GICKEYSRQ  GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPD
11.13	2493	A	9247	264	115	Pride Control of the
1143	2473	,				ARDSTSIIRMGPEIPPP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Giutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	Ì	ļ	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide	Sequence	/=possible nucleotide deletion, \=possible
		1	1	sequence	1	nucleotide insertion
	0.004	<del>  </del>	9260	Sequence	401	KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCGI
1144	2494	A	9200	1	101	SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE
	Į.	1	Ì	1	1	AMEESDRPCEISEIDDNPKISENPRRSPTHEKN
	1			ļ		TMGAQEAHIYVKTVAGSEEPVHDRYRPTIEM
	1	1	1			ERRR
1146	2495	A	9264	175	411	METIWIYOFRLIEIGDSTVGKSCLLHRFTQGRI
1145	2493	A	9204	173	1 ***	PGLRSPACDPTVGVDFFSRLLEIEPGKRIKLLL
		1				WDTAGOERFISIT
1146	2406	A	9277	592	814	MFTYLEGREGIKSOPKMEPHSVT\RLECSGMI
1146	2496	A	9211	392	014	SAHCSLNLPGTSDSPASASR/VAGTTGMRHHA
		ļ		1		WLIFAFLVETGF
1147	2407	A	9279	1255	2	FRRGRRGEEEKEEEEEEEGWVNGMENSHPF
1147	2497	1 ^	32.13	1 1233	-	HHHHOOPPPQPGPSGERRNHHWRSYKLMIDI
						ALKKGHHKLYRYDGQHFSLAMSSNRPVEIV
		ļ				DPRVVGIWTKNKE\LELSVPKFKIDEFYVDQ\
	1	İ			ļ	PPKOVTFAKLNDNIRENFLRDMCKKYGEVER
		ŀ	1			VEILYNPKTKKHLGIAKVVFATVRGAKDAVO
	1		1		1	HLHSTSVMGNIIHVELDTKGETRMRFYEL\L\
						TGRYTPQTLPVGELDAVSPIVNETLQLSDALI
		1	1			RLKDGGLSAGCGSGSSSVTPNSGGTPFSQDT
	1	ļ	1		}	YSSCRLDTPNSYG/QGTPLTPRLGTPFSQDSSY
		ł			1	SSRQPTPSYLFSQDPAVTFKARRHESKFTDAY
	1	i i	1 .		NRRHEHHYVHNSPAVTAVAGATAAFRGSSD	
	1		1		LPFGTVGGTGGSSGPPFKAQPQDSATFAHTPI	
	}	1	1		J	PAQATPAPGFR
1148	2498	A	9302	1026	6	IASIQNADTMPGVGLLVSHFSTLVSRQRCPNY
			ľ	1	·	ADPONLTDVSIFLLLEVSGDPELQPVLAGLFL SMCLVTVLGNLLIILAISPDSHLHTPMYFFFSN
		1	1	]	1	LSLPDV\GFTSTTVPK\MIVDI\QSRSRVISYAG
			[	İ		CLTQKSLFAIFGGTEE\NMLLSVMAYDRFVA
	,		1			CHPLYHSAIMNPCFCAFLVLLSFFFLSLLDSQ
	1		1			HSWIVLQFTIIKNVEISNFVCDPSQLLKFACSI
	1	ł	ì	ł		SIINSIFIYFHKDPERQLVLAGLFLSMCLVTVL
		1	1			GNLIILDVSPDSHLPTPMYFFLSNLSLPDIGFT
		1				STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAI
	1				1	GGMEERHAPECDGL
	1	+	0202	<del>                                     </del>	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE
1149	2499	A	9303	1	1077	FRLVAADRSMGRYMLFGVINLICTGFLLMW
		1				SSTNSIALT\SYTYLTIFDLFSLMTCLISYWVT
				1		RKPSPVYSFGFERLEVLAVFASTVLAQLGAL
		j	1	1		ILKESAERFLEOPEIHTGRLLVGTFVALCFNL
			1			TMLSIRNKPFAYVSEAASTSWLQEHVADLSR
						SLCGIIPGLSSIFLPRMNPFVLIDLAGAFALCIT
	İ	]				YMLIEI
1150	2500	<del> </del>	9308	797	693	DRSTSVTRAGVQWCSLGSLQPRTPGLLRSSC
1150	2500	A	9308	1 '3'	""	SLP
1161	2501	<del> </del>	9309	205	406	VAIKELPVLWKWSKPTR\TAKEPPQTQQRAG
1151	2501	A	7307	1 203		SKTAAPPCQWSRMASEGPNIPCPGARHSDKC
						FLICTI
1155	2502		9314	913	504	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV
1152	2502	Α	9314	313	1 304	QGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRF
	1			1		PPPHR\EIFFVFLAETGFHRASQAGPDLPTS/S/
				1	1	PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL
	-				İ	GTNVSLRAA
				1202	1	HPHRPRPGFRSPARSSRPCPVLTSLLPPFPSPS
1153	2503	Α	9315	392	1,	PADDLVKAGRDRKDPQVR/ERRLRPNPGRLC
		1	1			GPR\PRPARARS/CHQPRLTRVCPRSPPPEARA
						PAPAAPARGRGAPKRNRPRTDTRAPRGSSAF
l		1	1		ļ	PGNS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ł	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
Ì			1	residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
	0.504		9321	sequence 331	433	MPCI/QAQYGTPAPSPGPRDHSASDPLTPEFIK
1154	2504	Α	9321	331	433	PT
	0505	<del> </del>	9324	180	275	MEEPQSDPSVEPPLSQETFSDLWKLLSENNVL
1155	2505	A		383	619	MISPSRTEGDPLPLPP/EGEGQEVRGFGGGPAK
1156	2506	Α	9326	303	019	EAAQRHCRASVSILRMRRPGQGSSRPARVPL
ı		{		l .	1	RGPDSHRLREPPPSPP
	0507	<del>  </del>	9327	152	292	YERRGRSQGGGSHPAGAQPGGRAIGAGWQS
1157	2507	A	9321	132	232	KEPLWEGLQRSGSPLPG
1150	2508	A	9328	1	430	QELKQGPNPLAPSPSAPSTSAGLGDCNHRVD
1158	2308	A	9328	1	1430	LSKTFSVSSALAMLQERRCLYVVLTDSRCFL
1			1		1	VCMCFLTFIQALMVSGYLSSVITTIERRYSLKS
						SESGLLVSCFDIGNLVVVVFVSYFRGRRRRP/
1	1		1			RVAAVGGLLDLEGGEMI
1159	2509	A	9334	108	383	KGNQVNGNGNQLKRKHESMCPVSLTQNTVR
1139	2309	A	3334	100	303	LMEAGLPOKQAERADELFEAGLVIYVKLDER
1						VLNAL\YSSVGLQWFKESDLSHLRLLEISFR
1160	2510	A	9338	2	430	FVGRPRGLSDRLEDLFLAGFRVGERLRTAAM
1100	2510	1	9556	1	130	KRYVRILLLGEGAEHVADPVPGGRGVPRGEA
	1					DHTDQELREEIHKANVERVVHDVSQEATIEKI
İ		1	4			RTKWIPLV/RWGDHA/EGPVGIKSYLPSGRSM
1		<b>,</b>	1	İ		EAELPIMSQLTEIETCVEC
1161	2511	A	9341	1	390	NSRVDDFVAPGLSEAGKLLGLEFPERQRLAA
1101	1 2311	1 **	133	1		AVG/CSPMSGVISMSAPFFLGKIIDAIYTNPTV
	1					DYSDNLTRLCLGLSGVFLCGAAANAIRVYLM
	1					QTSRQRVVKRLRTSLFSSILGQEVAFSDKAGT
j		1	1	]		GELI
1162	2512	A	9343	84	837	QGRFRAFCWQRDFLQPPGMRLSALLALASKV
1		1				TLPPHYRYGMSPPGSVADKRKNPPWIRRRPV
1		1			}	VVEPISDEDWYLFCGDTVEILEGKDAGKQGK
1			1	1		VVQVIRQRNWVVVGGLNTHYRYIGKTMDYR
			ł			GTMIPSEAPLLHRQVKLVDPMDRKPTEIEWR
		1				FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET
	1					WIDGPKDTSVEDALERTYVPCLKTLQEEVME
ĺ						AMGIKETR'NTRRSIGIEPGAEQLLPNFCPSLE
				<u> </u>	<u></u>	G
1163	2513	A	9346	967	616	DSLALSPRIECSGAISAHCNLTPPGFTPFSCLS
			1	1	}	LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ
				1	1	AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT
						FSSYQRNNPDLILNDTIMPNIK
1164	2514	A	9347	3	1099	SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL
1				1		FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV
1						VAGASVGAGVWARNPRYRTEGEACVEFKA
		1	1	1		MLIAVGIHLLLLMFEVLVCDRVERGTHFWLL
}		,		1	)	VFMPLFFVSPVSVAACVWGFRHDRSLELEILC
			1			SVNILOFIFIALKLDRIIHWPWLVVFVPLWILM
		1				SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH
					1	VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS
1		1			1	YVSIFVPLWLSLLTLMATTFRRKGGNHWWF
						AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA
		1				LPLQNKDRGSWPASRGSPRLL
	J	<del></del>	10000	547	001	DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP
1165	2515	Α	9362	547	991	VPEGVRLADGPGHCKGRVEVKHQNQWYTV
1					1	COTGWSLRAAKVVCRQLRCGRAVLT\QKRC
1	ļ				1	TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP
						LGEDTLFHVEYTSVHGRERLSAKD
	4	+	0262	201	707	PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS
1166	2516	A	9363	201	387	GAISAHLAHCNLCLPGSSDSPASAFQVAS
1.7=-	1222	<del></del>	0360	707	1087	AVLTPCLSPCSPSRIPRP\SRPYPGRRSLSHTPP
1167	2517	A	9368	707	1007	ATEIT CEGI COI GIGITA GIG IT GIGGESTITT

NO: of nucleotide sequence NO: of nucleotide seq	EQ ID NO: of exptide eq- ence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide	Predicted end nucleotide location corresponding to last amino acid residue of peptide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
nucl- eotide seq- uence  1168 2	eeptide eq- eence		in USSN 09/496	nucleotide location correspondi ng to first amino acid residue of peptide	location corresponding to last amino acid residue of peptide	F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
eotide se seq- uence ue	eq- eence		USSN 09/496	location correspondi ng to first amino acid residue of peptide	to last amino acid residue of peptide	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
seq- uence ue	ence		09/496	correspondi ng to first amino acid residue of peptide	to last amino acid residue of peptide	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
1168 2				ng to first amino acid residue of peptide	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
1168 2	2518		914	amino acid residue of peptide	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	2518			residue of peptide		T=Threonine, V=Valine, W=Tryptopnan,
	2518			peptide		
	2518				sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	2518				}	/=possible nucleotide deletion, \=possible
	2518			sequence		nucleotide insertion
	2518		i			PRPLILYAPAP\RPAGTAFIPHSHPPPPDLLRPT
	2518					ATPA/TPCPSLPPPPRPLHPTQPSTALLPDPPPW
	2518		1		1	PLPFPPPSS/RPPRPDCSTSYSPTFPPPT
	2310	Α	9375	511	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS
	•		1			PITVTSAVIIVLMLLMM/IFSPWLATHDPNAID
			1	[		LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS
				1		QQSILAGLVVVATTGMIGSPLECLFGELGGRA
						DAIFMRVMDIMRS/IPSLVLTMEKTAALGPSL
						FNAMQASSEH
1160	2519	Ā	9377	42	410	GNGRVAPRDPGAVASAEPGLTTHDSGVNPN
1169 2	2319	Α.	9577	172	1	NSARRMEAMASGSNWLSGVNVVLVMAYWS
			ļ.			LVFVLLFIFAKRQIMRFAMKSLRGPHGPVGH
1			1		ŀ	NAPKDLKEEIDILLSRVHNIKYEP\HLLADDDA
<b></b>		<u> </u>	9378	302	1303	GVSGFSASVLRQRRMEDELEPSLRPRTQIQGR
1170 2	2520	Α	93/8	302	1,303	ILLLTICAAGIGGTFQFGYNLSIINAPTLHIQEF
1		[		1		TNETWQARTGEPLPDHLVLLMWSLIVSLYPL
! !			1		1	GGLFGALLAGPLAITLGRKKSLL\VNNIFVVS
		1	1			AAILFGFSRKAGSFEMIMLGRLASWGVNAGV
1		ł	ł		1	SMNIQP\MLPGGESAPKELRGAVAMSSAIFTA
						LGIVMGQVVGLSTTAATGLRGL\AGELEELEE
1		ì				ERAACQGCRARRPWELFQHRALRRQVTSLV
		}	1	İ		VLGSAMELCGNDSVYAYASSVFRKAGVPEA
1			ļ			KIQYAIIGTGSCELLTAVVSVSLEGALPPPAL
1		1				WGGTPRSFALNQFTLQKKKK
		ļ.,—	9381	2	412	RGPASAQEDERARTAPLERVRARGRMTTSSA
1171 2	2521	A	9381	1 2	712	LFPSLLPCSWSTSNKYLAEFRAGKMSLKGTTE
1		1		1		TPDKRKGLAY/IQQTDDSLIHFCWKDRTSGNV
		ļ	ļ		İ	EDDLIIFPDDCEFKRLPQCPNGRVYVLKFKAG
1		1	ł			SKRLFFWMQEP
-	0.500	<del></del> -	0204	20	355	GWNGRSTEASPAAEAPHVPHKET\KAAMGTQ
1172	2522	Α	9384	20	1 333	CTHGGKVRPDPHDMLTTVVHKIKLFVLCHSL
1 1		ł	1		}	LQLCAIMISDYLKSSIYTVEKRLGLFRPTSGLL
						ASFNEVGNTALIVLESY
		<u> </u>	0202	120	87	LCQCIVPGQQKETFSLNPSSATVRFYL*LSLQ
1173	2523	A	9393	430	0/	QRKEDQ*IIL*YHLNKDCLHIFMSAITLYMKI*
				1		KIFVLFDFNIMFETPFYII*FIFLFSQNLKRIRQV
] ]		Ì	1	}	}	IRPPISFSKINNGP
<u></u>		<u> </u>	J	<del></del>	1274	ERLEIGRLGGERGSGPASCLRVIDVSGMWDQ
1174	2524	Α	9397	77	374	RLVKLALLQLLRAFYGIKVKGVRVHRDCGTF
1		1	1			ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF
1			1			
		<u> </u>			1	LGML HESSRADRDKMDTRGSTYTDADPVNKSGGT
1175	2525	A	9399	66	397	HESSKADKUKMUTKOSTTTDAUPVNKSOOT
		1	1	1	Í	AKMNKWSKGKVRDKLNNLVLFDTATYDKL
1						CKEVPNYKLITLAVVSERLKIPGSLARAALHE
		1	1			LLSRGLI*LVIQHIAQVIY
1176	2526	A	9408	2	299	LDLTHVLSLSISLTVTILGTTFGMVIPLLDVVY
	-	1				GERGYAQNGDF*DAQLDDYSFSCYSHAQVN
1		1		I	1	GAPNSLTRAYDDP*VKISGLECQKVGALVEV
		1				KCLNL
1177	2527	A	9416	2	402	CNFLRSSRIRVHSTPAASTMPPKVDPNEIKVV
1		1.,	- ' - '			YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD
					1	FV*ATGDWNVLIISVILTIRILLSHIFVVPPFFCF
		1		ł	1	DHLIAFWDLQSLIFLHVIFSLFITLLLFCFFSIF
1178	2528	A	9419	142	426	TPLFDLWPRVVLSWLETVLTSLRTRRAASGPP
	2220	^	7717	1		ACRIMPTTVDDVLEHGGEVHFLQKQMLYLL
11/0		1		}		ALI*DTFAPIYVGIVFLGFTPDHRCRSPGVAEL
1110		1		4	1655	LSSAGTKMNLN*KNYWPGASAHACNPSTLG
	2620	+	0420	1 1450	י וחוי	
	2529	A	9420	1450	1033	GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA

						Amino acid sequence (A=A)anine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN 09/496	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		1	correspondi ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
İ		ŀ		peptide	sequence	/=possible nucleotide deletion, \=possible
	,		1	sequence		nucleotide insertion
4400	2520		9422	176	375	HRPQTTRPDWKPRT*PQGK*GRLSSEISPASPP
1180	2530	A	7422	170	373	SRFSRSTKPVPPKADPPARQKLTGVLHAPLLK
		1				L
1181	2531	A	9436	2	274	PIAASLRMYNLQPYTEENLICTAFATMVETVP
1101	2331	1	/150	~		IARTILDRLTGIPHGYCFVE*ADWATADKCVH
	ì	1	Í	1		IYNGKPLPGATPLLSLQLHQLAHLGS
1182	2532	A	9442	3	240	VDKCSSKSIVLSEYCPHCMCSLSTDPKPFGQL
1102	2332	1.	1			SMILK*MGAGDEKISAMGKARVDHRELYLGL
						LYPTEDYKLTFRARH
1183	2533	A	9444	384	3	LKDFQPWALHDWPLFCCCTFLLFLVLECFTR
1105						KGCSGWAPWLSLQCQHFGRPRWADHLRSGV
		1				RDQPGQYSKTTFLPKIQKLAGHSGAHL*S*LL
1		]	į			ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT
						ERG
1184	2534	A	9462	391	655	LSGFKSLMPKIPLQYIYVRVRTTWSFCLPLDG
						RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV
İ			-	1	_	IHTCNPSTLGGRAGWIV*AQEFET
1185	2535	A	9467	215	566	RCPMWQGQASRMDPAKAKDREASTCCSLA
1100						WWWGWECWVRALKLSSGPAGPLACWVAK
Ì	1	İ				KKSLSLSGPVYPSEKGAGLYVF*DRVSLCHPG
						WSAVVQFWLTAASNSCFSLLSSWDYRCA
1186	2536	A	9468	275	452	HIPQLHTKTHYVPTRMVNKI*QIDNSKPWQR
			İ			GG*TGILTHCW*ESKLVQPLWKIVWHYQ
1187	2537	A	9469	388	3	EVAPGPSQILPRRVTDGGDRPQFSLPGPRLPQ
						SSRGAEPCLSNCIHSPAPRKQRMGDSDQ*STP
1	1	ì		Ì		NPASPHPEAPQEPWDSASGSVGSFSLGRGAK ASS*VPGKGRGPRQGSELLAETILELFLALAN
						S S
			0.151	104	397	TMDKKNRHGNSLDMASEIHMTGPMCLIENTT
1188	2538	A	9471	124	397	GRLMANPEALKILSAITQPMVEEAIAGLYRAC
	}	į				*FYLTNNLAGMKKGLCLGSTEQAHTIGI
		<del> </del>	9480	584	769	GHVQSQHFGRPRRADHLRSGDRDHPG*HDET
1189	2539	Α	9460	364	103	PSLLKIQKISWAWWRAPVVPATWEAEAEEW
		}	]	}	ļ	R
1190	2540	$+_{\overline{A}}$	9483	463	86	VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL
1190	2540	^	7103	102		PROHCTLOTHRHLHPEAPVKV*KT*RLFPGLR
		1				GASSCRRRRCNPVLAARKAGSPRSHSTRENC
		İ		1		RRSRCPDTAHRRRRRGRRRNPSCVRSPRWR
1191	2541	+A	9489	1	411	LADALCLSAAATGAVRPGARAQPSTRRRLSP
1171	2271	1	1	1		SVRVCCRAAAASNLLYSSCLQRHSERASEEG
		,		1		ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI
				1		MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ
						KEEELTAVNVK
1192	2542	I A	9497	389	161	VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI*
					1	CEEDERKMAREFLAEFMSTYVMMNIHMIVE
1		1				KDTYSDHEEINTS
1193	2543	A	9509	186	1	IAKSQ*KRWQRSGAMETLKHGWWECKLVQF
				1		FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM
1194	2544	A	9512	58	433	PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL
				}		LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA
	-	1				SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI
}				<u> </u>	<u> </u>	RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ
1195	2545	A	9515	595	1223	GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP
1		1	1			AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC
1			1			PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP
1	- 1	1				LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL*
1	- 1					
	1		1			PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP
						APGSGPCGATARPSRGGRAGGSRARRPIPPGP GTRRTPSGCQNPAASGG

		154	Loro	D-distant	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of peptide	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
neuce	delice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ucija		{	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	1 '	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
1196	2546	A	9518	229	468	RSPTATPAPHAMGPGAPFARGGRPLPLLGAM
						AERVAPGWDLHTPYLPRTNSRRTPHL**EPHA
		1	}		1	GYIGALFPMSGGWPGGQ
1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG
		İ	1			HAMRHLTGNTSMAIRFL*ADSRFQVQRARYE
					<u> </u>	APNWKYKYGY*IPVDMLC
1198	2548	A	9524	204	1	KNKKTTKCLSIVTLNISGPNQ*NKRHRVAEWI
	İ		Ì			VKQEPNICHL*ETHFPFRDTYRLKEREQKKRK
		ļ				SSYS
1199	2549	A	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA
	_				<u></u>	V*QRGDGKNPGVTHLNRPVGTX
1200	2550	Α	9548	186	1-1-	VNAEKEF*KIQHYFMTKSQNKLHIEHTYLKPI
		<u> </u>				KAIYDKWTSDIMLNLQKL*AFFLRVIVRQI SSVVEFPRGPRSSLPPLDSTFPCGSSPNWTGGO
1201	2551	Α	9549	591	2	GSCPSGE*LVSPGSEQRKKYSNSNVIMHETSQ
						YHVQHLATFIMDKSEAITSVDDAIRKLVQLSS
			Į.	ļ		KEKIWTQEMLLQVNDQSLRLLDIESQEELEDF
		i				PLPTVQRSQTVLNQLRYPSVLLLVCQDSEQSK
	1	1				PDVHFFHCDEVEAELVHEYMESALTDCRLGK
		}			}	AMRP
1202	2552	<del> </del>	9552	428	<del>                                     </del>	KYGNEGHWSRQCPNPGKPIRPCPLCRGPHWK
1202	2552	2552 A 9552	9332	420	1	LDCERPPQGPLPSLPELAKTSYSDLTGLATED
						*WGPGMDAPATTIASSKTRVTLMVAGRPVFF
						LI*YRATYSALPNFSGPTQSSQVSVVGIDGQV
						SKPRATPPLFCSLHTF
1203	2553	A	9568	517	738	RRKFERKQKQ*RYREGKQYRQRDKMKEWG
	0.2.2.5	1				EKEKRRREKGEREERKMRHRERKGESGQRD
		İ				TMENWRVERLTEKER
1204	2554	A	9573	83	415	EDKRLRLVDGDSRCAGRV*IYHDGFWGTICD
	}	]			1	DGWDLSDAHVVCQKLGCGVAFNATVSAHFO
		1				EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ
						HDCRHKEDAGVICSEFTALR
1205	2555	. A	9577	64	424	ARGSCPTRPRTANGRMGETKDAPQMLVTFK
			1			DVAVTFFREEWRQLVLVHRTLYR*GMLETC
						GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE
						VSHSPCAGDMRELFTREATLTPHPYNNGA TLGAVLFSEVSKESSTSHSGGOLGRONRHPKL
1206	2556	A	9584	38	476	SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV
						NPQPLSTPSWQIETKYSTKVLTGNWMEERRK
		}		1	}	GLPYKHLITHHQEPPHRYLISTYDDHYNRHG
						YNPGLPPLRTWNGQKLLWL
		<del>   </del>	-	<del> </del>	412	LRSSPAALLRALCITTVTGTALALRSRVATTN
1207	2557	A	9586	2	412	PDGCRNVLRPKYYRLCDKAESWGIALETVPT
		1	1	1		GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP
				1		THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL
						FGILFSICFS
1000	10555	<del>   </del>	0507	122	3	IKNYWPGMVAHACNPSPLGGRGRWIA*AQK
1208	2558	Α	9597	122	٦	FADAWADAW
1200	2550	+	0611	148	558	KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK
1209	2559	Α	9611	140	ا ا	GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ
	1	ĺ				RIRDHDLLDKRKTVTALKAGEDRAILLGLAM
		1	]			MVCSIMM*FLLGITLLRSYMQSVWTRESQCT
		1		1		LLNASITETFNC
1010	1000	+	0610	284	2	SLHDMLMLAEQQQKQKWAVNTQNTAWSNA
1210	2560	A	9618	384	1 4	DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI
		-				KVQVKNNDLGLQATINNEANWIAHQDDFNW
		1		1	}	LLAELNTCQRQETADS***WSPKNSHVGKDS
				1		GELSAK
101-	10000	<del> </del>	0620	216	610	OKHPGGGQLGRSPQEDSRFHNKASSGVSRVR
1211	2561	A	9620	316	1010	ATTH GOOGLOTAL GEDORG THE RESIDED . BICKE

			650	Dedistad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ	ļ	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	{		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		Į.		residue of	sequence	/=possible nucleotide deletion, \=possible
		t		peptide		nucleotide insertion
	j	ł		sequence		LGRAWWLTPVIPTLWEAKAGGSPE*D*AGRG
						LGRAWWLIPVIPILWEARAUGSE'D AURU
	l .			1		GSRL*SQHFGRPRRVDHLRSAVQDQPGQHGE
	ì	ļ		}		TPSLLKIQKIN*VWGRRL*SSYSEAEAGESL
1212	2562	A	9623	297	344	QFPVDGDYQKIEKITQLFQAQNLSLCLAMTR
12.2	1					TREL*KGGGKGRHE*AVVPFLKKGGYGVKAP
	1	1				AILNTSNCT*CF*ETKMLSDDPKACVFEVSSA
		1		ļ		DL*NTSFGVIR
1213	2563	A	9624	2	356	AELSLASTACGRNTSGDSLPDYDRAPISSPLA
1213	2303	' *	302.	_		TSGTILSAISCLWDLPTPVLRVGLSCQPSMSSQ
		1		l .		IPRMYSTDVEAAVNSLEDLYLQAYYAYLCVG
	j	}	j		'	LYFHRDDMALEGVSRFL*ELAE
1014	2564	A	9634	776	912	SLSRWVRAKL*VPYNQENCLNPRGGGCSEPR
1214	2304	^	7054	1 // 0		SHYCTPAWATEKDS
	0000	+	9636	220	426	KPGNFAVSSEY*DITSGQLKTAVRG*IEMTST
1215	2565	Α	9030	220	120	EENFGEKLHDIGFGNGFLDKT*KAQATKAKI
					1	DK
	<del></del>		9637	391	76	CELEDGCTOAS*AEEAAVSPSMAEEEQGSTSC
1216	2566	A	9637	391	/*	RERRSIRFKMKNHSPDDTIKENVTISNIRTRKI
					1	NHLPETERNLLEHGLMYIRLNAAFCSLVAHS
	İ					LFGFILKAT
				2008	2432	LHCKMGALETQTHPCSQNMLRSLQKCCCKV
1217	2567	A	9655	2008	2432	EEHHLQPVQVLQTLLHSATAGTGCRRPARPP
	1	1				PAPPTPTPWRSRQSGKQSERAS*LKGRGRYGL
			ĺ			GALGGRGGRALGGSRWPPPLPGETLFSGCKH
	ļ	ì				RRRRGSDAAPGEEAGT
			0.650	<u> </u>	405	HASARALLSPNLSPNNKMAISGGPVLGFFIIA
1218	2568	Α	9658	3	403	VLMSAQEPWAIKEEHVIIQAEFYLNPDQSGEF
	i			<b>\</b>		MLDFEGEDTFHGDMAKKETVWRLE*LARLD
	1	1	1			NFEAQRALANIAADQAALEIMDMGSDYTLIP
	ì	-				NVPPKVTVL
					284	PDWTEKRKMQDTGSILPLHWFGFGYAALVA
1219	2569	A	9662	3	284	YGGIIGYVKAGSVPSLAAGLLFGSLSGLGAYQ
		İ	ı	l		LSQDPRNVWVFLATSGTLAGIMGMRFYHSG
ł						KL
					(00	LLLTGYIQTLQNQQLSGNQQEMQAVDNLTSA
1220	2570	Α	9669	200	699	PGNTSLCTRDYKITQVLFPLLYTVLFFVGLITN
ļ	1	1			1	GLAMRIFFQIRSKSNFIIFLKNTVISDLLMILTF
ļ			-		1	PFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYI
1			1			SISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
		}				
	1	<u> </u>			J.,	KERDSSTFSAAMTTMQGMEQAMPGAGPGVP
1221	2571	A	9676	164	562	QLGNMAVIHSHLWKGLQEKFLKGEPKVLGV
1				1		QLUNMAVIDALWAULQEATLAGERAVLUV
				1		VQILTALMSLSMGITMMCMASNTYGSNPISV
1			1			YIGYTIWGSVMFIISGSLSIAAGIRTTKGLVRG
1			1	[		SLGMNITSS SLGMNITSS
1222	2572	A	9688	43	412	VAKMVKCCSAIGCASRCLPNSKLKGLTFHVF
1.222	23/2	' '		1		PTDENIKRKWVLAMKRLDVNAAGIWEPKKG
		1				DVLCSRHFKKTDFDRSAPNIKLKPGVIPSIFDS
						PYHLQGKREKLHCRKNFTLKTVPATNYNH
1000	2573	+	9696	308	564	RTSMGILYSEPICQAAYQNDFGQVWRWVKE
1223	25/3	A	7070	1 300	1	DSSYANVODGFNGDTPLICACRRGHVRIVSFL
					1	LKKECLCOPOKPERENLLALCCE
			0700	<del> </del>	632	DAWASGGELGSLFDHHVQRAVCDTRAKYRE
1224	2574	Α	9700	3	032	GRRPRAVKVYTINLESQYLLIQGVPAVGVMK
						ELVERFALYGAIEQYNALDEYPAEDFTEVYLI
	1					KFMNLQSARTAKRKMDEQSFFGGLLHVCYA
1						PEFETVEETRKKLQMRKAYVVKTTENKDHY
ļ			}	1		VTKKKLVTEHKDTEDFRQDFHSEMSGFCKA
1		ļ	1	1	(	ALNTSAGNSNPYLPYSCELPLCYFSSK
j	- (	1				

SEQ ID   SEQ ID   Met NO: of nucl-   NO: of nucle-   No: of nucle-   seq-   uence   uence   vence	GKWS TVDT TLLYG /NYI RVCQ RGNG
nucl- eotide seq- uence unce unce unce vence unce venc	TVDT TLLYG /NYI RVCQ RGNG
eotide sequence   USSN   10 cation corresponding to last amino acid residue of peptide sequence   2575   A   9710   1   163   163   17   17   17   17   17   17   17   1	TVDT TLLYG /NYI RVCQ RGNG
to last amino acid residue of peptide sequence  1225   2575   A   9710   1   163   163   163   164   1	TVDT TLLYG /NYI RVCQ RGNG
1225   2575   A   9710   1   163   RSGCVLRMTEWETGAPAVAETPDIKLF	TVDT TLLYG /NYI RVCQ RGNG
uence    914   ng to first amino acid residue of peptide sequence   pe	TVDT TLLYG /NYI RVCQ RGNG
amino acid residue of peptide sequence	TVDT TLLYG /NYI RVCQ RGNG
peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide insertion   peptide insertio	TVDT TLLYG /NYI RVCQ RGNG
1225   2575   A   9710   1   163   RSGCVLRMTEWETGAPAVAETPDIKLFI   TDDVHINDISLQDYIAGVRLILL   1226   2576   A   9713   82   492   QGLPSFLPAFGPSGSWLGPAPTLGSSCN   CHGYSEIRPLFYLSFCDLLLGLCWLTET   ASVANKDIICYNLQAVGQIFYISSFLYTWYLYTELRMKHTQSGQSTSPLVIDYTC   MAFVFSSLI   GKWKRTQVPLLGECADMDLARKEFL   LAAGKMNISIDLDTNYAELVLNVGRVT   NRKKMKDCQLRKQQNENVSRAVCALL   GVIKAEVENKGYSYKKDGIGLDLENSF   PFVPNFLDFMQNGNYF   EASSNTVASNVADKTDPHSMNSRVFIGTLVLQKSDVEAVF   1229   2579   A   9725   121   902   LFAMSGFENLNTDFYQTSYSIDDQSQQ   GGSGGPYSKQYAGYDYSQQGRFVPDD   QQPYTGQIYQPTQAYTPASPQPFYGNN   PLLEELGINFDHIWQKTLTVLHPLKVAI   NETDLAGPMVFCLAFGATLLLAGKQF   GISAIGCLGMFCLLNLMSMTGVSFGCV   GYCLLPMILLSSFAVIFSLQGMVGIILTA   WCSFSASKIFISALAMEGQQLLVAYPCA   VFALISVF   TFVLNMNTPKEEFQDWPIVRIAAHLPD   HFSPERPFMDYFDGVLMFVDISGKCKR	TVDT TLLYG /NYI RVCQ RGNG
1225	TVDT TLLYG /NYI RVCQ RGNG
1225   2575   A   9710   1   163   RSGCVLRMTEWETGAPAVAETPDIKLE   TDDVHNDISLQDYIAGVRLILL	TVDT TLLYG /NYI RVCQ RGNG
TDDVHINDISLQDYIAGVRLILL  1226 2576 A 9713 82 492 QGLPSFLPAFGPSGSWLGPAPTLGSSCN ICHGYSEIRPLFYLSFCDLLLGLCWLTET ASVANKDIICYNLQAVGQIFYISSFLYTV WYLYTELRMKHTQSGQSTSPLVIDYTC MAFVFSSLI  1227 2577 A 9720 3 416 GKWKRTQVPLLGEECADMDLARKEFL LAAGKMNISIDLDTNY AELVLNVGRVT NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF  1228 2578 A 9723 278 411 EASSSNTVASNVADKTDPHSMNSRVFIGTLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQ GGSGGPYSKQYAGYDYSQQGRFVPPD QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHELKVAL NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGILLTAWCSFSASKIFISALAMEGQQLLVAYPCALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	TLLYG /NYI RVCQ RGNG
ICHGYSEIRPLFYLSFCDLLLGLCWLTET ASVANKDIICYNLQAVGQIFYISSFLYTV WYLYTELRMKHTQSGQSTSPLVIDYTC MAFVFSSLI  1227 2577 A 9720 3 416 GKWKRTQVPLLGEECADMDLARKEFL LAAGKMNISIDLDTNYAELVLNVGRVT NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF  EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQ: GGSGGPYSKQYAGYDYSQQGRFVPPD QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPC VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	TLLYG /NYI RVCQ RGNG
ICHGYSEIRPLFYLSFCDLLLGLCWLTEJ ASVANKDIICYNLQAVGQIFYISSFLYTV WYLYTELRMKHTQSGQSTSPLVIDYTC MAFVFSSLI  1227 2577 A 9720 3 416 GKWKRTQVPLLGEECADMDLARKEFL LAAGKMNISIDLDTNYAELVLNVGRVT NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF  EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQI GGSGGPYSKQYAGYDYSQQGRFVPPD QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAL NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	/NYI RVCQ RGNG
ASVANKDIICYNLQAVGQIFYISSFLYTY WYLYTELRMKHTQSGQSTSPLVIDYTC MAFVFSSLI  1227 2577 A 9720 3 416 GKWKRTQVPLLGEECADMDLARKEFL LAAGKMNISIDLDTNYAELVLNVGRVT NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQ: GGSGGPYSKQYAGYDYSQQGRFVPPD QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPC VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	/NYI RVCQ RGNG
WYLYTELRMKHTQSGQSTSPLVIDYTC   MAFVFSSLI	RVCQ RGNG
MAFVFSSLI	RGNG
1227 2577 A 9720 3 416 GKWKTQVPLLGEECADMDLARKEFL LAAGKMNISIDLDTNYAELVLNVGRVT NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF  1228 2578 A 9723 278 411 EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQ GGSGGPYSKQYAGYDYSQQGRFVPPO QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGILLTAWCSFSASKIFISALAMEGQQLLVAYPCAVFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	RGNG LGEN
LAAGKMNISIDLDTNYAELVLNVGRVT NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF  EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQI GGSGGPYSKQYAGYDYSQQGRFVPPDI QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	LGEN
NRKKMKDCQLRKQQNENVSRAVCALI GVIKAEVENKGYSYKKDGIGLDLENSF PFVPNFLDFMQNGNYF  EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQI GGSGGPYSKQYAGYDYSQQGRFVPPDI QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	
GVIKAEVENKGYSYKKDGIGLDLENSF. PFVPNFLDFMQNGNYF  EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQI GGSGGPYSKQYAGYDYSQQGRFVPPDI QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	NSGG
PFVPNFLDFMQNGNYF  1228 2578 A 9723 278 411 EASSSNTVASNVADKTDPHSMNSRVFIG TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQQ GGSGGPYSKQYAGYDYSQQGRFVPPDI QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	SNML
1228 2578 A 9723 278 411 EASSSNTVASNVADKTDPHSMNSRVFIGURE TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQGGSGGPYSKQYAGYDYSQQGRFVPPDIQQPYTGQIYQPTQAYTPASPQPFYGNN. PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMYFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGILLTAWCSFSASKIFISALAMEGQQLLVAYPCAVFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD. HFSPERPFMDYFDGVLMFVDISGKCKR	
TLVLQKSDVEAVF  1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQQQYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAL NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGILLTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	TNIN
1229 2579 A 9725 121 902 LFAMSGFENLNTDFYQTSYSIDDQSQQQGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	311211
GGSGGPYSKQYAGYDYSQQGRFVPPDI QQPYTGQIYQPTQAYTPASPQPFYGNN PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	שלעטע
QQPYTGQIYQPTQAYTPASPQPFYGNN. PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	MACO
PLLEELGINFDHIWQKTLTVLHPLKVAI NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	CEDED ATMIGI
NETDLAGPMVFCLAFGATLLLAGKIQF GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	CODA
GISAIGCLGMFCLLNLMSMTGVSFGCV GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	ODIM I
GYCLLPMILLSSFAVIFSLQGMVGIILTA WCSFSASKIFISALAMEGQQLLVAYPC VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	GIVI
WCSFSASKIFISALAMEGQQLLVAYPCA VFALISVF  1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	ASVL
1230 2580 A 9739 11 247 VFALISVF HFSPERPFMDYFDGVLMFVDISGKCKR	GIIG
1230 2580 A 9739 11 247 TFVLNMNTPKEEFQDWPIVRIAAHLPD HFSPERPFMDYFDGVLMFVDISGKCKR	LLYG
HFSPERPFMDYFDGVLMFVDISGKCKR	
HFSPERPFMDYFDGVLMFVDISGKCKR	LIVYG
	DVCL
MWMSNRLAWEFTCRA	
1231 2581 A 9744 37 1100 TPLFDFWPGFVLSWLQPLSASLRARRA	ASGPP
ACRIMPTTVDDVLEHGGEFHFFQKQMI	FLLA
LLSATFAPIYVGIVFLGFTPDHRCRSPG	VAELS
I.R.C.G.W.SPAEELNYTVPGPGPAGEASPR	QCRR
YEVDWNOSTFDCVDPLASLDTNRSRLI	PLGPC
RDGWYYETPGSSIVTEFNLVCANSWM	LDLFQ
SSVNVGFFIGSMSIGYIADRFGRKLCLL	TTVLI
NAAAGVLMAISPTYTWMLIFRLIQGLV	SKAG
WLIGYILITEFVGRRYRRTVGIFYQVAY	TVGL
LVLAGVAYALPHWRWLQFTVALPNFF	FLLY
YWCIPESPRWLISQNKNAEAMRIIKHIA	KKNG
KSLPASL	
PGPGMOGPPPITPTSWSI PPWRAYVAA	AVLC
1232 2582 A 9753 164 517 PGPGMQGPPPITPISWSLPPWRAYVAA YINLLNYMNWFIIAGVLLDIQEVFQISD	NHAG
LLQTVFVSCLLLSAPVFGYLGDRHSRK	ATMS
FGILLWSGAGLSSSFISPRYSWLF	· - <del>-</del>
L PARWTER VPK SEGI VGTCL GDPMAS	PRTVT
1233 2583 A 9757 25 419 LPAPWTERVRKSEGLVGTCLGDPMAS	YSEM
KRAYKSYVRALPLIKKMGINSILLRKS	IGALE
VACGIVMTLVPGRPKDVANFFLLLLVL	AVIF
FHQLV	ATTION
1234 2584 A 9765 71 456 RLELDWGFSLHFLPVAYLCPLSSGFEM	UDANO.
CSRCGYGVYPAEKISCIDQIWHKACFH	UE Y U
KMMLSVNNFVSHQKKPYCHAHNPKN	X1519
VYHTPLNLNVRTFPEAISGIHDQEDGEO	<b>JCKSV</b>
FHWD	
1235 2585 A 9767 52 559 IRSGAMSVDKAELCGSLLTWLQTFHVE	
SPODI SSGLAVAYVLNOIDPSWFNEAV	PSPCA
SEDPGPNWKLKVTSGLLIRGOTGEEM	PSPCA VLQGI
ARHMSWVMGRKRDRCLVINHLFIHSS	PSPCA VLQGI TRDGP
CARPGHSARNNTDKNLPHTAILLVTSN	PSPCA VLQGI TRDGP MEYSP
KINFQAGRSGSCL	PSPCA VLQGI TRDGP MEYSP
CDCCAL TVDEL TVDELGEVASNEESLYK	PSPCA VLQGI TRDGP MEYSP
1236   2586   A   9770   352   608   FRGEALT VELLER FIGURE TASKEEST TR	PSPCA VLQGI TRDGP MEYSP TYTTI

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
					Sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide	}	nucleotide insertion
				sequence		LERKQLNLEIYDPCSQTQKAKFSLTSELHWA
	ļ			Ì		DGFVIVYDISDRSSFAFAKALI
		<del> </del>	0703	266	515	NILAHYFPFPRLFLLRDSQSNPKAFALTLCHH
1237	2587	Α	9793	200	1 313	QKIKNFQILPVSIDALTPPLVVCFLVSFLTHFS
		1				RVKPTRPVCITOFOGCS
		<del>  </del>	9802	537	967	ELGAGRSDREAMEAAVKEEISVEDEAVDKNI
1238	2588	Α	9802	337	100	FROCNKIAFYRROKOWLSKKSTYRALLDSVT
		1				TDEDSTREOINEASKVPLLAEIYGIEGNIFRLK
	1	İ	1			INEETPLKPRFEVPDVLTSKPSTVRLISCSGDT
	1		1			GSLILADGKGDLKC
1000	0.500	<del>  </del>	9805	105	540	VPGDPAMVRAGAVGAHLPASGLDIFGDLKK
1239	2589	A	7003	103	1	MNKROLYYOVLNFAMIVSSALMIWKGLIVLT
		Ì			1	GSESPIVVVLSGSMEPAFHRGDLLFLTNFRED
		i			Į	PIRAGEIVVFKVEGRDIPIVHRVIKVHEKDNG
ł		ł		İ		DIKFLTKGDNNEGDDRGSYK
1240	2590	A	9819	3	305	TDGRDPLPCAARRGGGGECCGAGWVAEWS
1240	2390	^	7017	-		PQPLDPAMLLWMQGFVLEAVACQDNDDYLR
}	1					YGILFEDLDCNGDGVVDIIELQEGLRNWSSAF
			1			DPNSEEHG
1241	2591	A	9834	841	1209	SPARGKSNRTDVMITAPKNKKMTENLAAPEA
1241	1 2391	1	100.			LDSSTHSSSTATQSRAKMNTPAPTPSTVPAIPR
]		}				GGSGGPPPCAPHDRVSSVLQCDTQAMDHKTE
	1	}	ì	•	1	SSHSVVEFLFKRTKTPSPFHPAVRENRN
1242	2592	A	9843	3	589	TISCGPATEPPASLLSSASSDDFCKEKTEDRYS
1242	2372	1				LGSSLDSGMRTPLCRICFQGPEQGELLSPCRC
					1	DGSVKCTHQPCLIKWISERGCWSCELCYYKY
					}	HVIAISTKNPLQWQAISLTVIEKVQVAAAILGS
					1	LFLIASISWLIWSTFSPSARWQRQDLLFQICYG
						MYGFMDVMIVAVDSEDMVQAAKEVGKRWS
	}	İ		·		DIPP   WRISHHAGKMPVMKGLLAPQNTFLDTIATRF
1243	2593	A	9846	198	411	DGTHSNFILANAQVAKGFPIVYCSDGFCELAG
	-					DGIHSNFILANAQVARGITIV I CSDGI CEBITO
1				1		FARTEVMQ PICGFLYLCSAMASESSPLLAYRLLGEEGVAL
1244	2594	Α	9848	116	650	PANGAGGPGGASARKLSTFLGVVVPTVLSMF
1				}	1	PANGAGGPGGASARALSTFLGVVVVTVLSMI SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA
	1			1		LTVLSVCAIATNGAVQGGGAYCILQHRWTG
	1					VWPVLPAREVMISRTLGPEVGGSIGLMFYLA
		1		1	1	NVCGCAVSLLGLVESVLDVFGA
					1.00	KSKCRFPEGLSEGFGPMRKEALSSGSVQEAE
1245	2595	Α	9849	573	1620	AMLDEPQEQAEGSLTVYVISEHSSLLPQDMM
	1					SYIGPKRTAVVRGIMHREAFNIIGRRIVQVAQ
		1			1	AMSLTEDVLAAALADHLPEDKWSAEKRRPL
						KSSLGYEITFSLLNPDPKSHDVYWDIEGAVRR
		1				YVQPFLNALGAAGNFSVDSQILYYAMLGVNP
		į			1	RFDSASSSYYLDMHSLPHVINPVESRLGSSAA
					1	SLYPVLNFLLYVPELAHSPLYIQDKDGAPVAT
		1				NAFHSPRWGGIMVYNVDSKTYNASVLPVRV
		1				EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL
						LSGPTSEGLMTWELDRLLWARSVENLATATT
						TLTSLA
					1	PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS
1246	2596	Α	9850	114	464	ARSLGRRPRIAMVTVGNYCEAEGPVGPAWM
		1	l			QDGLSPCFFFTLVPSTRMALGTLALVLALPCK
						RRERPAGADSLSWGAGPRISSYV
						FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF
1247	2597	A	9851	2	327	HQFPTDTIQRSKWIRAVNRVDPRSKKIWIPGP
		1		1	1	I HOLLIDITOKOV MIKOVAJAVADI VOKOMIL QI
	ŀ	ì	İ	i	İ	CAT CEVETEOESDEESVGIDEKI KKGAVPSVS
						GAILCSKHFQESDFESYGIRRKLKKGAVPSVS LYKVFKYSSRCTS

			7.000	- F - F - F	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	İ	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		l	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Í	[		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	İ		peptide	sequence	/=possible nucleotide deletion, \=possible
		1		sequence	<b>\</b>	nucleotide insertion
10.40	2598	A	9853	58	444	RVDDFVYSKGGKDAGGADVSLACRRQSIPEE
1248	2398	A	9633	30	1777	FRGITVVELIKKEGSTLGLTISGGTDKDGKPR
	İ					VSNLRPGGLAARSDLLNIGDYIRSVNGIHLTR
	1					LRHDEIITLLKNVGERVVLEVEYELPPPGGCP
	]	j				WT
1249	2599	A	9856	2	1265	LPPPRPSRHRRGRAGTRASAAAAAGPTVSAV
1249	2399	A	9636	2	1203	RAPVRGQDSGAGTPQGRLAGRGAHLSRVGA
		1				SGSGVAAGPAARHAPRRRCADAGEAVGASC
	1					GRCAVALLSGVCTLVSTHVCVGSGCPGAAGT
						PMGAGDAGASAESAVTTAPQEPPARPLQAGS
						GAGPAPGRAMRSTTLLALLALVLLYLVSGAL
	1	1			1	VFRALEOPHEOOAQRELGEVREKFLRAHPCV
]						SDOELGLLIKEVADALGGGADPETNSTSNSSH
1		1				SAWDLGSAFFFSGTIITTIGGGGDWHVGGGK
	-	}				ELPHGGRCRETEGSQVAPRLPASPLCPGYGN
	1	ŀ				VALRTDAGRLFCIFYALVGIPLFGILLAGVGD
	1	1			ļ	RLGSSLRHGIGHIEAIFLKWHVPPELVRVLSA
			1			MLFLLIGCLLFVLTPTFVFCYMEDWSKLEAIY
		i			1	FVIVTLTTVGFGDYVA
1250	2600	A	9873	2	652	FVVPSPCGGIPGRAPNGASRPTMGNSASRNDF
		' '				EWVYTDQPHTQRRKEILAKYPAIKALMRPDP
	i	1				RLKWAVLVLVQMLACWLVRGLAWRWLL
	j					FWAYAFGGCVNHSLTLAIHDISHNAAFGTGR
	1					AARNRWLAVFANLPEGVPYAASFKKYHVDH
					1	HRYLGGDGLDVDVPTRLEGWFFCTPARKLL
		-		-		WLVLQPFFYSLRPLCVHPKAVTRMEVLNTLV
1		-				QLA
1251	2601	A	9875	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSR
Į	ļ	1			1	LESYRPOTOLSREDTGCNLQHISDRENIDDLN
	1	1				MEFNPSDHPRASTIFLSKSQTDVREKRKSLFIN
	1	}				HHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTI KCVALATYYHIKNRDPDGRMLLDIFDENLHPL
	ł	1				SKSEVPPDYDKHNPEQKQIYRFVRTLFSAAQL
	i	}				TAECAIVTLYYLERLLTYAEIDICPANWKRIV
		}				LGAILLASKVWDDQAVWNVDYCQILKDITVE
		1				DMNELERQFLELLQFNINVPSSVYAKYYFDL
1		i				RSLAEANNLSFPLEPLSRERAHKLEAISRLCED
	1	ļ				KYKDLRRSARKRSASADNLTLPRWSPAIIS
1000	0.00=	<del></del>	0070	6	376	KRPDSRPPAQYRAGPTRPRTRGCELLYWKAT
1252	2602	A	9879	0	370	KAVGIKMGSLSTANVEFCLDVFKELNSNNIG
1						DNIFFSSLSLLYALSMVLLGARGETEEQLEKV
	1	1				WNSSEVCSEPRSLSCSRSGSAKLILSLYQ
10.00	0.000	<del> </del> _	0000	180	388	KEQAELLYGLYCQCDLTLSSHPSSVPAMSSC
1253	2603	A	9880	100	300	NFTHATFVLIGIPGLEKAHFWVGFPLLSMYVA
1						AMFGNC
100	0001	<del>  _</del> _	0001	19	494	VISFQIITDTIMDSSTAHSPVFLVFPPEITASEYE
1254	2604	A	9881	17	דינד	STELSATTFSTQSPLQKLFARKMKILGTIQILF
1				i		GIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWG
		-	-			SVLFINSGAFLIAVKRKTTETLIILSRIMNFLSA
1		1	1	1	1	LGAIAGULLTFEFHPRSKLHL
1066	1200		9896	72	386	RPGREQRDCFQAPPLGLGGRQTDMMHHPLT
1255	2605	A	9890	1/2	360	GATCVGLPNVGMCPQLSGALTFMYLQQGNQ
1		1				EATVAPDTMAQPYASAQFAPPQNGIPGEYTA
1	İ	$\perp$	}	1	1	PHPHPAPEYTGQTT
100		<del> </del>	0000	105	399	SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG
1256	2606	Α	9902	95	לדכ	DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK
1		1				PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH
				1		KEELE
<u> </u>	1	<del> </del>	0000	274	459	EHLKSTPNRLGVVAHTCNPSTLGGRGGW
1257	2607	Α	9905	374	439	LIEROTT TOTAL CONDITIONS OF

FO 110	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID IO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid E=Glutamic Acid,
ucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	ł	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1 1	residue of	sequence.	/=possible nucleotide deletion, \=possible
		l	1	peptide		nucleotide insertion
			<u> </u>	sequence	1074	AGPGVPAVGGRWASGPGLGGRTLCSGPPDH
258	2608	A	9911	364	1974	ODDGDCGASGDPOCVGSPHPORARPLLARP
	ł	1				CARLL PGHI PSPRPPRLPTGOPPAAAFRGPVK
	)					POGGGHTHPL PTPGGRPCFAVSEGSGSALLLS
						VIGEOGSSSYVTGAACISPVLRCREWFEAGLP
	1		1	1	ì	WPVFRGFLLHOKIALSRYATALEDTVDTSRL
		1		1		EDGRGI REFEEALFCHTKSFPISWDAYWDKND
		-		1		DI POVDE A AVPVI.CICSADDPVCGPPDHTLTT
		1		1		FLEHSNPYFFLLLSRHGGHCGFLRQEPLPAWS
	}	}		ł		LUCYTI ESERAL TEFFRTEERIKGLSKHRASILU
	1	· ·				GRRGGALQRREVSSSSNLEEIFNWKRSYTRL
		ł	-		{	MAAAAGAAAAPGSREPQDRPECGAGHPGPR
					1	YYRHPERWLLRPEAFLGPLRTRAPSAEDSQR
		1		1		ERPAARSGPEMRVRYPVVAAVLAPYLALSQD
	İ	}	}	1		PMVKSSASGQGASGSYNHVREEMLIKAGGA
		1		1		MSRRVVRQSKFRHVFGQAAKADQAYEDIRV SKVTWDSSFCAVNPKFLAIIVEAGGGGAFIVL
	l	ļ		1		
						PLAK GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA
1259	2609	A	A 9919	693	935	TLSKAERLRSQPGPEQGGSSYRPRTPTAAAIL
			1			PPRPGRSHRKRKLVSTK
	İ	-				QRSCLCSAIEKDGGDVKALYRRSQALEKLGR
1260	2610	A	9921	455	1082	T DO A VI DI ORCVSLEPKNKVFQEALKNIGGQ
			1			10EKVDVMSSTDAKVEOMFOILLDPEEKGTE
		- }			i	I VVOKASONI VVI AREDAGAEKIFRSNG VQLI
	1	Ì				OPI I DMGETDLMLAALRTLVGICSEHQSKI V
		- [				ATLSILGTRRVVSILGVESQAVSLAACHLLQV
		j				MEDAI KEGVKKGFRGKEGAIIV
			9928	+	438	GERGAEARGAAOAPKKKKPRPTEGGPGAGSC
1261	2611	A	9928	1		PCKDPVRGPTLLHOPKPPKDEFLSSLESYEIA
		Ì	}	ļ		DTDVDINGALLAFSPPPPORORRGIGALAES
		- 1		1		RLFYKEASPSTHFLLNLTRSSRLLAGHVSVEY
		1				WTREGLAWQRADRPHCLYA
1262	2612	A	9931	168	435	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA
1202	2012	1	777			PPRLPFCLQELQGRHALHTFSLERTCSYQDFL
		1				WADEGRLLHVGAQDLATWHTLSPLGLW
1263	2613	A	9938	247	488	RMSATSVDQRPKGQGNKVSVQNGSIHQKDG CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY
1203	2015		ļ	l l		YAPSIGFPYSLGEAAWSQL
		l	Ì			ESIGLTALGPRRPWEHRWSDPITLKMKGWG
1264	2614	A	9941	61	277	WLALLEGALLGTAWARRSQDLHCGACKAV
	1	1	(			RRVRQFNIYDY
		1				FVASEVSKMPVPASWPHPPGPFLLLTLLLGL
1265	2615	A	9956	2	522	EVAGEEELQMIQPEKLLLVTVGKTATLHCTV
	ļ		Į	l .		TSLLPVGPVLWFRGVGPGRELIYNQKEGHFP
	ł	- {				PUTTUSDLTKRNNMDFSIRISSITPADVGTY
	1	ł		Ĭ		CVKFRKGSPDHVEFKSGAGTELSVRGEYSVC
		ł	1	{		FI SOVWWWI.SSHPFMN
					387	PKNNACHLLFTAVCQPRCKHGECIGPNKCK
1266	2616	A	10002	243	307	HPGY AGKTCNOGRKTV
		_		120	707	IDAPASTWSVARETMASSSVPPATVSAATAG
1267	2617	A	10004	36	/0/	PGPGFGFASKTKKKHFVOOKVKVFRAADPL
	}		1			GVEL WGVAHSINELSOVPPPVMLLPDDFKA
[			1			CVIVANIALI FHRENI PSHFKFKEYCPOVEKN
ì		)	}			PDPEGIDDODYLVSLTRNPPSESEGSDGRFL
	1					VDRTI VIKEVSSEDIADMHSNLSNYHQVKPI
1		}			1	SDILSE SSELLTYSSATVSNRCOLGRKLIGRENE
1			10005	2	209	GEGYELFVPSNGVPAVCHMVGRRPHRAVLS SQDELEHSLGESAAQGAAGVVLWVSWENT
1268	2618					

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	}	1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Sequence	/=possible nucleotide deletion, \=possible
		l l	1	sequence		nucleotide insertion
	<u> </u>	<b></b>	<del> </del>	sequence		TKVSLGLA
		<del> </del>	10010	245	688	FGMLKNKGHSSKKDNLAVNAVALQDHILHD
1269	2619	A	10010	243	1 000	LOLDNI SVADHSKTOVOKKENKSLKRDTKAL
	1		1		1	IDTGLKKTTOCPKLEDSEKEYVLDPKPPPLIL
	1	1				AOKLGLIGPPPPPLSSDEWEKVKQRSLLQGDS
		1		1		VOPCPICKEEFELRPOVFSIRG
	2620	+A	10011	2	588	RVDDFVRPLPPGLMSRSRASIHRGSIPAMSYA
1270	2620	A .	10011	1		PFRDVRGPSTHRTQYVHSPYDRPGWNPRFCII
				1		SGNQLLMLDEDEIHPLLIRDRRSESSRNKLLR
	1	1	· I			RTVSVPVEGRPHGEHEYHLGRSRRKSVPGGK
	<u> </u>	}			ł	QYSMEGAPAAPFRPSQGFLSRRLKSSIKRTKS
[		Ì	Į	ļ		QPKLDRTSSFRQILPRFRSADHDRYRGWSMW
		1		l .		DEIDV
1001	2621	- A	10013	209	363	LPAPPNLSPRLSFGFQFPGGNDNYLTITGPSHP
1271	2021	1^	10015	1	1	FLSGAEVSQSCRRRGGRA
1272	2622	A	10014	+7	388	SAVTISWKWRSVMGIQTSPALLASLGAGLVT
12/2	2022	^	1001.	) '		LLGLAVGSYLVRRSRRPQVTLLDPNEKDLLR
1	1	Ì	- 1			LIDKTLSARSPCKHIYLSTRIDGSLSIRPYTPVT
]	Ì					SDEDQGYVDIDIKVYLKGVHPTFPEGGKMSH
1273	2623	A	10016	1	1339	MAARTLGRGVGRLLGSLRGLSGQPARPPCGV
12/3	2023	\ \hat{\chi}	100.0		l	SAPRRAASGPSGSAPAVAAAAAQPGSYPALS
)		]	1	1		AQAAREPAAFWGPLARDTLVWDTPYHTVW
1	ł	1				DCDFSTGKIGWFLGGQLNVSVNCLDQHVRKS
		İ				PESVALIWERDEPGTEVRITYRELLETTCRLA
ļ	1		1			NTLKRHGVHRGDRVAIYMPVSPLAVAAMLA CARIGAVHTVIFAGFSAESLAGRINDAKCKVV
ł	1	1	1	1		TTFNQGLRGGRVVELKKIVDEAVKHCPTVQH
1						VLVAHRTDNKVHMGDLDVPLEQEMAKEDP
1						VCAPESMGSEDMLFMLYTSGSTGMPKGIVHT
	ì		<b>!</b>	· I		QAGYLLYAALTHKLVFDHQPGDIFGCVADIG
1	ł	ł	1	į.		WITGHSYVVYGPLCNGATSVLFESTPVYPNA
1	i	1	ŀ	ļ		GRYWETVERLKINQFYGAPTAVRLLLKYGD
	1	İ	ļ	l		AWVKKYDRSSLRTLGSVGEPINCEAWEWLH
Ì	}	1				RVVGDSRCTLVDTWWQT
					3750	FRPOGTPRSPASHVLTMSAPDEGRRDPPKPKG
1274	2624	A	10017	1	3/30	KTI GSFFGSLPGFSSARNLVANAHSSARARPA
	1			1	1	ADPTGAPAAEAAOPOAQVAAHPEQTAPWIE
				1		VELOPSEKMVSGAKDLVCSKMSRAKDAVSS
		1	1	1	1	GVASVVDVAKGVVOGGLDTTRSALTGTKEV
1		1	1	1		VSSCVTGAMDMAKGAVOGGLDTSKAVLIG
1		1				TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV
}		1	[		İ	T TGTK DTVTTGVMGAVNLAKGTVQTGVE1S
1		1				KAVI TOTKDAVSTGLTGAVNVARGSIQIGV
1		}	-			DTSKTVLTGTKDTVCSGVTGAMNVAKGIIQ1
1	1		-			GVDTSKTVLTGTKDTVCSGVTGAMNVAKGT
1						IOTGVDTSKTVLTGTKDTVCSGVTGAMNVA
1		1				KGTIOTGVDTTKTVLTGTKNTVCSGVTGAVN
İ						1 AKEAIOGGLDTTKSMVMGTKDTMSTGLTG
		1	1			AANVAKGAMOTGLNTTONIATGTKDTVCSG
			1		1	VTGAMNI ARGTIOTGVDTTKIVLTGTKDTVC
	-	- !	1	İ		SGVTGAANVAKGAVOGGLDTTKSVLTGTKD
			1	1	1	AVSTGLTGAVNVAKGTVOTGVDTTKTVLTG
1						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV
			}			VIGTEDTMSTGLTGAANVAKGAVQTGVDIA
						KTVI TGTKDTVTTGLVGAVNVAKGTVQIGM
1	1	1	1	1		DTTKTVI TGTKDTIYSGVTSAVNVAKGAVQI
1	1	1	1	1		GLKTTQNIATGTKNTFGSGVTSAVNVAKGAA
			i i	I		(ILKITONIMIOTIZITI 000 I ISTITI
	į					OTGVDTAKTVLTGTKDTVTTGLMGAVNVAK
						QTGVDTAKTVLTGTKDTVTTGLMGAVNVAK GTVQTSVDTTKTVLTGTKDTVCSGVTGAAN

PCT/US01/03800 WO 01/57188

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met		Predicted	nucleotide	D-Aspertic Acid F=Glutamic Acid,
O: of	NO: of	hod		beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-		USSN		to last amino	M=Methionine N=Asparagine, P=Proline,
eq- {	neuce		09/496	correspondi	acid residue	O=Glutamine R=Arginine, S=Serine,
ence			914	ng to first	of peptide	T=Threonine V=Valine, W=Tryptophan,
ļ			1	amino acid		V-Tyrosine X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
		ļ	1 1	peptide		- valentide insertion
		1	ll	sequence		TUAK GAJOGGI DTTKSVLTGTKDAVSTGLTGA
			}		1	AVIAVICTUOTIGMDTTKTVLIGIKDAVIGGV
	ì	]	1		Ì	TGAANVAKGAVQMGVDTAKTVLTGTKDTV
	l	ļ	1 1			CSGVTGAANVAKGAVQTGLKTTQNIATGTK
	ł	<b>\</b>	1			NTLGSGVTGAAKVAKGAVQGGLDTTKSVLT
	•	Ì	1			GTKDAVSTGLTGAVNLAKGTVQTGVDTSKT
	}	ļ	1			VLTGTKDTVCSGVTGAVNVAKGTVQTGVDT
	t	1	Į.			AKTVLSGAKDAVTTGVTGAVNVAKGTVQTG
		1	1		}	VDASKAVLMGTKDTVFSGVTGAMSMAKGA
		1	1			VDASKAVLMGTKDTVFSGVTGAMSKI III
	}	1	ì	1	•	VQGGLDTTKTVLTGTKDAVSAGLMGSGNVA
		ì				TGATHTGLSTFQNWLPSTPATSWGGLTSSRT
		1	ŀ	}	1	TDNGGEQTALSPQEAPFSGISTPPDVLSVGPEPTTG
	1		ł	1		AWEAAATTKGLATDVATFTQGAAPGREDTG
			i			LLATTHGPEEAPRLAMLQNELEGLGDIFHPM
		1	1	· ·		NAEEQAQLAASQPGPKVLSAEQGSYFVRLGD
	1	1		•		LGPSFRQRAFEHAVSHLQHGQFQARDTLAQL
		1		1	}	QDCFRL QDCFRL
	0.00	A	10025	124	415	TILARKKEKTCPCKKEIGRNSRSGMYSRKAM
1275	2625	A	10025	124		YKRKYSAANTKVEKKKKEKVLAPVTKPVGG
	1	i	Ì	1		DKNGGTRVVKLPTMPRYYPTEDVPRKLLSHO
	1	1	1	1	1	KKPFS TO THE TOTAL THE PARTY OF
			10030	3	507	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMS
1276	2626	A	10030	-		ASRPOSPTTPWCLPRRYMKHKRDDGPEKQEI
	1	1	l l	İ		- LEAVIDUMTCVFVVMCCSMLVLLIIFIUL
	ļ		l	1		LVYVVIGIFCLASATGLYSCLAPCVRRLPFGK
	1		}	1	į	CRIPNNSLPYFHKRPQARMLLLALFCVAVSV
	1				1	VWGVFRNEDQ
	0.605		10035	51	869	YSRFTVPLPATMASSEVARHLLFQSHMATKT
1277	2627	A	10033	1 3.	1	TCMSSQGSDDEQIKRENIRSLTMSGHVGFESI
			1			- L PROT ANTESTOOGECENIL CYGETGIGKSTELD I
		1	ļ			T ENTERNY ESCHECPNYKLKAUTTELQESIN
		1	ļ	ì	1	VQLKLTIVNTVGFGDQINKEERQLGRSQSTE
			1	j	1	POW OBSECUTO TERM TO A MANUAL OF A MANUAL
ľ	į.	- [		1		- Leggoga COPYLPINSPPHRLADVAD VALLESS V
<b>\</b>	}	i	1	1		I SGAFGCYHLDVTVNEFKKQQNKDEQEG 13
1	)	1			İ	L COOROGSWKHGADPLRGGEM
			10026	3	457	- TRACOVERVEST RPCCPRDFHAGCLIVSGPSI
1278	2628	A	10036	3	1 '5'	UNICAVICESI SVOCRYEEKYKII NKY WURQ
1		\	Į.	l l		CI DIWLIENVETGGSEGVVKSDOVILLDELUD
	1		Ì	{		TETYTI ENI TADDAGKYRCGIAI ILQEDOLO
			ļ.	1	1	EL PODEFOVOVI VSSASSIENSVKIP
					435	NIDST VPMSSWRSCARAPSSESAWKKSAATK
1279	2629	A	10039	214	733	SRKCLRTKRKRWSSGKGTQMQSTLSETPRR
}		1		1		OMPCMWWYPFWG
1					344	DATWHNAGKEREAVOLMAGAEKRVKASH
1280	2630	A	10043	2	344	EL DOLEGGNTRIEFACEMYTRAANMIKMAL
				}		NWSAAGNAFCOAAKLHMQLQSKHDSAISF
1	ľ		-	ĺ	1	DAGNAVKKADPOGKTARHVACYLCV
						VIYKLDSSLFSYFIYFFIFETESHFLPLMKWT
1281	2631	A	10080	620	818	DDAAUCSI KII ASRNSADSAFLSAGDI SLSH
		}				CASHIDGOKRASGEVGIAPSSRHILIGEPSAK
1282	2632	A	10084	. 3	1640	NGTAIISLVRGPGILGEVTVFWRIFPPSVGEF.
1.202	2002	1	-	Į.		ETSGKLTMRDEQSAVIVVIQALNDDIPEEKS
	İ	1	İ			YEFQLTAVSEGGVLSESSSTANITVVASDSP
1	-		j	1		YEFQLIAVSEUUVLSESSSIAITII VYASBUI
					1	GRFAFSHEQLRVSEAQRVNITIRSSGDFGHV
1	-			1		LWYKTMSGTAEAGLDFVPAAGELLFEAGE
1	1			1		RKSLHVEILDDDYPEGPEEFSLTITKVELQGI GYDFTIQENGLQIDQPPEIGNISIVRIIIMKND
	1				,	F CODETIONNEL OHNORFRIGNISI A KITMATATA
j		ì	1	1		AEGIIEFDPKYTAFEVEEDVGLIMIPVVRLHO

					- T - 1 - 1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	DLQ	Predicted	Predicted end nucleotide	D=A spartic Acid. E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	,		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		Ì	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
		1	1	sequence		YGYVTADFISQSSSASPGGVDYILHGSTVTFQ
						HGQNLSFINISIIDDNESEFEEPIEILLTGATGG
	1	1	{			AVLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIA
	ì					NPNSTMILSLVLERTGGLLGEIQVNWETVGPN
						SQEALLPQNRDIADPVSGLFYFGEGEGGVRTII
	1	l	1			LTIYPHEEIEVEETFIIKLHLVKGEAKLDSRAK
		1			1	LTTYPHEEIEVEETFIIKLHLVKGEAKLDSGAR
		ļ				DVTLTIQEFGDPNGVVQFAPETLSKKTYSEPL
	1	İ				ALEGPLLITFFVRRVKGTFGEIM
	2622	A	10088	316	516	MGSKTLPAPVPIHPSLQLTNYSFLQAVNGLPT
1283	2633	^	10000	] 3.0		VPSDHLPNLYGFSALHAVHLHQWTLGYPAM
	1	\		1	1	HLXRS
	-	<del> </del>	10091	2	569	FVSPSRAMASALIYVSKFKSFVILVVTPLLLLP
1284	2634	Α	10031	1 4	1 337	I VII MPAKEVRCAYVIILMAIYWCTEVIPLAV
	1	1		ļ		TSI MPVI LEPLEOILDSROVCVQYMKDINML
•	1	1.		ļ		FI GGLIVAVAVERWNLHKRIALRTLLWVGA
	1	1				KDARI MI GEMGVTALLSMWISNTATTAMMV
		1		l		PIVEAILQQMEATSAATEAGLELVDKGKAKE
	1	1	1	1		I P
_				1-00-	728	KOSTRPDVMTLYPLHWOEEMSGESVVSSAVE
1285	2635	Α	10092	290	120	A A ATRITISEK GTSPSSKYVKLNVGGAL Y Y I I
		ļ.		}	}	MOTI TKODTMLKAMFSGRMEVLTDSEGWIL
		[		1		IDRCGKHFGTILNYLRDGAVPLPESRREIEELL
	1					AEAKVVI VOGI VEECOAALQV
	ł			<u> </u>		DDD GR GAWAGPGGDYSGVRROORRK I KISGS
1286	2636	Α	10100	1	574	OPGSDA AGTMGCCTGRCSLICLCALQLVSAL
	1	1	1	1		ERQIFDFLGFQWAPILGNFLHIIVVILGLFGTIQ
1	l	1		l .		YRPRYIMVYTVWTALWVTWNVFIICFYLEVO
		l				GLSKDTDLMTFNISVHRSWWREHGPGCVRR
1	ł	1				VLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI
•		)	}			
			ŀ	1		HSA RSRMGDKPIWEQIGSSFIQHYYQLFDNDRTQI
1287	2637	A	10103	252	376	GAIYVSFQL
120						MEEEDESRGKTEESGEDRGDGPPDRDPTLSPS
1288	2638	A	10107	1	478	AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL
1200	1 2000			ì		RWRRCRSPRSEPRSQESGGTDTATVLDMATI
1	I	1				SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM
	ı	İ				SFLAGLVSVLDPPDI W VPSKLDLKI GESEDIN
		1		1		LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG
l	1	1				KT COVERNEY COVERNEY F
1000	2639	-	10113	237	438	LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLF
1289	2039	^	10113	1		DLREIGHGSFGAAYFARDVRTNEVVAIKKMS
						YSG
		<del>-  </del>	10114	367	856	RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSP
1290	2640	Α	10114	707	""	TEATRATAMSKSLKKKSHWTSKVHESVIGKI
						PEGOLGEELKGGAENGOFPYLGEVKPGKVA
1	}		1	l		FSGSKLVSEELLLEVNETPVAGLTIRDVLAVI
1				i		KHCKDPLRLKCVKQGESSGLLSVLPGGGTAI
		Ì		1		GAGO
	1	L			601	PTIRETERRSALSCSVLKSEPLPGLQPQASQQ
1291	2641	Ā	10116	128	591	PDDI PGRROVOVOEGGGSGLRAWVLAMAS
	[	- 1		1		LGSGRGSGGLSSQLKCKSKRRRRRRSKRKDI
		1			1	VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE
1			1	1		VKENRNVGNLAARPPPSGDRARGGATR
1			}			QRRRFRAGLWGGHGLTDGLRRNGGCGCSA
1292	2642	- A	10121	1	749	QKKKFKAGLWGGGGGGGCGGA
1292	2042	1"				VPRVGERLRGHRCPDPLCLLLDMLFLSFHAC
		i				SWESWCCCCLIPADRPWDRGQHWQLEMAD
		- 1		İ		RSVHETRFEAAVKVIQSLPKNGSFQPTNEMN
1	İ			l l	1	LKFYSFYKQATEGPCKLSRPGFWDPIGRYKV
i		1		l	ì	DAWSSLGDMTKEEAMIAYVEEMKKIIETMP
	j	l l	1		ì	D11,10000000000000000000000000000000000
				(		MTEKVEELLRVIGPFYEIVEDKKSGRSSDITS

			CEO.	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=Aenartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		1	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	ļ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ł	Į.	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ			sequence	/=possible nucleotide deletion, \=possible
	1	ł		peptide		nucleotide insertion
	1	l		sequence		LGNVLTSTPNAKTVNGKAESSDSGAESEEEE
	ł	1	}	_		AC PLMSLVRVVEFVAASSAQKTPSRLENYYMVC
1293	2643	A	10124	2	989	PLMSLVRVVEFVAASSAQRIFSREENT IN CO
1293	2043	1	1			KADEKFNQLVHFLRNHKQEKHLVFFRYSSGL
	1	1	1			CGRGIRDSARMCSTCACVEYYGKALEVLVK
	1	1	i	1	1	GVKIMCIHGKMKYKRNKIFMEFRKLQSGILV
	1	1			1	CTDVMARGIDIPEVNWVLQYDPPSNASAFVH
	1	ĺ				RCGRTARIGHGGSALVFLLPMEESYINFLAIN
		1				OK CPI OEMKPORNTADLLPKLKSMALADKA
•	\	1	1			VEEKGMKAEVSYVOAYAKHECNLIFRLKDL
	1		-			DFASLARGFALLRMPKMPELRGKQFPDFVPV
	1	1	l	}		DVNTDTIPFKDKIREKQRQKLLEQQRREKTEN
	1	İ	ı	1	l	EGRRKFIKNKAWSKQKAKKK
	i	1	1			EGRRKFIKNKA WSKQKAKKK
1294	2644	A	10129	91	1042	VTMYKDCIESTGDYFLLCDAEGPWGIILESLA
1294	2044	1	1012	} -	}	ILGIVVTILLLLAFLFLMRKIQDCSQWNVLPTQ
1			1	1		LLFLLSVLGLFGLAFAFIIELNQQTAPVRYFLF
	l l		1		1	GVLFALCFSCLLAHASNLVKLVRGCVSFSWT
		1	1	1		TUCIAIGCSLLOIIIATEYVTLIMTRGMMFVN
	}	1.			1	MTPCOLNVDFVVLLVYVLFLMALTFFVSKAT
1	ł	'		ļ		ECGPCENWKOHGRLIFITVLFSIIIWVVWISML
ļ	1	1		}		I RGNPOFOROPOWDDPVVCIALVTNAWVFL
ļ				1	}	LLYIVPELCILYRSCRQECPLQGNACPVTAYQ
	Ì	1			ļ	HSFQVENQELSRDKWKVLLNSDFLSHSGA
		1	1 '			RPRVVTHNSQWCFLPQDHPGWLPGQSGAPG
1295	2645	A	10133	376	518	RPRVV I HNSQWCFLFQDIII GW DI GQGGIA G
1293	2043	1		i		GRGAPRQEGPGSSWRQV
1206	2646	A	10135	3	551	EWSLDPFMGIMSGQVGDLSPSQEKSLAQFRE
1296	2040	1 ^	10133		1 .	NIQDVLSALPNPDDYFLLRWLQARSFDLQKS
ļ	i				'	EDMLRKHMEFRKQQDLANILAWQPPEVVRL
	1	ł	1		1	VNANGICGHDGEGSPVWYHIVGSQDPKGLLL
1			-			SASKOELLRDSFRSCELLLRECELQSQKLGKR
ļ	ļ			1		VEKTIATEGLEGLGLRDLWKPGIELLQE
				10	407	MVSSCCGSVCSDOGCGODLCQETCCRPSCCE
1297	2647	Α	10138	48	407	TTCCPTTCCRPSCCVSSCCRPOCCOSVCCQP1
1	İ		ŀ			CSRPSCCQTTCCRTTCYRPSCCVSSCCRPQCC
	l					QPVCCQPTCCRPSCCETTCCHPXCC
]	1	1	1		_	OPVCCOFICCRI SCCEFFCCIE NO
1298	2648	A	10156	94	453	GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG
1270	2070	11		1		QEMYLRFDQTTRRSPYRMSRILARHQLVTKI
1		1			,	QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP
1		1				INITY A VICIDITY OF THE PROPER
		+	1010	<del>-                                     </del>	393	PRESEL VINGRGRVSARFGGSPSKAATVRSQPT
1299	2649	Α	10161	1	1 3/3	ASAOI ENMEEAPKRVSLALOLPEHGSKDIGN
1		1		[		VPGNCSENPCONGGTCVPGADAHSCDCGPGF
			1		1	KGRRCELACIKVSRPCTRLFSETKAFPVWEGG
1			1	(		VCHHV
				1		AKIASLERIMPANYTCTRPDGDNTDFRYFIYA
1300	2650	A	10162	98	391	AKIASLEKIMPANI ICIRPUUNITIIRITIIR
1300	2030	1 **		1		VTYTGILGPGLIGNILALWVFYGYMKETKRA
1			1	1		VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF
		1			}	VPV
			10000	<del></del>	7545	PGIP VGITSOTGL SSNLOENCSKLAFISSHGTE
1301	2651	A	10165	] 1	1545	KOT OCMPMEGRGRASSSISDLQGKGFEKGTU
1	1			1		FKHVPGVGSARHSPOASAGGSPWQRGKAQI
1		1			1	RWLGKPDPGRKRRGSPQEEGGLRVSAAAR
		1				LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP
				1		LLCSGANKCKVLVKQINSTRITQQCAVIII STI
1		1				PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA
		İ		1	!	LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP
1		1		ļ		RTLSVEEPGVECNQLCLYADVTDPVLCLGQK
1		ĺ				DPGVEGKHCEKEKISSSKELKHVHAKSEPSKE
	1				1	ARRLSESLHVVDENKNESKIEREHKRRTSTPV
1	1		1			
		l		1		IMEGVQEETDTRDVKRQVERSEICTEEPQKQ

SEQ ID Not of north bot much of much of much optical peptide sequence (a) and bot much optical peptide sequence (a) and bot much optical peptide sequence (a) and bot much optical peptide sequence (a) sequence (b)							
SO of No-of node of the node of peptide of the node of	CEO ID	SEO ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucio de sequence 914 914 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		,				nucleotide	D=Aspartic Acid, E=Glutamic Acid,
uence    Solidation   Solidatio	1	_				location	F=Phenylalanine, G=Glycine, H=Histidine,
uence  914  914  914  914  914  914  914  91		,				corresponding	I=Isoleucine, K=Lysine, L=Leucine,
enice  ### spin of first among and residue of peptide residue of peptide sequence  ### spin of first among and the spin of peptide sequence  ### spin of first among and the spin of first among and t	4						M=Methionine, N=Asparagine, P=Proline,
amino acid residue of peptide sequence peptide sequence of peptide	1 .	dence				acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of popular procession and control pro	uence	ł		117	, ,	of pentide	T=Threonine, V=Valine, W=Tryptophan,
peptide nucleotide insertion nucleotide insertion kSTILKNEKHLKKDOSETPHLKSLLKKEVKSS KERPEREKTYSEOKLSVKHKYKGOMIKTG DETELHISSEKGILKVEENIQKQSQOTKLSSDDK TERKSKHRERKI SVLKGNGKPKSYSVIIKTDE NVRKENNKKERRI SAEKTKAEHKSRKSSDSK IQKDSLGSKOHGTILGREGSTYSEDKOMDST NMDSNLKPEEVVHKERRITKSLLEEKLVLKS SKTOGKOVKVVETELGGGATKQATTPKPD KEKNTEENIDSEKQRKSKVEDKPFEETGYEPV LETASSSAHTOGKDSSHFAKLPLAKEKYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKEKYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKEKYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKEKYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKEKYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKERYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKERYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVDSSHFAKLPLAKERYKSD KONTSTRILERALSOGHKSRSLKHSSKDIKKKD ENSDDKOKGEVENSHFAKLPKSCH ENSTADALSOGHKSGSLATHSSKOKKKND ENSDSKOKGKONTOK SKOKEN SOGSHAKOBEKLAANTLST SGSSLOFHKSGOMTLPGOFFENDER SOGSLOFHKSGOMTLPGOFFENDER KEPHREGTEVINDSETYHRMLLSAFSRGTOV NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHREGTEVNIDSETYHRMLLSAFSRGTOV NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHREGTEVNIDSETYHRMLLSAFSRGTOV NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHREGTEVNIDSETYHRMLLSAFSRGTOV NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHREGTEVNIDSETYHRMLLSAFSRGTOV ORNIKANTALEHVAQGDATLEHSTNLDSSPOS GGATVTVLRESVTYTKREGGLAVTHLOSSER GGATTAKANTALVTRESETYLKGSTA KKENDLAMANTALSTRICKTOR KERNELLY ALVERTING AND AND AND AND AND AND AND AND AND AND			ļ				Y=Tyrosine, X=Unknown, *=Stop codon,
nucleotide insertion  SEQUENCE  KETERKEHLEKUDSETPHLKSLLKKEVKSS  KERFEREKTPSEDKLSVKHRYKODCMIRTO DETELLISSEKGILKVERNIQKOGOGNIKTO DETELLISSEKGILKVERNIQKOGOGNIKSTO DETELLISSEKGILKVERNIQKOGOGNIKSDDK TERKSKHRNERKLSVLGKDGRYSEYVIIKTDE NYRKERNIKKERILSSKEKTKAHEKRSSDSK IQKDSLGSKOHGITLQRESESYSEDKCDMDST NDESNILKPEEVVHLEKRITKSLLEEKLVLKS KEKTQGKQVKVVETELQEGATKQATTPKPD KEKNTERDISKGRIKSKYENEKSTEGYBEV LETASSSAHSTQKDSSIRHAKLPLAKERYKSD KONSTITILERKLSDGHKSSILKHSSODIKKKD ENKSDDOKDGKEVDSSHEKARGNSSILMEKL SRILCERRGSLGORMAKGEKLAANTLSTP SGSSLORPKKSGDMTLIPEOEPMEIDSPOVE NNEVSKSTODNRINNISHQDDSSINMOKQKTS ATVQKDELRICTADSKATAPAYKRORGTOV NNESHAHADHRSTLTKKMHIGGANYSKIMPGE KEPHREGTTEVNIDSETVHRINLSAPSEDHOVY QENLKINTAAEEHVAGGATLEHSTILDSSPS LSSVTVVPLRESVDPDVPLFDKRIVLGGSTA SISPADHASALPNOSLTVESEVLKTSDSKEGG EGFTVDTPAKASITSKRHIPBAHQATLLDGKQ GEVIMPHGSKLTGVYTENENTKEGGLVDMA KKENDLNAEPNIKGTIKATVENGKKDGIAVD HVGLINTERYNAETVIKLHKRSPGKVKDISID VERRNENSEVDTSAGGGGASPSVLHQRNOGTE  VERRNENSEVDTSAGGGGASPSVLHQRNOGTE  UPSTROMENSEVDTSAGGGGASPSVLHQRNOGTE  OPATGPRAEKTSVATISTEGKDEVDTLSPVK AGPATTTSSETRQSEVALPCTSIRADEGLIGT HSRNNPLHVGABASECTVFAAAEEGGAVTE GPASSETHLTSTKEGESGGCAVATSEDRAADL LAVIAVAKIBANNSVTEEKDDANTSAGSEE KCDGSLSRDSEIVEGTITTISEVESDGAVTSAG TIRAGSISSEEVDGGONMARMORKETEG TVTCTGABERSDNFVICSVTGAGFREERMVT GGSAVTSTGTIEDGEGPASCTGSEDSSEGFALS SESSENGESAMDSTVVSTEKGDAVTSAGGE TIRAGSISSEEVDGGSONMATMSKRKETEG TVTCTGABERSDNFVICSVTGAGFREERMVT GGSAVTSTGTIEDGEGPASCTGSEDSSEGFALS SESSENGESAMDSTVAKEGTDVAAGFCD DEGIVTSTGAKEEDEEGEDVYTSTGRGNEIGH VEARAGAAMANNENNDSNIGTERGSKEDT SESSENGESAMDSTVAKEGTDVAAGFCD DEGIVTSTGAKEEDEEGEDVYTSTGRGNEIGH VEARAGAAMANNENNDSNIGTERGSKEDT SESSENGESAMDSTVAKEGTDVAAGFCD DEGIVTSTGAKEEDEEGEBOVTSTGRGNEIGH VEARAGAGAMANNENNDSNIGTERGSKEDT SESSENGESAMDSTVAKEGTONPUT WORD GEGAPTSTTOATEFFERAPPSAVGODEVTYPGGC GPMTSAASDOSDSQLEKVEDTITSTGLVGGS TOALVESENERAGTVANGEFEEFEINSTITKCAES LOPVAAAVEERERATGPVLISTAJDFGGMPSAPP BEASPCAASTSCEKEEGEFEINSTSVEDC  GOVERSENERAGTVANGEEGEFEINSTSVEDC  GOVERSENERAGTVANGEFEINSPSKEDELANDERG GILDSATEVSSHAW PYPSALGEFEINSTSVEDC  GOVERSENERAGTVANGERGEFEINSTSVEDC  GO	)	ŀ	l	l	1	50425	/-possible nucleotide deletion, \-possible
KSTLKNEKHLKKIDDSETPHLKSLLKKEVASS  KERFEREKTSPEGNL, SVAHKYKGOCHMIKTO  DETELHISSEKGILKVEENIOKOSQOTKLSSIDDK  TERKSKHRPEKLISVLKGHGKPVSYVIIKTDE  NYRKENNIKKERRLSAEKTKAEHKSRRSSIDSK  IQKDSLOSKOHGTI, ORRESSYSBUCKDMDST  NAMDSNLKPERVYHKERRITISLLEEKLVLKS  KSKTOKOKOVKVVETEL GOGATKOATTPKPD  KENTTENDISKORKSKVEDKPFEETGVEPV  LETASSSAHSTIGKDSSHAAKDERSKLLEKEKLYKSS  KONTSTILLERKLSOHKSRSLKHSSKDIKKKD  ENKSDIKKDOKGVEVOSTERLAENISKDIKKKD  ENKSDIKKDOKGVEVOSTERLAENISKDIKKKD  ENKSDIKKDOKGEVOSTERLAENISKDIKKKD  ENKSDIKKDOKGEVOSTERLAENISKDIKKKD  ENKSDIKKLORGENISTERLAENISKOHKSKL  SRRLCENRROSLSQEMAKGEEKLAANTLSTP  SGSSLQRRKKSGOMTLPEOEPMELDSEPOVE  NNEFUKKTONISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNEFUKRTORISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNISKARTORISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNISKARTORISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNISKARTORISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNISKARTORISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNISKARTORISKOHMSSHQDIDSENMKOKTS  ATVOKDELRICTADSKATAPAYKPGRITOV  NNISKARTORISKOHMSSHQDIDSENMKOKTS  OKNIKATABENTALASSANAMA  KEPILRIGTTEVNIDERVITRAGLELAENISKOHMO  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKA  (RIVIMPLEKSTOHMULDSKATAPAKSHOLMULDSKATAPAKS		1	1	ĺ		ļ	nucleotide insertion
KEKPEREKTYSEDKLSVKHKYKGDCMHKTG DETELHSSEKGIK VERMIOKOGYCTKLSSDDK TERKSKHRNERI SYLOKDOKPVSEYHIKEDE NYKEKNINKERRIK SYLOKDOKPVSEYHIKEDE NYKEKNINKERRIK SYLOKDOKPVSEYHIKEDE NYKEKNINKERRIK SAENT KALHEKRIKSSDSK IQKDSIGSKOHGITLORRSEYSEDKCOMMOTS NIMDSNIK KPEVVYHEKERRITSKILERU VLKS KSKTOGKOVK VYETELQEGATKOATTPKYD KIKNTEENDSEKORKSKYVENPERTGVERPY LETASSSAHSTOKDSSHRAKLPLAKEKYKSD KIKNTEENDSEKORKSKYVENPERTGVERPY LETASSSAHSTOKDSSHRAKLPLAKEKYKSD KONTSTELERKLSJOHKSSHLAKLSKIKKD ENKSDDKLOGHKSNSLAHAMTLSTP SOSSLORPKKSGDMTLDEPGPMEIDSEPOVE NYFEVSKTOONTNNSHODDESDMKQKTS ATVOKDELTCTADSKATAPAYKPGGTOU NSESKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDSETVHRMLSAPSENDEN VON LIKNTAAEEHVAQGDATLEHSTNLDSSPS LSSVTVYPLRESYDPDVIPLDKRTVLEGSTS SISPADHSALPHOGATUSTENSKHADGE KEPHRGTTEVVIDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDDSETVHRMLSAPSENDEN VON SINSEKHADHRSTLTKKMHIQSAVSKMNPGE KEPHRGTTEVVIDSETVIKAKTSENSENG KEPHRGTTEVVIDSETVIKAKTSENSENG VON SINSEKHADHRSTLTKSHRIPSANGATALBAPS LSSVTVVPLRESYDPDVIPLDRKTVLLGARSE KEPHRGTAVTVLKHKRSPGKVDISID VERRNENSEVDTSAGSGSAPSVLHORNOGTIF UNTGOFRAEKTSVATSTECKDKDVLTSPVK AGPATTISSETRQSEVALPCTSIEADGGLIGT DATGOFRAEKTSVATSTECKDKDVLTSPVK AGPATTISSETRQSEVALPCTSIEADGGLIGT TOTATGOFRAEKTSVATSTECKDKDVLTSPVK AGPATTISSETRQSEVALPCTSIEADGGLIGT HENDRIPHLYGAGASECTVFAAAGGAVVTE GRASSETFILTSIKGEGSGECAVAESEDRAADUT GRASSETTILTSIKGEGSGECAVAESEDRAADUT GRASSETTILTSIKGEGSGECAVAESEDRATOVAT GRASSETTILTSIKGEGSGERATESEDGAVTTAGGAT TICKGAGGSGSAVTOTTGGGGGSVIDOTT GRASSTSTAGSGGGAMBRATHATOVATSTGGGGGGNATTGGGGSVIDOTT GREAVITSTGTLTGGGGGGSVIDOTT GREAVITSTGTLTGGGGGGANGATTGGGGSTATT NEGGGAVTSTGGGGEPLITTSTGLVGGSSDATE ENNEGTRAVTTERFARMFRAVSGODSOLTATE				<del> </del>	sequence		KSTLKNEKHLKKDDSETPHLKSLLKKEVKSS
DETELHSSEKGIK VEENIQKOŞOQTKLISSDIK TERKSKIRINERIL SALEKIKAEHKSRISSDIK NYKENINKERILSAEKIKAEHKSRISSDIK NYKENINKERILSAEKIKAEHKSRISSDIK NYKENINKERILSAEKIKAEHKSRISSDIK NODSIL KPEVVIKERRITISILLEKLULKS NODSIL KPEVVIKERRITISILLEKLULKS KIKTOĞKOYK VVETELOĞGATKATIPKID KEKNITERDISEKORKSK VEDKPFETIGUPEV LETASSAHISTOKDSIKTAKIRLAKEKYKSDI KIKKLERILSSAHISTOKDSIKTAKIRLAKEKYKSDI KOSTSTELERKLISDGHKSRILKHSSKDIKKKL BIKISDALDÇKEV VEDKSHERARONSIMEKKL SIRILCENRROSISOGEMAKĞEEKLANTISTIP SOSSLOPPKSSODMITLIPFOPPENEDISPEVYE NYFEV SKIDONININISHODDISENIKOKIT ATVOKDELITICIADISATATA PAYPERGITOV NISHEKHALDIRSTITIKKHIQSAVSKMINGE KEPHROTTEVANDISTIVIRMLISTISINISTISIS ATVOKDELITICIADISATIATAYAPERGITOV NISHEKHALDIRSTITIKKHIQSAVSKMINGE KEPHROTTEVANDISTIVIRMLISTILDISKO QOKUMITAAEHNAQODATLEHSTINLDSSIS LISSIVIVPLERSIPDDIVIPLIPKINISTISISIS LISSIVIVPLERSIPDDIVIPLIPKINITUSSIS LISSIVIVPLERSIPDDIVIPLIPKINITUSSIS LISSIVIVPLERSIPDDIVIPLIPKINITUSSIS LISSIVIVPLERSIPDIVIPLIPKINITUSSIS LISSIVIVPLERSIPOLITITISTISHOLIDGIK QOKUMITAAEHNAQODATLEHSTINLOSIS GEOFTYDTIMAASITISKHIPPEHALDIGIKO GOKUMITAKAEHNAQODATLEHSTINLOSIS LISSIVIVPLERSIPOLITITISTISHOLIDGIK GOKUMITAKAEHNAQODATLEHSTINLOSIS LISSIVIVPLERSIPOLITITISTISHOLIDGIK GOKUMITAKAEHNAQODATLEHSTINLOSIS LISSIVIVPLERSIPOLITISTISHOLIDGIKUMITAKAEHNAQODATLEHSTINLOSIS LISSIVIVPLERSIPOLITISTISHOLIDGIKUMITAKAEHNAQODATLEHSTINLOSIS DVATOPRAEKETSIVATSTEOKUKUNILSIVA AGRAVITSISHTOLIDATISAAGSAENAALEGGAVITE GFASETFILISTIKGGSGECAVAEEDGILISTIS GFASETSITISTISHOLIDATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITISTICADATISAAGSEE KCDGSLSRISSISTITICADATISAAGSEE KCDGSLSRISSISTITICADATISAAGSEE KCDGSLSRISTITISTICADATISAAGSEE KCDGSLSRISTITIAAASEE TYTCTGAEEGGECALTISTICADATISTICATORIOSISTITICADATISAAGOTATIAATATITITISTICATIONAAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		1					KEKPEREKTPSEDKLSVKHKYKGDCMHKTG
TERRSKHRNERLISVLOKDOKPVSEYHIKED NYRKENNIKKERRISSDES NOMSHIK SPEVVHKERRITSSLEKH.VLKS (AKINIKKERRITSSLEKH.VLKS NAMSHIK KPEVVHKERRITSSLEKH.VLKS NAMSHIK KPEVVHKERRITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.VLKS NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. SISPADHSALPNQSLTVRESEVLKTSDSSEGG GEFTVITTPAKASTIKKHPERALGATLLIGKO GKVIMPLGSKLTGVIVENEHITKEGGL VOMA NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. SISPADHSALPNQSLTVRESEVLKTSDSSEGG GEFTVITTPAKASTIKKHPERALGATLLIGKO GKVIMPLGSKLTGVIVENEHITKEGGL VOMA NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKARSSLEKH. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKER. NAMSHIKERITSSLEKH.NAMSHIKERITSSLEKH.NAMSHIKARSSLEKH.NAMSHIKER.	1			1			DETEL HSSEKGLKVEENIOKOSOOTKLSSDDK
NVRKENNIKERRLSAEKTKAEHKSRRSSDSK (QKDSIGSKQHOTTLORRSSYSTEDKCDMDST NMDSNLKPEVVHKERRRTKSLLEEKULKS. SKOGKOVYKVETELOGGATKQATTPKPD KEKNTEENDSEKORKSKVEDKPFETGUEVE LELASSAHSTOKDASTRAKULAKEYKSD KEKNTEENDSEKORKSKVEDKPFETGUEVE LELASSAHSTOKDSSHRAKULAKEYKSD KDSTSTELERKLSDGHKSRSLKHSSKDIKKKD DKKSDDKDGKEVDSSHEKARONSMEKKL SRILCENRRGSISOEMAKGEKLAANTLST SOSSLORPKSGOMTLTPEOPEMEDSPOYE NVFEVSKTODNRNNSHODDSENMKOKTS ATVQKDELRTCTADSKATAPAYPGGGTOV NSNSEKHADHRSTLTKKMHIQSAVSKMNGE KEPHRGTTEVNIDSSTVIRMLASPENDRY QKNLKNTAAEEHVAQGDATLEHSTNLDSSPS LSYNTYVPLRESYDPDVPLDENFLOKEGTA STSPADHSALPYQSLTVRESEVLKTSDSKEG GEGTVTVTPTAASTSKRHPEAHOATLLOGKO GKVMPLOSKLTOVIVSENTKEGGI.VDMA KENDLMAEPIALGTKATATSKHPEAHOATLLOGKO GKVMPLOSKLTOVIVSENTKEGGI.VDMA KENDLMAEPIALGTKATKSKHPEAHOATLLOGKO GKVMPLOSKLTOVIVSENTKEGGI.VDMA KENDLMAEPIALGTKATKSKHPEAHOATLLOGKO GKVMPLOSKLTOVIVSENTKEGGI.VDMA KENDLMAEPIALGTKATKSKHPEAHOATLLOGKO GKVMPLOSKLTOVIVSENTKEGGI.VDMA KENDLMAEPIALGTKATKATSKERGEKVEDISID VERRNENSEVITSAGGSASSASVATEAGGI.GAVVTE GRASETTILTSCAGGSASSASVATEAGGI.GAVTE GRASETTILTSCAGGSASSASVATEAGGI.GAVTE GRASETTILTSCAGGSASSASVATEAGGGGI.GAVTE GRASETTILTSCAGGSASSASVATEAGGGGI.GAVTE GRASETTILTSCAGGSASSASVATEAGGGGI.GAVTE GRASETTILTSCAGGSAGGASSASVATEAGGGG.GAVTE GRASETTILTSCAGGSAGGASSASVATEAGGGG.GAVTE GRASETTILTSCAGGSAGGASSASVATEAGGGGG.GAVTE GRASETTILTSCAGGSAGGASSASVATEAGGGGGGGAVTE GRASETTILTSCAGGSAGGASSASVATEAGGGGGGGAVTE GRASETTILTSCAGGSAGGAGGASVATEAGGGGGGGAVTE GRASETTILTSCAGGSAGGAGGASVATEAGGGGGGAVTE GRASETTILTSCAGGAGGGGGGAVTEAGGGGGGGAVTE GRASETTILTSCAGGGGGGGAVTEAGGGGGGGAVTEAGGGGGGGAVTEAGGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTEAGGGGGGAVTAGGAGGGGGAVTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	ł		1	i	1		TERK SK HRNERKI SVLGKDGKPVSEYIIKTDE
IQKISLOSKOHGITLQRRSESYSEENKCHMST NIMMSNILKPEEVHEKRRITSLLEEKLVILKS KSKTOGKOVKVVETELQEGATKQATTPKPD KEKINTEENDSEKORKSKVENPEETOVEPV LETASSSAHSTOKDSSHRAKLPLAKEKYKSD KOETSTRIERKISDGHKRSKIKSSOHKKKL ENRSDDKLOKEVDSSHRAKLPLAKEKYKSD KOETSTRIERKISDGHKRSKIKSSOHKKKL SRRLCENRRGSISQEMAKGEBELAANTLSTP SOSSLORRKKSGDWTLDEGEPMEIDSEPOVE NVFEVSKTODNENNSHSHODENMKQKTS ATVOKDELRTCTADSKATAPAYXPGRGTOV NSNSEKHADHRSTLTKEMHOSAVKMPGE KEPHRGTTEVNIDSETVHRMLLSAPSENDRY QKNLKNTAAEHVAQDATLEHSTNLDSSPS LSSVTVPLRESTOPDVIPLFDKRTVLEGSTA STSPADHSALPNOSLTVRESSVLKTSDSKGG GKVIMPLGSKLTGVIVENENITKEGGLVMA KKENDLNAEPNILKQTIKATVENGKUDGIAV HVVGLINTEKYAETVKLKHKRSPGKVKDISID VERRYNENSEVDTSAGSGASPKVIKTOSHOW HVVGLINTEKYAETVKLKHKRSPGKVKDISID VERRYNENSEVDTSAGSGASPKVIKTOSHOW HVVGLINTEKYAETVKLKHKRSPGKVKDISID VERRYNENSEVDTSAGSGASPKVIKTOSHOW HOVALTEKYAETVKLKHKRSPGKVKDISID VERRYNENSEVDTSAGSGASPKVIKTOSHOW HOVALTEKYAETVKLKHKRSPGKVKDISID VERRYNENSEVDTSAGSGASPKVIKTOSHOW HOVALTEKYAETVKLKHKRSPGKVKDISID VERRYNENSEVDTSAGSGASPKVIKTOSHOW HOVALTEKYAETVGSKVALPCTSIGADGEGLIGT HSRNIPLHYGAEASECTVFAAAEEGGAVVTE GFAESETFLISTIKEGESGECATSIGANGE KCDOSLSRDSEIVGGTTIFTESTEADEGLIGT HSRNIPLHYGAEASECTVFAAAEEGGAVVTE GFAESETFLISTIKEGESGECATSIGASGEE KCDOSLSRDSEIVGGTTIFTESTEVSDOAVTSAG TEIRAGSISSEEVDGSQONMMRMOPKKETEG TVCTCAGAGGSISPLVGTTTIGTGSPEEDSTGFAIS SESEENGESANDSTVAAEGTNVPLVAAGPCD DEGITYSTGAKEEDEGEADVTSTGGRFEERMVT GAGVVLGDNDAPFGTSASGEGOGSVDDGTE GESAVTSTGTTEDGEGPASTGONSUSTEKGHEND GAGAVTTGTETDEGEPASTGTTSGGNEIGH ASTCTCLGESEGGVLICSSAGGSOSQITVEH VEAEAGAAMMANENVONDSMGTEKGSKDT DICSSAKGVESSYTSAVSKKDEVTPVEGGCE GPHTSTAASDOSDSOLEKVETISTGLVGGGE GPHTSTAASDOSDSOLEKVETISTGLVGGGE GPHTSTAASDSOSDSOLEKVETISTGLVGGGE GPHTSAASDSOSDSOLEKVETISTGLVGGGE GPHTSAASTOSDSSOLETISTSAEECEASVS GVVVESENERAGTVUISTAADFEGPPARP EAESPLATSTSKEKEEDGLANTS GGCEAVMGGAVLODEDRITTITECLIDAD ALISTSTACCMPRASSERICHERONVICCOPPAR GGKPGPVLVANTEGENGPGFAGRGOKSTIL HLINAEENVILNSLOKERDSVIKFSAOCGH PSAVCACKEERIGKECPGGFFAGGGOKSTIL HLINAEENVILNSLOKERDSVIKFSAOCGH PSAVCACKEERIGKECPGGFFAGGGOKSTIL HLINAEENVILNSLOKERDSVIKFSAOCGH	1			Į		1	NVRKENNKKERRLSAEKTKAEHKSRRSSDSK
NMDSNLKPEEVVHEKERRITKSLLEEKU VLS KSKTOGKOWKVVETELOEGATKQATTPKPD KEKNTEENDSEKQRKSKVEDRPFEETIOVEPV LETASSASHATSKODSSHRAKLPLAKEKYKSD KDSTSTRI ERKLSDGHKSRSLKHSKOLKKU ENKSDDKJOKKEVDSSHEKARKONSSLMEKKL SRRJCENBROGLSQEMAKGEEKLAANTSP SOSSLQRPKKSGDMTLPEGEBEDSPOVE NVFEVSKTODRNINNSHQDIDSENMKQKTS ATVQKDELRICTADDSKATAPAYKPGRGTOV NSNSEKHADHRSTLTKKMHQSAVSKMRDGE KEPHRGTTEVNIDSETVHRAKLSAPSERDAV QKNLKNTAAEHVAGDATLEBSTADVS QKNLKNTAAEHVAGDATLEBSTADVS LSSVTVVPLRESYDPDVPLFDKRTVLEGSTA STSPADHSALPNOSLTVERSEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEAHQATLLDGKQ GKVMPLGSKLTGVIVENSITKEGGLVDMA KKENDLNAEPNLKQTIKATVENGKKDGIAVD HVVGLATIEKYAETVALKIKRSPGKVKDISID VERRIENSEVDTSAGSGAPSVLHORNOQTE DVATGPRAREKTSVATSTEGOKDVTLSPVX AGPATITSSETRQSEVALPCTSIEADEGLIGIT HSRNNPLHVQBAASECTVA-AAEEGGAVVTE GFAESETLTSTKEGESGCAVAESEDRADL LAVHAVKERANNSVYTEEKDDAVTSAGSEE KCDGSLSRDSENVEGTITFISEVSSDGAVTSAG TEHAGSISSEEVDGSQGNMARMOPKKETEG TVTCTGAEGRSDNFVICSVTGAGPBERMVT GAGVVLGDNDAPPGTSASQECDGSVNDOTE GESAAVTSGTTEDGEGPASCTSGROSSEGFAIS SESEENGESAMDSTVAKEGTNVPILVAAPDC DEGITYTSTGKEEDEGGDVVTSTGACPBERMVT GAGVVLGDNDAPPGTSASQECDGSVNDOTE GESAAVTSGTTEDGEGPASCTSGROSSEGFAIS SESEENGESAMDSTVAKEGTNVPILVAAPDC DEGITYSTGKEEDEGGBOVVTSTGACPBERMVT GAGVVLGDNDAPPGTSASQECDGSVNDOTE GESAAVTSGTTEDGEGPASCTSGROSSEGFAIS SESEENGESAMDSTVAKEGTNVPILVAAPDC DEGITYSTGKEEDEGGBOVTSTGACPBERMVT GAGVVLGDNDAPPGTSASQECDGSVNDOTE GESAAVTSGTTEDGEGPASCTSGROSSEGFAIS SESEENGESAMDSTVAKEGTNVPILVAAPDC DEGITYSTGKEEDEGGBOVTSTGACPBERMVT GAGVVLGNDAPPGTSASQECDGSVNDOTE GESAAVTSGTTETEGGEGFANSTSGROSEIGSTSVECC GPWTSAASSGSSOLGEVTFVTGGCE GPWTSAASSGSSOLGEVTFVTGGCE GPWTSAASSGSSOLGEVTFTGGCE GPWTSAASGGSSOLGETTASFEKEDEDITTSVE NEEGGLAMATTASGDTTNORNLAGGENGGC GPWTSAASGGSSOLGETTASFEKEDEDITTSVE NEEGGLAMTTASGDTTNORNLAGGENGGC GPWTSAASGGSSOLGETTATGCASS LQPVAAAVEERATGSVLISTSAECCASVS GVVVESNERAGTVMEKLGGGUSSTSSVECC GFWSSAVPGEGGPSVTTAAFERMGTAMBETS GGCEAVMGGAVLQDEDRLTTTREELBOLADA AIISTTAECMPRASSIDHELERNCTADPFECPOPN GGKEPGPVLAVSTEEGHNGFSVHKSAGOGH PSAVCACKEEKHGKECPGGPTFAGGGGCKSTL HLIMPEENNVLINSLOKERDSVHTENGGGTAK SVSAGREGGRANSPAHLRGPFOTSGGTAK	)		1		1		JOKDSI GSKOHGITLORRSESYSEDKCDMDST
KSKTOGKOVK-VYETELQEGATKQATTPKPD KEKNTEENDSEKORKSKVENPEETGVEPY LETASSSAHSTQKDSSHRAKLPLAKEKYKSD KOPTSTRIERKLSDGKKSSKLNSKSDKKKKD ENKSDKJOKEVDSSHRAKLPLAKEKYKSD KOPTSTRIERKLSDGKKSKLEKSKDKKKKD ENKSDKJOKEVDSSHRARGNSSLMEKKL SRRLCENRRGSLSQEMAKGERSLAANTLSTP SGSSLQRPKKSODMTLIPEQEPMEIDSEPGVE NVPEVSKTQDRNRNNSHQDIDSENMKGTS ATVQKDELRTCTADSKATAPYKPGRGTGV NSNSEKHADHRSTLTKKMHIQSAVSKMPGE KEPHRGTTEVNIDSETVIRMLISAPSENDRV QKNLKNTAAEEHVAQDATLEHSTNLDSSPS LSSVTVVPLRSSTYDPDVPLPDKRTVLEGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVVPLRSSTYDPDVPLPDKRTVLEGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVVPLRSTYNDSETVIRMLSAPSENDRV QKNLKNTAAEEHVAQDATLEHSTNLDSSPS LSSVTVVPLRSTYDPDVPLPOKRTVLEGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVVPLRSTYDPOVPLPOKRTVLEGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVPLRSTYNDSTYTERSEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVPLRSTYNDSTYTERSEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVPLRSTYNDSTYTERSEVLKTSDSKEGG EGFTVDTPAKASTISKRHIPEATLLDSSPS LSSVTVPLRSTYNDSTYTERSEVLKTSDSSPS LSSVTVPLRSTYNDSTYTERSEVLKTSDSSPS LSSVTTATTSSETTRGSEVALPCTSTEAGEGAVTBA LKAMENDLANGSTYNDSTYTERSEVLKTSTORGATERSE DVATGRRAKETSVATSTEGKEKDAVTSAGGEAVTE GFAESETTLTSTKEGESGECAVAESBDRAADL LAVHANKERANNSVYTEEKDDAVTSAGGEAVTSAG TEIRAGSISSEEVEDOSQONMARMOPKKETEG TVCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPFGTSASGEGOGSVNDGTT GEGSAVTSTGTTEDGEGPASCTGSEDSSEGAIS SESEENGESANDSTYAKEGTNYPLVAAGPCD DEGITTSTGAKEEDEEGDVTSTTGRGNEIGH ASTCTOLGEESGVLICESAFGDSQIGTVVELVAGG DEGITTSTGAKEEDEEGDVTSTTGRGNEIGH ASTCTOLGEESGVLICESAFGDSQIGTVVELVAGG TVCTGAEGRSDVFLCSVTTGAGRSETITSVE NEEGCAMTSTGIGEFFELPISSATTIKACAS LQPVAASCHERAGTVYPLVAGGENSSVDGATA SESEENGESANDSTVAKEGTNYPLVAGGENGEA ULISTSTTACMTASGDITTNYBNLAGESTSSVEDC GFWTSANDADATTASGDITTNYBLAGESTSSVEDC GFWTSANDADATTASGDITTNYBLAGESTSSVEDC GGRSSATYTAGGEFFELPSSATTIKACASS LQPVAASTEGENGPSSVERGTAGGSTSSVEDC GGRSSATVTAGGEFFELPSSATTIKACASS LQPVAASTEGENGPSSVERGTAGGSTSSVEDC GGRSSATVTALTSGSGTSSVEDC GGRSSATVTALTSGGTSSVERGTSSTSVED		1	1	1	ļ		NADSNI KPEEVVHKEKRRTKSLLEEKLVLKS
KEKNTEENDSEKQRKSYEDRFFEET(VEPV LETASSASHATS(DSSHRAKL)LAKEKYKSD KDSTSTRLEKK1.SDGHKSRSI.KHSSKDIKKKL ENKSDDKJOKKEVDSSHEKARGNSSI.MEKKL SRILCENBROGI.SQEMAKGEELLAANTLSTP SOSSLQPRKS.GOMTLJEPGEDPMEIDSEPOVE NVFEVSKTQDRRNNNSHQDIDSENMKQKTS ATVQKDELRTCT.ADSKALTA-YERGGTIOV NSNSKEHADHRSTI.TKKMHIQSAVSKMPGE KEPHRGTTEVNIDSETVHMLI.SAYSEMPGE KEPHRGTTEVNIDSETVHMLI.SAYSEMPGE SESTIVOVELRESYDPVPLFDKRTVLLGSTA STSPADHSALPNOSILVRESESVLKTSDSKEGG EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ GKVMPLGSKLTGVIVENEMITKEGGLVDMA KENDLNAEPNI.KQTIKATVENGKKDGIAVD HVVGLNTEKYAFTVALKIKKSPGKVKDISID VERRINSEVDTSAGSGSAPSVLIQRTNGOTE DVATGPRAREKTSVATSTEGOKDVTLSPVK AGPATTTSSETRQSEVALPCTSIEADEG.LIGIT HSRNNPLHVGGAASECTVAAAEEGGAVVTSAY GFALSKALVSVALVALVALKIKSPGKVKDISID LAVHAVKIERAVNSVVTEEKDDAVTSAGSEE TVTCTGAEGRSDNFVICSVTGAGPBERMVT GFAESETLTSTKEGGSGCAVAESEDRADL LAVHAVKIERAVNSVTEEKDDAVTSAGSEE TVTCTGAEGRSDNFVICSVTGAGPBERMVT GAGVVLODNDAPPGTSASGEGOGSVNDGTE GESAVTSTGTIEDGEGPASCTGSEDSSEGFAIS SESEENGESANDSTVAREGTNVPILVAGRICH GAGVVLODNDAPPGTSASGEGOGSVNDGTE GESAVTSTGTTEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAREGTNVPILVAGGCE GPWTSTGAKEEDEGEDVYTSTGRONEIGH ASTCTGLGESEGVLICESAEGDSQIGTVVEH VEAEAGAABMANENNVDSMGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTFVGGCE GPWTSASSGSSPSQLECHTISTELLYGGG VPULVSGEVPECEVAHTSPSEKEDEDITITSE VSGC GPWTSASSGSSPSQLECTTSTELERAGESSGLANTS SEEEDECAMISTSIGEEFELPISSATTIKAES LQPVAAAVEERATASGDITNONSLAGGRNQGK VLLISTSTTNDTPTPQSAITDVEGGESDSLATE ENNEGTEVTTEFFEAPPMSAVSGLOGSVDALTE ENNEGTEVTTEFFEAPPMSAVSGLOSDSLATS ENEGGEGAMNTSTVASGEFFELPISSATTIKAES LQPVAAAVEERATASGDITNONSLAGGRNQGK VLLISTSTTNDTPTPQSAITDVEGGESPOSLATS SEEEDECAMISTSIGEEFELPISSATTIKAES LQPVAAAVEERATGSPLISTSLAECCASVS GVVVESENERAGTVTPBLAAGDITNYE GERPANTASGDITNONSLAGGRNQGK VLLISTSTTNDTTPGPSASIDELETENQLTADPEGF GDLSATTVSKEKEDEGEGPSVTFAEEMGDTAMISTS TSEGCEAVMGGAVLQDEDRLITTRELDIADA ALISTSTAECCMPASSASDELEEROUTADNECTCOPVR GGKEPGPVLAVSTEEGHINGSVTKPSAGQGH PSAVCAKEEKHGKECPEIGPFAGGGGKSTL HLIMPEENSANDKLEEROUTADNECTCOPVR GGKEPGPVLAVSTEEGHINGSVTKPSAGQGH PSAVCAKEEKHGKECPEIGPFAGGGGKSTL HLIMPEENSCHLINSLONCECTCOPVR		1	l l		ļ		VSKTOGKOVK VVETELOEGATKOATTPKPD
LETASSAHSTQKDSSHRAKLPLAKEYKSD KDSTSTILERKILSIGHKSSLKHSSKDIKKKL ENKSDDKDGKEVDSSHEKARGNSSLMEKKL SRRILCPNRGOSLSQEMAKGEEKLAANTLSTP SGSSLQRPKKSGDMTLPFGCEMEIDSPOVE NVFEVSKTQDNRNNISHQDDSEMMKQKTS ATVQKDELRTCTADSKATAPAYKPGGTGV NSNSEKHADHRSTLTKKMHIQSAVSKMPGE KEPHRGTTEVNIDSETVHRMLISAPSENDRV QKNLKNTAAEEHVAQGDATLEHSTLDSSPS LSSYTVVPLERSYPDVIPLFDKRTVLEGSTA STSPADHSALPNQSLTVRESEVLXTSDSKEGG GEGTVDTPAKASITSKRHIPEHQATLLDGKQ GKVIMPLGSKLTGVIVENENITKEGGLVDMA KKENDLNAEPNLAGTIKAVENGKEGIGAV HVVGLNTEKVAETVKLKHKRSPGKVKDISID VERRIENSEVDTSAGGSGSVHORNGOTE DVATGPRAEKTSVATSTEGKDKDVTLSPVK AGRATTSSETRQSEVALTSGKBCBLUGT HSRNNPLHVGARASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVAESEDRAADL LAVHAVKIRANNSVYTERKDDAVTSAGSEE KCDGSLSRDSEIVEGTTITTISEVESDGAVTSAG TEIRAGSISSEVDGSGOMMRMGPKKETEG TVTCTGAEGRSDNFVICSVTGAGFRERMYT GAGVVLGDNDAPPGTSAGGEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSEGFAIS SESEENGESGAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEGEDVYTSTGROREIGH ASTCTGLEGESSGVLICESSEGFAIS SESEENGESSGAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEGEGDVYTSTGROREIGH ASTCTGLEGESSGVLICESSEGFAIS SESEENGESSBOMSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEGEGDVYTSTGROREIGH ASTCTGLEGESSGVLICESSEGFAIS SESEENGESSBOMSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEGEGDVYTSTGAKEGTNUFL VEAEAGAAMNIANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSKGVEVTPVPGGCE GPMTSAASDQSBOQLEKVEDTTTTTGLVGGS YDVLVSGEVPECEVAHTSPSKEEDEDITTSVE NEECOGLMATTASGDTINONSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRYTTTEFFARPASAGGDSGGTVSEH VEAEAGAAMNIANENNVDSMSGTEKGSKDT SEGCEAVMGAWTASGSDTINONSLAGGKNQGK VLISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRYTTTEFFARPASAGGDDGGTAMSTS TSEGCEAVMGAWAUQDEDRLTTTRVELLSDA AIISTSTAECMPRASATTRAEER STREEKDECALISTSTAEECEASVS GVVVSENERAGTVMPERSAGGDGGTSNSPED GGREPGFBVANTEEFFALPISTATHCAES LQPVAAVERERATGPVPULSTADFEGRMPSAPP EASPLASTTSKEEKDECALISTSTAEECGASGG GFPGSAVPQEEGDPSVTPAEEMGGTAMSTS TSEGCEAVMGAWAUQDEDRLTTTRVELLSDA AIISTSTAECMFALSATIKAERSKELDEGGAMSTSAHL HLINAEEKNVLINSLOKECKFGFFTAGGSST ASYSAGRGLGGNANSTAHLRGPGOTSGGTAK BLILLINAEEKNVLINSLOKECKFGFFTAGGSST		i		1	j		VEKNITEENDSEK ORK SK VEDKPFEETGVEPV
KDSTSTRLERKI.SIOGHKSRSILKEKDL EINSJÖNDIGKEVDSSILEKARGNSIS.MEKEKL SRILCENRRGSI.SOEMARGEEKLAANTI.STP SGSSLORPKGSODMILPGEPMEIDSEPOYE NVFEVSKTQDNRNINSHQDIDSERMIQKTS ATVQKDELRTCTADSKATAPAYKPGRGTOV NSNSEKHADHRSTITKKMLINGSAVSKMNPGE KEPIHRGTTEVNIDSETVIRMLISAPENDRV QKNLKNTAAEHVAQGDATLEHSTNLDSSPS LSSVTVVPLRESYDPDVPLFPKRYTLGSTA STSPADHSALPNOSLTVRESEVLKTSDSKEGG GEFTVDTPAKASITSKRHIPEAHQATLLDGKQ GKVMPLGSALTGVIVENTKEGGLVDMA KKENDLNAEPNLKOTIKATVENGKEGIAVD HVVGLNTEKYAETVKLKHRSSPGKVKDISID VERNIENSEVDTSAGSGSAPSVLHORNGOTE DVATGPRRAEKTSVATSTEGKDKVTLSPVK AGPATITSSETRIGSEVALPTSIDEAGGLIGT HSRNIPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFILTSTKEGESGECAVAESEDRAADL LAVHAVKIEANVNSVYTEEKDDAVTSAGSEE KCDGSLSRDSEVGGTITISEVESDGAVTSAGS EKCOGSLSRDSEVGGTITISEVESDGAVTSAGS TEIRAGSISSEEVDGGGONMKRMOPKKETEG TVTCTGAGRESDNFVICTAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVITSTGTIEDGEPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKGTNPVLVAAPCD DEGIVTSTGAKEEDEGEDVVTSTGRENEIM ATCTGGGEESGEVLICESSAGDSOGIOTVEH VEAEAGAAINNANENNVDSMSGTEKGSKDT DIGSSAKGIVESSYTSAVGETORVPTPYGGCE GPMTSAASDQSDSOLEKVEDTITISTGLVGS VDVLVSGEVPECEVALTSSEKEEDEDIITSVE NECCOGLMATTASGDITNONSLAGGKNQGK VLISTSTTNDYTPQVSAITDVEGGLSDALRTE ENNEGTRYTTEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVALAVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVALSVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVALSVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVALSVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVALSVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVALSVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVASAVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVASAVERRATOPVITEEFEARPSAVSGDDSQLTAS RSEEKDECAMISTISIGEFEILBISSATIKCAES UPVASAVERRATOPVITEEFEARPSAVSGDSGCTAMISTS TSEGCEAVMGGAVLQDEBGCTAMISTS TSEGCEAVMGAVLQDEBGCTAMISTAT HILMAEEKNYLLNSI,QUECKLECEGFSGAGESTIL HILMAEEKNYLLNSI,QUECKLECEGFSGAGGESTIL HILMAEEKNYLLAN VALAADDMOGTVA	{	l.		1			LETASSSAHSTOKDSSHRAKLPLAKEKYKSD
ENKSDIKDGKEVDSSHEKARGNSKIMEKKL SRRICENRRGSLSQEMAKGEKLAANTLSTP SGSSLQRPKKSGDMTLIPFGCEMELBEPOVE NVEVSKTQDNRNNISHQDDSEMMKQKTS ATVQKDELRTCTADSKATAPAYKPGRGTGV NSNSEKHADHRSTLTKKMHIGSAVSMMPGE KEPIHRGTTEVNIDSETYHRMLISAPSENDRV QKNLKNTAAEEHVAQGDATLEHSTLDSSEPS LSSVTVVPLRESYPDVPUFPKRTVLEGSTA STSPADHSALPNQSLTVRESEVLXTDSKEGG EGFTVDTPAKASITSK RHIPEAHQATLLDGKQ GKVIMPLGSKLTGVIVENENITKEGGLYDMA KKENDLNAEPNLKOTIKATVENGKKDGIAVD HVVGLNTEKV AETVKLKHKRSPGKYKDISID VERRINESSEVDTSAGSGSAPSVLHQRNGQTIE DVATGPRRAEKTSVATSTEGKDKDVTLSPKY AGPATTTSSETRQSEVALPCTSEBADGLIIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVAESEDRAADL LAVHAVKIEANYNSVVTEKDDAVTSAGSEE KCDGSLSRDSEIVEGTTTFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGMMARMGPKKETEG TVTCTGAEGRSDNFVICSVTGAGGREERMVT GAGVVLGDNDAPPGTSASQEGDSVNDGTE GESAVTSTGTTEDGEGRSDNFVICSVTGAGGREERMVT GAGVVLGDNDAPPGTSASQEGDSVNDGTE GESAVTSTGTTEDGEGRSDNFVICSTGRGREERMVT GAGVVLGDNDAPPGTSASQEGDSVNDGTE GESAVTSTGTTEDGEGRSDNFVICSTGRGREERMVT GAGVVLGDNDAPPGTSASQEGDSVNDGTE GESAVTSTGTTEDGEGRSDNFVICSTGRGREERMVT GAGVVLGDNABARGNTGKENSVNDGTE GESAVTSTGTTEDGEGRSDNFVICSTGRGREERMVT GAGVVLGDNABARGNTGKENSVNDGTE GESAVTSTGTTEDGEGRSDNFVICSTGRGNEIGH ASTCTGLGEESGEVLICESAEGDSQIGTVVEH VEAEAGAAMNANENNYDSNSGTEKGSKD SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGITYSTGAKEEDEEGEDVYTSTGRGNEIGH ASTCTGLGEESGEVLICESAEGDSQIGTVVEH VEAEAGAAMNANENNYDSNSGTEKGSKD SESEENGESAMDSTVAKEGTNVPLTAAGPCD DICSSAKGIVESNYTSAVSKOEVTPVPGGCE GPMTSAASDQSSDQLEKVEDITISTSCLAGGS TVDVLVSGEVPECEVAHTSPSKKEDEDLITSVE NEECGGLMATTASGDITNONSLAGGKNQGK VLIISTSTTNDYTPQVSAITUTVEGGLSDALRTE ENMEGTRVTTEFFAPMPSAVSGDDSQLTAXS REEKBECAMISTSTREEKDECALISTSTAECECASVS GVVVESENERAGTVMERECGGSBISTSSVEDC GGPVSSAVPQEEGDPSVTTAEEMGCTAMISTS TSEGCEA VAMGGAVQOBERLITTREVELISDA AIISTSTAECMPISASURHEENQLTADNPEGN GCREPGPVLAVSTEECHHOPSVHRPSAGQH PSAVCAEKERHGGECFEIGFFAGGGKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHR GPFQTSGGTAKA BSSVSTRYLAANTIGALKADDMPPOGTVA		1	1				KNOTSTRI ERKI SDGHKSRSLKHSSKDIKKKD
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ATVOKDELRICTADSKATAPAYRGRGTGV NISNSEKHADHRSTLTKMIQSAVSKIMPGE KEPIHRGTTEVNIDSETVHRMILSAPSENDRV QKNILKINTAAEEHVAQGDATLEHSTNLDSSPS LSSVTVVYPLRESYDPDYPLFDKRTVLEGSTA STSPADHSALPNQSLTVRESEVLATSDSKEGG GGTVTDTPAKASITSKRHIPEAHQATLLDGKQ GKVIMPLGSKLTGVIVENENITKEGGLVDMA KKENDLNAEPPILKQTIKATVENGKLOGIAVD HVVGLNTEKY AETVYLKIKKRSPGKVKDISID VERRNENSEVDTSAGSGAPSVLHQNINGGTE DVATGFRAEKTSVATSTECKDKDVTLSPVK AGPATITSSETRQSEVALPCTSIBADEGLIGT HSRNIPLHVGAEASECTVFAAAEEGGAVVTE GFAESETITLTSTKEGESGECAVAESEDRAADL LAVHAVKEANVNSVTEKDDAVTSAGSE KCOGSLSBDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEVDOSQONMMRMOPKKETEG TVTCTGAGGRSDNFVCSTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGITEDGEOPASCTGSEDSSEGFAIS SESENGESAMDSTVAKEGTINVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVYTSTGRONEIGH ASTCTGL GESSEGVLICESAEGDSQIGTVVBH VEAEAGAAMMANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDITTSVE NECDGLMATTASGDTNONLSKAEGENOK VLIISTSTINDYTPQVSAITUVEGGLSDALRTE ENMEGTRVTTEFEFAPMPSAVSGDDSQLTAS RSEEKDECAMISTSTGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTAGGKNOK VLIISTSTINDYTPQVSAITUVEGLSDALATIE ENMEGTRVTTEFEFAPMPSAVSGDDSQLTAS RSEEKDECAMISTSTGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTAGEKDDSQLTAS RSEEKDECAMISTSTGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTAGERNOKOK VLIISTSTINDYTPQVSAITUVEGGLSDALRTE ENMEGTRVTTEFEFAPMPSAVSGDDSQLTAS RSEEKDECAMISTSTGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTAGERNOKOK VLIISTSTINDYTPQVSAITUVEGLSDALATIS ENMEGTRVTTEFEFAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGISTSSVEDC GOPVSSAVPQEEGPSVTPAEEMGDTAMISTS TSGCCEAMMGSVLQDEDRLTTITREDLSDA AIISTSTAECMPISSASDRHEENDGTAMISTS TSGCCEAMMGSVLQDEDRLTTITREDLSDA AIISTSTAECMPISSASDRHEENDGTAMISTS TSGCCEAMMGSVLQDEDRLTTITREDLSDA AIISTSTAECMPISSASDRHEENDGTAMISTS TSGCCEAMMGSVLQDEDRLTTITREDLSDA AIISTSTAECMPISSASDRHEENDGTAMISTS TSGCCEAMMGSVLQDEDRLTTITREDLSDA AIISTSTAECMPISASDRHEENDGTAMISTS TSGCCEAMMGSVLALQEDRSFTGTAGGSST ASYSAGRGLEGRANSSPAHLRGSPETYOGGTVA	1				}		NVERVSKTODNENNNSHODIDSENMKOKTS
NSNSEKHADHRSTLTKKMHIQSAVSKMYGE KEPHRGTTEVNIDSAPSENDRY QKNLKNTAAEEHWAQGDATLEHSTNLDSSPS LSSVTVVPLRESYDPDVPLFDKRTVLGGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTFAKASITSKRHIERAHQATLLOKQ GKVIMPLGSKLTGVIVENENITKEGGLVDMA KKENDLNAEPNLKQTIKATVENGKKDGJAVD HVVGLNTEKYAETVKLKHKRSPGKVKDISID VERRNENSEVDTSAGSGSAPSVLHQRNGQTE DVATGPRRAEKTSVATSTEGKDKDVTLSPVK AGPATTTSSETRQSEVALPCTSIEADEGLIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGGCAVAESEDRAADL LAVHAVKIEANVISVYTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTTIFIESEVSEDGAVTSAG TEIRAGSISSEEVDGSQGNMMRMGPKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGTEDGEGPASCTGSEDSSEGFAIS SISSEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVTSTGRGNEIGH ASTCTGLGESSEGVLICESAEGDSQITVVEH VEAEAGAAMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSKGDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECFVAHTSPEKEDEDIITSVE NECCDGLMATTASGDITNQNSLAGGKNOGK VLIISTSTTNDYTJPQVSAITDVEGGLSDALTTE ENMEGTRVTTEFFAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIK CAES LQPVAAAVERATOPVLISTADFEGFMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSVEDC EGFVSSAVJQEEGDPSVTTAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRILTTRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNFEGR GDLSATEVSKHKVPMPSLAEENCCFOPMTS ANISTSTAECMPISASIDRHEENQLTADNFEGR GDLSATEVSKHKVPMPSLAEENCCFOPMTS GGKEPOPVLAVSTEEGHNGPSVHKPSAGOGH PSAVCAEKEEKHGKECPEIGPFAGROKESTL HLINAEENNYLLINSLQKEDKSTLA			ì	1	1	1	ATVOUDEL PTCTADSKATAPAVKPGRGTGV
KEPHRGTTEVNIDSETVHRMLISAPSENDRV QNALKNTAAEEHVAQGDATLEHSTNLDSSPS LSSVTVVPLRESYDPDVPLFDRRTVLEGSTA STSPADHSALPNQSLTVRESEVLXTSDSKEGG EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ GKVIMPLGSKLTGVIVENENITKEGGLOMA KKENDLNAEPNLKOTKATVENOKKDGIAVD HVVGLNTEKYAETVKLKHKRSPGKVKDISID VERRNENSEVDTSAGSGSAPSVLHQRNGQTE DVATGPRRAEKTSVATSTEOKDKDVTLSPVK AGPATTTSSETRQSEVALPCTSIEADEGLIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVESEDRAADL LAVHAVKIEANVSVYTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMMMGPKKETEG TYTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGGNDAPPGTSASGEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVTSTGRGREIGH ASTCTGLGEESEGVLICESAEGDSQICTVVEH VEAEAGAAINNANENNVDSMGTEKGSKDT DICSSAKGIVESSVTSAVSKGEVTYPVGGG GPMTSAASOQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTPSFKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNOOK VLISTSTTNDYTPQVSAITDVEGGLSDALTE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDSQLATRE ENNMEGTRYTTEFEAPMPSAVSGDTAMISTS TEGGCEAVMGGAVLQDEDRITITRVEDLSDA AIISTSTAECMPISASIDHEENQLTADNPEGN GDLSATEVSKHKVANIQAEMERQLATSDHAECCASVS GVVVESENERAGTVMEEKDGSGISTSSVEDC EGGYSSAVPQEEGDPSVTPAEEMGDTAMISTS TEGGCEAVMGGAVLQDEDRITITRVEDLSDA AIISTSTAECMPISASIDHEENQLTADNPEGN GDLSATEVSKHKVANIQAEMERQCFGFPFFGRGQKESTL HINAEEKNYLLINSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPPETGGTAK DSSVSREYLAAVNIGAIKADDMPPSQGTAK	İ	İ	1		1		NENSEKHADHRSTI TKKMHIOSAVSKMNPGE
OKNLKNTAAEEHVAQGDATLEHSTNLDSSPS LSSVTVPLRESYDPDVPLFDKRTVLGGTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTFAKASITSKRIIFEAHQATLLDGKQ GKVIMPLGSKLTGVIVENENITKEGGLVDMA KKENDLNAEPNLKQTIKATVENGKKDGIAVD HVVGLNTEKYAETVKLKHKRSPGKVKDISID VERRNENSEVDTSAGSGSAPSVLHQRNGQTE DVATGPRAAKTSVATSTEKDKDVIVTSVK AGPATTTSSETRQSEVALPCTSIEADEGLIGT HSRNNPLHVGAEASECTVFAAEEGGAVVTE GFAESTFLTSTKEGSCGAVAESEGRAAVI LAVHAVKIEANVNSVYTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITTIESVESDGAVTSAG TEIRAGSISSEEVDGSGGNMMKMRGYKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGHEDEGGPASCTGSEDSSEGFAIS SSEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEGEDVYTSTGRNEIGH ASTCTGLGEESEGVLICSSAEGDSQIGTVVEH VEAEAGAAMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSYTSAVSGKDEVTPVPGGCE GFMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSKEEDEITTSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLLISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFRAMPSAVSGDDSQLTAX RSEEKDECAMISTSIGEFFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTNKEEKDECALISTSIAECECASVS GVVYESENERAGTWAEKDGSGISTSSVEDC EGPVSSAVPQEEGDSTYTAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRITTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GGKEPGPVLAVSTEEGINGPSVHKPSAGQGH PSAVCAEKEKHKKEVPPGSPAGROGKESTL HLINAEENNYLLINSLQKEDKSPTTGTAGGSST ASYSAGRGLEGNANSPAHLROPEDTSGGTAK		1			1		VEDIUD GTTEVNIDSETVHRMLLSAPSENDRV
LSSVTVVPLRESYPDVPTLPDKTTVLEGSTA STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASITSK RIIPEAHQATLLDGKQ GKVIMPLOSKLTQVIVENENTIKEGGLVDMA KKENDLNAEPNLKQTIKATVENGKKDGIAVD HVVGLNTERYAETVKLKHKRSPGKVKDISID VERRHENSEVDTSAGSAPSVLHQRNGQTE DVATGPRAEKTSVATSTEGKDKDVTLSPVK AGPATITSSETRQSEVALPCTSIEADEGLIGIT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVESEDRAADL LAVHAVKEANVNSVVTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMMRMGPKKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASGEDGSSVDGTE GESAVTSTGTEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGDVTSTGRGNEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENVNDSMSGTERGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVFGGGE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASDDITNQNSLAGGKNQGK VLISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVERAATGPVLISTAAPEGPBAPP EAESPLASTSKEREDDEGLAISTSIAECCEASVS GVVVESENERAGTWEKDGSGISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMGAVLQEDGRLTITRVEDLSDA AIISTSTAECMPISASIDHEENQLTADNPEGN GDLSATEVSKHKVPMPSLLAENNCCPGPVR GGKEPGPVLAVSTEEGRINGPSVHKPSAGQGH PSAVCAEKEKHGKECPEIGPFAGRGQKESTL HLINAEEKNYLLINSLQKEDKSPETGTAGGSST ASVSAGRGLEGNANSPAHLRGPEGTSGOTAK			1		1		OKNI KNTA A FEHVA OGDATLEHSTNLDSSPS
STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKSITSKRHPBARQATLLDGKQ GKVMPLGSKLTGVIVENENITKEGGLVDMA KKENDLNAEPNLKQTIKATVENGKKDGIAVD HVVGLNTEKYAETVKLKHKRSPGKVKDISID VERRIENSEVDTSAGSGSAPSVLHQRNGQTE DVATGPRRAEKTSVATSTEGKDKDVTLSPVK AGPATTTSSETRQSEVALPCTSIEADEGLIIGT HSRINPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKGESGECAVAESEDRAADL LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTTTFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGMMMRMGPKKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSAOSEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVYSTGRREIGH ASTCTGLGESSEGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTIGLYGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNOGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMTEEKDGSGIISTSSVEDC EGPVSSA VPOGEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLITITRVEDLSDA AIISTSTJAECMPISSAGGGIESTSSVEDC GGKPEGPVLAVSTEEGHNGPSVYKPSAGGOGESTL HLINAEEKNVLLINSLQKEDKSSETGTAAGSST ASYSAGRGLEGNANSPAHLRGPPQTSQQTAK	1	1					I SSUTVUPI RESYDPDVIPLFDKRTVLEGSTA
EGFTVDTPAKASITSKHPPEAHQATLDGKQ   GKVIMPLGSKLTGVIVENENITKEGGLVDMA    KKENDLNAEPNLKQTIKATVENGKKDGIAVD    HVVGLNTEKYAETVKLIKHRSPGKVKDISID    VERRIENSEVDTSAGSGSAPSVLHQRNGQTE    DVATGPRRAEKTSVATSTGKDKDVTLSPVK    AGPATITSSETRQSEVALPCTSIEADEGLIGT    HSRINPLHVGAEASECTVFAAAEEGGAVVTE    GFAESETFLTSTKEGESGECAVAESEDRAADL    LAVHAVKIEANVISVVTEKEDDAVTSAGSEE    KCDGSLSRDSEIVEGTTIFISEVESDGAVTSAG    TEIRAGSISSEVDGSQGMMRMROPKKETEG    TVTCTGAEGRSDNFVICSVTGAGFREERMVT    GAGVVLGDNDAPPGTSASQEGDGSVNDGTE    GESAVTSTGITEDGEGFASCTGSEDSSEGFAIS    SESEENGESAMDSTVAKEGTNVPLVAAGPCD    DEGIVTSTGAKEEDEEGEDVTTSTGRNEIGH    ASTCTGLGEESEGVLICESAEGDSOJGTVVEH    VEAEAGAAMNANNNVDSMSGTEKGSKDT    DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE    GPMTSAASDQSDSQLEKVEDTITSTGLVGGS    YDVLVSGEVPECEVAHTSPSEKEDEDITSVE    NEECDGLMATTASGDITINONSLAGGKNQGK    VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE    ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS    RSEEKDECAMSTSIGGEFLIPISSATTIKCAES    LQPVAAAVEERTGPVLISTADFEGPMPSAPP    EAESPLASTSKEEKDECALISTSIAEECEASVS    GVVVESENERAGTVMEEKDGSGUSTSSVEDC    GEPSSAVPQEEGDPSVTPAEEMGDTAMISTS    TSEGCEA MIGGAVLQDEDRITITRVEDLSDA    AIISTSTAECMPSSATPHEENQLTANDFEGN    GGKEPGPVLAVSTEEGHOFSVYKPSAGQGH    PSAVCAEKEEKHGKECPEIGFPAGRGOKESTL    HLINAEEKNVLLINSLQKEDKSPETGTAGGSST    ASYSAGRGLEGNANSPAHLRGPFQTSQCTAK			l	ł	1	1	STSPADHSAI PNOSLTVRESEVLKTSDSKEGG
GK VIMPLGSKL TGVIVENENTIKEGGLVDMA KKENDLNAEPNI. KOTIKA TVENGKKDGIAVD HVVGLNTEKYAETVKLKHKRSPGKVKDISID VERRNENSEVDTSAGGSAPSVLHQRNGQTE DVATGPRRAEKTSVATSTEGKDKDVTLSFVK AGPATITTSSETRQSEVALPCTSIEADEGLIIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLITSTKEGESGECAVAESDRAADL LAVHAVKIEANVNSVYTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTTFTISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMRMRMPKKETEG TVTCTGAEGRSDNFVICSVTGAGGREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAIMANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGGE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTINDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEKNOGSISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGG GGKEPGPVLAVSTEEGINGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGGKESTI. HLINAEEKNYLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK		1	1	1			EGET VIDTPAK ASTTSK RHIPEAHOATLLDGKQ
KKENDLNAEPNLKOTIKATVENGKKDGIAVD HVVGLTVKLKIKRSPGKVKDISID VERRNENSEVDTSAGSGSAPSVLHQRNGQTE DVATOPRRAEKTSVATSTEGKDKDVTLSPVK AGPATITISETTROESVALPCTSIEADEGLIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETITLTSTKEGESGECAVAESEDRAADL LAVHAVKLEANVNSVVTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEEVDGSQONMMRMGPKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDOTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGDVVTSTGRGNEIGH ASTCTGLGESSEVLICESAEGDSQIGTVVEH VEAEAGAAMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTITSTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDITTSVE NEECDGLMATTASGDTNQNSLAGGKNQGK VLISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAECEASSVS GVVVESNERAGTVMEKDGSGISTSSVEDC EGPVSSAVPQEEGDPSVTTAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITTRVEDLSDA AIISTSTTAECMPISASIDHEENQLTADNPEGN GDLSATEVSKHKVPMPSLLAENNCRCPGPVR GGKEPGPVLAVSTEEGINGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGGKESTI. HLINAEEKNVLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK	1		1	1			GKVIMPI GSKI TGVIVENENITKEGGLVDMA
HVVGLNTEKYAETVKLKHKRSPGKYKDISUD VERRINENSEVDTSAGSGSAPSVLHORNGOTE DVATOPRRAEKTSVATSTEGKDKDVTLSPVK AGPATTTSSETROSEVALPCTSIEADEGLIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLISTKEGESGECAVAESEDRAADL LAVHAVKIEANVNSVYTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTTFTISEVESDGAVTSAG TEIRAGSISSEVDGSQONMMRMGPKKETEG TVTCTGAEGRSDNFVICSVTGAGGFREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDOTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGRNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTISAECEASVS GVVVESENERGTVMEEKEDGSGISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMGAVLQDEDRLTITRVEDLSDA AIISTSTAECMTSAGDHERNOLSDA			1	1			KKENDI NAEPNI KOTIKATVENGKKDGIAVD
VERRNENSEVDTSAGSGSAPSV-HQRNGQTE DVATGPRAEKTSVATSTEGKLKDVTLSPVK AGPATTTSSETRQSEVALPCTSIEADEGLIIGT HSRNNPI-HVGAASECTVFAAAAEGGAVVTE GFASSETFLTSTKEGESGECAVAESEDRAADL LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITTISEVESDGAVTSAG TEIRAGSISSEEVDGSVGNMMRMGPKKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEGEDVVTSTGRGNEIGH ASTCTGLGEESGGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTINDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEFELPISSATILKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMGGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISSAGDREENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGSPSVHKPSAGQGH PSAVCAEKEEKHIGKECPEIGSPFAGRGOKESTL HLINAEEKHRKVPLINSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTEVIA AVNTGAKADDMEPVOGTVA			1	}			HVVGI NTEKYAETVKLKHKRSPGKVKDISID
DVATGPRRAEKTSVATSTEGKDKDVTLSPVK AGPATTTSSETRQSEVALPCTSIEADEGLIGT HSRNNPHVGAEASECTVFAAAEEGGAVVTE GFAESETFI.TSTKEGESGECAVAESEDRAADL LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITTISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMMRMOPKKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVVTSTGRONEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSCKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTITISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALATE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RESEKDECAMISTSIGEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EASSPLASTSKEEKDECALISTSIAECCEASVS GVVVESENERAGTVMEEKDGSGISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMGGAVLQDEDRLITITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEECHNGPSVHKPSAGGH PSAVCAEKEERHGKECPEIGPFAGRGQKESTI HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGGTAK	1	- [	)	•	•		VERRNENSEVDTSAGSGSAPSVLHORNGQTE
AGPATTTSSETRQSEVALPCTSIEADEGLIGT HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVAESEDRAADL LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMMRMOPKKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASQEGDGSVNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVVTSTGRONEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNONSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFFAPMFSAVSGDDSQLTAS RSEEKDECAMISTSIGEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EASPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGISTSSVEDC EGPVSSAVPQEEGDPSVTTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRITTRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGOKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGIANNSPAHLRGPEQTSGCTAK	1	ĺ	- \		1		DVATGPRRAEKTSVATSTEGKDKDVTLSPVK
HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVAESEDRAADL LAVHAVKIEANVNSVTIEKDDAVTSAGSEE KCDGSLSRDSEIVEGTITIFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMRMOPKKETEG TVTCTGAEGRSDNFVICSVTGAGPREERMVT GAGVVLGDNDAPPGTSASOEDGSSVDNDGTE GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD DEGIVTSTGAKEEDEEGEDVVTSTGRONEIGH ASTCTGLGEESEGVLICESAEGDSQIGTVVEH VEAEAGAAIMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LOPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSLAECCEASVS GVVVESENERAGTVMEEKDGSGIISTSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGGNANSPAHLRGPEGTSGQTAK		1					AGPATITSSETROSEVALPCTSIEADEGLIIGT
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VEAEAGAAIMNANENNVDSMSGTEKGSKDT DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK		1	1		,		ASTCTGLGEESEGVLICESAEGDSQIGTVVEH
DICSSAKGIVESSYTSAVSGKDEVTPVPGGCE GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSAITIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVQGTVA	1	1	Į	1	1		VEAEAGAAIMNANENNVDSMSGTEKGSKDT
GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHINGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVQGTVA	-			1			DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE
YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHINGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI.AAVNTGAIKADDMPPVQGTVA	1			1	ļ	1	GPMTSAASDOSDSQLEKVEDTTISTGLVGGS
NEECDGLMATTASGDITNQNSLAGGKNQGK VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVOGTVA		1	1	}	1		YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE
VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVOGTVA	1						NEECDGLMATTASGDITNONSLAGGKNOGK
ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVOGTVA					1		VLUSTSTTNDYTPOVSAITDVEGGLSDALRTE
RSEEKDECAMISTSIGEEFELPISSATTIKCAES LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVOGTVA		1	{				FINEGTRATTEEFEAPMPSAVSGDDSQLTAS
LQPVAAAVEERATGPVLISTADFEGPMPSAPP EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVOGTVA	1						RSEEKDECAMISTSIGEEFELPISSATTIKCAES
EAESPLASTSKEEKDECALISTSIAEECEASVS GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVQGTVA	}		1	-	{		LOPVAAAVEERATGPVLISTADFEGPMPSAPP
GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVQGTVA	}		1				FARSPLASTSKEEKDECALISTSIAEECEASVS
EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVQGTVA		1			1		GVVVESENERAGTVMEEKDGSGIISTSSVEDC
TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTIL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYI AAVNTGAIKADDMPPVQGTVA							EGPVSSAVPOREGDPSVTPAREMGDTAMISTS
AIISTSTAECMPISASIDRHEENQLTADNPEGN GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHINGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA					1		TSEGCEAVMIGAVI.ODEDRI.TITRVEDLSDA
GDLSATEVSKHKVPMPSLIAENNCRCPGPVR GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA	l	1		1			AUSTSTAFCMPISASIDRHEENOLTADNPEGN
GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA					1		CDI CATEVER DEVIDENDE LA ENNOR CPGPVR
PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA					1		CONTROL A VETER CHARGASTICKET OF A K
HLINAEEKNVLLNSLQKEDKSPETGTAGGSST ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA			1				DOVELOR A FWA STEEDUNG SALING SWOODL
ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA	1				}		TOAVUAENEENTUNEUTEIUTTAUNUVAESTE
DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA	1	-	1	ĺ	J		HLINALENIA YLLINOLUNEUNOTE I UTAUGOST
EHSFLPAEQQGSEDNLKTSTTKCITGQESKIAP	-	1			ļ		ASYSAURULEUNANSFAILRUFEQISOQIAR
EHSFLPAEQQGSEDNLK1511KC11GQESKLAF			-		}		D22A22IK I LYA ANT GYIYYOLI COLECTIVE
	1	1	1	1	[		EHSFLPAEQQGSEDINLK 1511KC11GQESKIAP

		<del></del>	CEO 1	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid E=Glutamic Acid.
NO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		USSN	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
eotide	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uenœ	t		914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ĺ	l	} !		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	)	1	] .	residue of	sequence	/=possible nucleotide deletion, \=possible
	İ		1	peptide		nucleotide insertion
			<u> </u>	sequence		SHTMIPPATYSVALLAPKCEQDLTIKNDYSGK
			1			WTDQASAEKTGDDNSTRKSFPEEGDIMVTVS
	1		1			SEENVCDIGNEESPLNVLGGLKLKANLKMEA
		]	1			YVPSEEKNGEILAPPESLCGKPSGIAELQRE
	1	1	1			PLLVNESLNVENSGFRTNEEIHSESYNKGEISS
	]			}		GRKDNAEAISGHSVEADPKEVEEEERHMPKR
	1	1	l			KRKQHYLSSEDEPDDNPDVLDSRIETAQRQC
	ì	1	ŀ			PETEPHATKEENSRDLEELPKTSSETNSTTSRV
			ĺ	1	1	PETEPHATREENSRULEELI RISSETTOTI SOF
	1	1	1			MEEKDEYSSSETTGEKPEQNDDDTIKSQE
1302	2652	A	10167	321	842	EPSLFPFLRPSPARPPPRPPAPFPSPELAGPEPH
1302	1	1	1			FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG
	1		ł .	1		NSTVAGRGTSVRCLSPSPRPLPPLLPLLADLLE
	}	}				DGFGEHPFYHCLVAEVPKEHWTPEGNPSPFP
	1	1	]	1		EARETKCYVRSSVGCVEPLTTQAEVTENLDR
			1	1		KNSQQVFKLLKKK
1303	2653	A	10171	206	429	NMILLKKRRLLINSLGEGTINGLLDELLETNV
1303	2033	1				LSQEDTEIVKCENVTVIDKARDLLDSVIRKGA
	1	ł	1			RACEICITYI
1204	2654	$\frac{1}{A}$	10184	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSFAQNGF
1304	2034	Δ.	10101	1 , , ,		YHEAVVLFTQALKLNPQDHRLFGNRSFCHER
	1	1	l			I GOPAWALADAOVALTLRPGWPRGLFRLGK
			İ			LAIMGLOREREAAAVFOETLRGGSOPDAAKEL
		1	1			RSCLLHLTLOGORGGICAPPLSPGALQPLPHA
		Ì	į	ļ		FLAPSGLPSLRCPRSTALRSPGLSPLLH
	<del> </del>	<del> </del>	10194	2	394	TOLLGRRERVDGAAMAACEGRRSGALGSSQ
1305	2655	A	10194	2	1 374	SDEL TPPVGGAPWAVATTVVMYPPPPPPPHR
1	}	)	1	}		DEISVILSEGESYDNSKSWRRRSCWRKWKQL
[	l.	}	j	}		SRLQRNMILFLLAFLLFCGLLFYINLADHWKG
			1	ì		IRNTCT
			10105	1	410	IPGSTISI FGPI SKWTNVMKGWOYRWFVLDY
1306	2656	A	10195	1	410	NAGLLSYYTSKDKMMRGSRRGCVRLRGAVI
	l		ļ			GIDDEDDSTFTITVDQKTFHFQARDADEREK
ļ	ł	1	ł	1		WIHALEETILRHTLQLQVRVFTWFPDSSLVGA
1	- 1	1		ľ		FFFWI VSGFFFK
l			<u> </u>	<del> </del>	308	OGLPSTMVKLGCSFSGKPGKDPGDQDGAAM
1307	2657	Α	10205	85	306	DSVPLISPLDISQLQPPLPDQVVIKTQTEYQLS
}	1					SPDOONYTKSR
1	t _				452	ECGGIRQPGPPPALASAPAATMNRVGGSPS
1308	2658	A	10214	2	453	AAANYLLCTNCRKVLRKDKRIRVSQPLTRGP
1		1	}	1		SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL
1	1		1		1	DNITQVMSLHTQYLESFLRSQFYMLRMDGPL
		j	}	1	}	PLPYRHYIAIMAAARHQCSYLINM
	1	)	L	1		RGWPEQQSTGRPRDVARQPRCQKEEGRRLRP
1309	2659	A	10233	45	421	RGWPEQQSTGRPRDVARQPRCQREEGRACKI RALESRTFQGSERSRWGPPLESTKENVQCGH
1					}	RALESKI FQUSEKSK WUFFLEST KEN VQCUIT
1		1				RPAFPNSSWLPFHERLQVQNGECPWQVSIQM
1				1		SRKHLCGGSILHWWWVLTAAHCFRRTLLDM
1 .			1			AV ODNIUTIVI VDDV
1310	2660	A	10241	243	442	AFQLFNAKCESAFLSKRNPLQRNWTVLYRRK
1210	2000	^	10241	= ·· <del>·</del>	1	HKKGQSAEIQKKRTRRAFKFQRAITGASLADI
ſ			1	1	i	MAK
1000	<del>-  </del>		10261	751	176	LPGADYGGGHLSLRLFHLLLTSAAWVPDESQ
1311	2661	Α	10201	(3)	1	VTI NSAICVLSTVLIMEFPDLGKHCSEKTCKQ
		1		1		LDFLPVKCDACKODFCKDHFPYAAHKCPFAF
		1		1	1	OKDVHVPVCPLCNTPIPVKKGQIPDVVVGDHI
1						DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML
						QMVCAQCHGNFCIQHRHPLDHSCRHGSRPTI
1		}		1		KAG
1.						STSSDEGSPSASTPMINKTGFKFSAEKPVIEVP
1212	2662	A	10270	3	669	SMTILDKKDGEQAKALFEKVRKFRAHVEDSD
1312	2002	1				T OVERLY DANDEROVE OF ERRARATION

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						(A-Alexina C-Custains
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	}		914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	1		sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
		<b></b> -	<del> </del>	sequence		LIYKLYVVOTVIKTAKFIFILCYTANFVNAISF
	}		ļ	]		EHYCKPKVEHLIGYEVFECTHNMAYMLKKL
	1	Ì	1			LISYISIICVYGFICLYTLFWLFRIPLKEYSFEKV
	}	ł	1			REESSFSDIPDVKNDFAFLLHMVDQYDQLYS
	i	1			1	KRFGVFLSEVSENKLREISLNHEWTFEKL
1313	2663	A	10287	1221	266	GAHRVLSPAQGAQPRLRSAASVEVSMVGQR
1212	2003	1 **	1020.			VLLLVAFLLSGVLLSEAAKILTISTLGGSHYLL
					1	LDRVSQILQEHGHNVTMLHQSGKFLIPDIKEE
		1			1	EKSYQVIRWFSPEDHQKRIKKHFDSYIETALD
		ł	1			GRKESEALVKLMEIFGTQCSYLLSRKDIMDSL
ł	1	1	İ		1	KNENYDLVFVEAFDFCSFLIAEKLVKPFVAIL
Į	1	-				PTTFGSLDFGLPSPLSYVPVFPSLLTDHMDFW
}	1	1				GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF PEGSRPVLSHLLLKAELWFVNSDCAFDFARPL
	1	1		}		LPNTVYIGGLMEKPIKPVPQVSEPSAFSLGFT
					1000	NVQLAKFSSTLVFFFSCDADPSALAKYVLAL
1314	2664	A	10288	536	1890	VKKDKSEKELKALCIDQLDVFLQKETQIFVEK
						LFDAVNTKSYLPPPEQPSSGSLKVEFFPPQEK
	ł	\				DIKKEEITKEEEREKKFSRRLNHSPPQSSSRYR
}	į.	1	}			ENRSRDERKKDDRSRKRDYDRNPPRRDSYRD
İ	1					RYNRRRGRSRSYSRSRSRSWSKERLRERDRD
ļ					•	RSRTRSRSRTRSRERDLVKPKYDLDRTDPLEN
Ì		1			1	NYTPVSSVPSISSGHYPVPTLSSTITVIAPTHHG
1	Ì				[	NNTTESWSEFHEDQVDHNSYVRPPMPKKRC
1						RDYDEKGFCMRGDMCPFDHGSDPVVVEDVN
		1				LPGMQPFPAQPPVVEGPPPPGLPPPPPILTPPPV
	1	ŀ			1	NLRPPVPPPGPLPPSLPPVTGPPPPLPPLQPSG
		I				MDAPPNSATSSVPTVVTTGIHHQPPPAPPSLFT
	ł				1	ADTYDTDGYNPEAPSITNTSRPMYRHRVHPR
	İ	1	ŀ	_		AKLG
1315	2665	A	10293	447	1331	SHPLLSCPEKVSAKLRAAAEAAAEERRTRGA
		1				GSRGICAGLRSVAPGPEPLKQEEGRREWGSSI GTPSPCGSAQAAAAAAAEEATEKIPALRPALL
						WALLALWLCCATPAHALQCRDGYEPCVNEG
1		}		1		MCVTYHNGTGYCKCPEGFLGEYCQHRDPCE
		1			1	KNRCQNGGTCVAQAMLGKATCRCASGFTGE
1						DCQYSTSHPCFVSRPCLNGGTCHMLSRDTYE
1		1		-		CTCQVGFTGRNPKCPGGNLNYQFNGIIVVYS
1		1				GGSVPPSGTKTSKPAEHNAMGTGSKNFASGT
	1	1	İ	1		LWVMVSGATSTSTSTL
	1	<del>-   -</del>	10004	118	572	SLSMESNHKSGDGLSGTOKEAALRALVQRTG
1316	2666	Α	10294	110	312	YSLVOENGORKYGGPPPGWDAAPPERGCEIF
						GKLPRDLFEDELIPLCEKIGKIYEMRMMMDF
						NGNNRGYAFVTFSNKVEAKNAIKQLNNYEIR
					Ì	NGRLLGVCASVDNCRLFVGGIPKTKK
1015	- 000	<del></del>	10301	158	1956	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQ
1317	2667	Α	10301	130	[ 1550	DRPTKSSMRSAAKPWNPAIRAGGHGPDRVRP
				1		LPAASSGMKSSKSSTSLAFESRLSRLKRASSE
Ì		Ì				DTLNKPGSTAASGVVRLKKTATAGAISELTES
	1		İ	1		RLRSGTGAFTTTKRTGIPAPREFSVTVSRERSV
					1	PRGPSNPRKSVSSPTSSNTPTPTKHLRTPSTKP
1		Į.	1	1	1	KOENEGGEKAALESOVRELLAEAKAKDSEIN
ì		1	1		İ	RLRSELKKYKEKRTLNAEGTDALGPNVDGTS
	1	1	1			
					İ	VSPGDTEPMIRALEEKNKNFQKELSDLEEENR
						VSPGDTEPMIRALEEKNKNFQKELSDLEEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ
						VSPGDTEPMIRALEEKNKNFQKELSDLEEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ ESSFGSPTGNQLSSDIDEYKKNIHGNALRTSG
						VSPGDTEPMIRALEEKNKNFQKELSDLEEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ ESSFGSPTGNQLSSDIDEYKKNIHGNALRTSG SSSSDVTKASLSPDASDFEHITAETPSRPLSSTS
						VSPGDTEPMIRALEEKNKNFQKELSDLEEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ ESSFGSPTGNQLSSDIDEYKKNIHGNALRTSG

WO 01/57188

	_					Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ		ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Sequence	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		<u> </u>	<del> </del>	sequence		NEKLVDEKTILETSFHOHRERAEQLSQENEKL
		j		)	ļ	MNLLOERVKNEEPTTOEGKIELEQKCTGILE
		1		<b>t</b>		OGREEREKLLNIOOOLTCSLRKVEEENQGAL
		1	1	1		EMIKRLKEENEKLNEFLELERHNNNMMAKTL
	}	1	į	[		FECRYTLEGLKMENGSLKSHLQG
1210	2668	A	10303	333	879	GECFIMAAVVQQNDLVFEFASNVMEDERQL
1318	2000	Α	10303	} 333		GDPATEPAVIVEHVPGADILNSYAGLACVEEP
		1			ĺ	NDMITESSLDVAEEEIIDDDDDDDTTLTVEASCH
			j	}		DGDETIETIEAAEALLNMDSPGPMLDEKRINN
						NIFSSPEDDMVVAPVTHVSVTLDGIPEVMETQ
	1			}		QVQEKYADSPGASSPEQPKRKKK
1319	2669	A	10322	169	654	MEVRMSGSVAVTRAIAVPGLLLLLIIATALSL
1317	2007	1	1			LIGAKSLPASVVLEAFSGTCQSADCTIVLDAR
		1		1		LPRTLAGLLAGGALGLAGALMQTLTRNPLAD
		ì	1	1	ĺ	PGLLGVNAGASFAIVLGAALFGYSSAQEQLA
		İ				MAFAGALVASLIVAFTGSQGGGQLSPVRLTL
	}	ļ	1			AGVXL
1320	2670	A	10323	441	2	KMNQVAVVIGGGQTLGAFLCHGLAAEGYRV
1320		1	]		}	AVVDIQSDKAANVAQEINAEYGESMAYGFG
{		}	İ			ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI
	1		ł		1	AKAAFISDFQLGDFDRSLQVNLVGYFLCARE
1		f	·			FSRLMIRDGIQGRIIQINSKSDE RHRTAGPGSTISSRTDSASAPAARAMPCEYTY
1321	2671	A	10332	1	453	AKLTSDCSRPSLQWYTRAQSKMRRPRLLLKD
		ļ	Ì		j	ILKCTLLVFGVRILYILKLNYTTEECDMKNMH
		İ	•	1		YVDPDHVKRAQKYAQQVLQKESPPKFAKTS
l	Ì	İ	1			MALLFEHRYSVDLLPFVQKAPTDSEA
			<del>                                     </del>	105	423	EPSNGPVVYSALGNEDDEILLLGKDIIGTFAAS
1322	2672	Α	10333	25	423	ERKMRAHQVLTFLLLFVITSGASENASTSRGC
		1	}	1	ļ	GLDLLPONVYLCDLDAIWGIVVEAVAGAGA
		1		1		LITLLLMLILLGRLPFIKEKEKKSPAVLHFLFL
		1			}	LGTLG
1000	2673	+	10334	52	426	SSLGNEDDEILSLAKDITGMFVASHRKMRAH
1323	2073	^	10334	1 2 2	1	QVLTFLLLFVITSVASENASTSRGCGLDLLPQ
		1		1	j	YVSLCDLDAIWGIVVEAAAGAGALITLLLMLI
						LLVRLPFFKEKEKKSPVGLHFLFLLGTLGP
1324	2674	A	10336	1	932	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEE
1324	2014	, ,				NSVTHHEVKCQGKPLAGIYRKREEKRNAGN
1		'		1		AVRSAMKSEEQKIKDARKGPLVPFPNQKSEA
				-		AEPPKTPPSSCDSTNAAIAKQALKKPIKGKQA
1		1		1		PRKKAQGKTQQNRKLTDFYPVRRSSRKSKAE
}		1	}	1		LOSEERKRIDELIESGKEEGMKIDLIDGKGRG
1		1		1		VIATKOFSRGDFVVEYHGDLIEITDAKKREAL
1		1		1		YAQDPSTGCYMYYFQYLSKTYCVDATRETN
		1	}	1		RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS RDIAAGEELLYDYGDRSKASIEAHPWLKH
						PGSTISCSELKGTQCRATAGSRGRRPPMTCWL
1325	2675	A	10338	3	870	RGVTATFGRPAEWPGYLSHLCGRSAAMDLG
				1		PMRKSYRGDREAFEETHLTSLDPVKQFAAWF
		1	1			EEAVQCPDIGEANAMCLATCTRDGKPSARML
	}	}		1		LLKGFGKDGFRFFTNFESRKGKELDSNPFASL
		- }		1		VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS
	}	1			-	RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE
1	}	1	}			QLYQDQEVPKPKSWGGYVLYPQVMEFWQG
1		- 1		1		OTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE
	1.	1				TOTAL TANGENT AND THE PROPERTY OF THE PROPERTY
				}		DWI YERLAP
					084	DWLYERLAP
1326	2676	A	10344	2	984	DWLYERLAP  ARAAAHCGICRLVRWWRKRRSVMGIQTSPV
1326	2676	A	10344	2	984	DWLYERLAP

SEQ ID SEQ ID NO: of NO	e, ,
NO: of nucl- nucl- peptide eotide seq- uence uence    NO: of nucl- peptide eotide seq- uence   S	e,
Seq-   uence   USSN   location   corresponding   to last amino   acid   residue   of peptide   sequence   ue	e,
eotide sequence wence uence where the corresponding to first amino acid residue of peptide sequence wence wence wence where the corresponding to first amino acid residue of peptide sequence wence wence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid residue of peptide sequence where the corresponding to first amino acid	
sequence    Sequence   914   ng to first amino acid residue of peptide sequence   914   ng to first amino acid residue of peptide sequence   12   1327   2677   A   10345   1   968     10345   1   968   Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon /=possible nucleotide insertion   HHTLGLPVGKHIYLSTRIDGSLVIRPY   EDQGYVDLVIKVYLKGVHPKFPEGG   LDSLKVGDVVEFRGPSGLLTYTGKG   NKKSPPEPRVAKKLGMIAGGTGITPN   ILKVPEDPTQCFLLFANQTEKDIILRE   ARYPNRFKLWFTLDHPPKDWAYSK   MIREHLPAPGDDVLVLLCGPPPMVQ   LDKLGYSQKMRFTY   LQSAGEGVTHVLILLESPARPVAAV   RYHRLSDMSMLAERRRKQKWAVD   SNDDSKFGQRMLEKMGWSKGKGL   ATDHIKVQVKNNHLGLGATINNEDI   DDFNOL LAFLNTCHGOETTDSSDKE	
uence  amino acid residue of peptide sequence  amino acid residue of peptide sequence  sequence  T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon /=possible nucleotide deletion, \=possible nucleotide insertion  HHTLGLPVGKHIYLSTRIDGSLVIRPY EDQGYVDLVIKVYLKGVHPKFPEGG LDSLKVGDVVEFRGPSGLLTYTGKG NKKSPPEPRVAKKLGMIAGGTGITPN ILKVPEDPTQCFLLFANQTEKDIILRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY  LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI DDFNOL LAFLNTCHGOETTDSSDKI	١,
residue of peptide sequence sequence y=Tyrosine, X=Unknown, *=Stop codon /=possible nucleotide deletion, \=possible nucleotide insertion  HHTLGLPVGKHIYLSTRIDGSLVIRPY EDQGYVDLVIKVYLKGVHPKFPEGG LDSLKVGDVVEFRGPSGLLTYTGKG NKKSPPEPRVAKKLGMIAGGTGITPN ILKVPEDPTQCFLLFANQTEKDILLRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY  LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI DDFNOL LAFLNTCHGOETIDSSDKE	١,
/=possible nucleotide deletion, \=possible nucleotide insertion    HHTLGLPVGKHIYLSTRIDGSLVIRPY	'
nucleotide insertion  HHTLGLPVGKHIYLSTRIDGSLVIRPY EDQGYVDLVIKVYLKGVHPKFPEGG LDSLKVGDVVEFRGPSGLLTYTGKG NKKSPPEPRVAKKLGMIAGGTGITPY ILKVPEDPTQCFLLFANQTEKDILLRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY LQSAGEGVTHVLILLESPARPVAAV' RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	• 1
sequence    Inucleotide insertion	´
HHTLGLPVGKHIYLSTRIDGSLVIKT EDQGYVDLVIKVYLKGVHPKFPEGG LDSLKVGDVVEFROPSGLLTYTGKG NKKSPPEPRVAKKLGMIAGGTGITPN ILKVPEDPTQCFLLFANQTEKDIILRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	(12TV/QTV
LDSLKVGDVVEFRGPSGLLTYTGKG NKKSPPEPRVAKKLGMIAGGTGITPN ILKVPEDPTQCFLLFANQTEKDIILRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI DDFNOLLAFLNTCHGOETIDSSDKE	LILAISD
NKKSPPEPRVAKKLGMIAGGTGITPI ILKVPEDPTQCFLLFANQTEKDIILRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	INMOO I
ILKVPEDPTQCFLLFANQTEKDILLRE ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	HINIQI HINIQI
ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY  LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	VILQLIKA
ARYPNRFKLWFTLDHPPKDWAYSK MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY  LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	DLEELQ
MIREHLPAPGDDVLVLLCGPPPMVQ LDKLGYSQKMRFTY  1327 2677 A 10345 1 968 LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	GFVIAD {
1327 2677 A 10345 1 968 LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGLU ATDHIKVQVKNNHLGLGATINNEDI	LACHPN
1327 2677 A 10345 1 968 LQSAGEGVTHVLILLESPARPVAAV RYHRLSDMSMLAERRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI DDFNOLLAFLNTCHGOETTDSSDKE	
RYHRLSDMSMLAERRRKQKWAVD SNDDSKFGQRMLEKMGWSKGKGL ATDHIKVQVKNNHLGLGATINNEDI	TQVQRR
SNDDSKFGQRMLEKMGWSKGKGLO ATDHIKVQVKNNHLGLGATINNEDI DDFNOLLAFLNTCHGOETTDSSDKI	PUNIAW
ATDHIKVQVKNNHLGLGATINNEDI DDFNOLLAFLNTCHGOETTDSSDKI	GAQEQG
DDFNOLLAFI.NTCHGOETIDSSDK	NWIAHQ
I DDFNOLDAELNICHGQDIIDODDIA	KEKKSFS
LEEKSKISKNRVHYMKFTKGKDLSS	RSKTDL
DCIFGKRQSKKTPEGDASPSTPEENI	TTTTSAF
DCIFGKRQSKK I PEGDASI STI LEIN TIQEYFAKRMAALKNKPQVPVPGSI	DISETOVE
RKRGKKRNKEATGKDVESYLQPKA	KRHTEG
RKRGKKRNKEAIGKUVESIECIKA	GPCWDO
KPERAEAQERVAKKSAPAEEQLR	Grewby
SSKASAQDAGDHVQPA	MDENICGI
1328 2678 A 10346 173 439 GSAAMKVKIKCWNGVATWLWVA	NDENCGI
1 1320   2070   11   1   CRMAFNGCCPDCK VPGDDCFL V W	GUCSHCF
UMHCII KWI.HAOOVOOHCPMCRQ	EWKIKE
OVER CAND TO IS FELLI GESO EPGLO	PFLFGLFL
1329 2679 A 10331 SAVIVIVI GNI LIILATISDSHLHII	MALLEDN
I SEADICVESTIPKMLMNIUIUNK	ALL ATACE
MOMVEEU FAGEENFLLSYMAYDK	FVAICHP [
T UVMVIMNPHI CGLI VLASWIMS	ALYSLLQI I
1 MVVRI SECTAL EIPHFFCELNQVI	QLACSDSr
I NHMVIVETVALLGGGPLTGILYS)	(2KH22H
AISSAOGKVKAFSTCASHLSVVSLF	YGAILGV
YLSSAATRNSHSSATASVMYTVVT	PMLNPFI
VSI PNIKDIKRAL GIHLL WGTMKGC	)FFKKCP
THE I VSCCCCCI EDEPPPPI DOVOE	ECEVERV
1330 2680 A 10352 34 2573 IPFLKSCCCCCLFDFPPPLDQVQEA	OFENDLE
TDPPNWQQLVSREVLLGLKPCEIK	ROEVINEL
FYTERAHVRTLKVLDQVFYQRVSF	EGILSPSE
FYTERAHVRILAVLING MEOMY AV	RKRNETS
LRKIFSNLEDILQLHIGLNEQMKAV	AATECSNO
VIDQIGEDLLTWFSGPGEEKLKHA	ESMDI CRR
PFALEMIKSRQKKDSRFQTFVQDA	TYTEWAT
LQLKDIIPTQMQRLTKYPLLLDNIA	TITEMET
	KEAENNY
predvorri de la	PKMPDFIK I
DVMIHEGPI VWKVNRDKTIDLYTI	LLEDILY
I I OKODDRI VI.RCHSKILASIADS	KHILDLAI
VI STVI VROVATDNKALFVISMSL	)NGAQIYE
TVAOTUSEKTVWODLICRMAASV	KEQSIKPI
DI POCTPGEGDNDEEDPSKLKEEU	HG12AIGL
OSPOPDI GI ESTI ISSKPOSHSLST	SGKSEVKD
I EVAEROFAKEOHTDGTLKEVGE	DIQIAIDS
HLPVSEERWALDALRNLGLLKQL	LVOOLGLT
EKSVQEDWQHFPRYRTASQGPQT	DSVIONSE
NIKAYHSGEGHMPFRTGTGDIATO	YSPRTSTE
NIKAYHSGEGHMFFRTOTOLIATE SFAPRDSVGLAPQDSQASNILVMI	HMIMTPE
SFAPRDSVGLAPQDSQASNLVNILL	HSDENPSE
MPTMEPEGGLDDSGEHFFDAREA	CALLANDE
GDGAVNKEEKDVNLRISGNYLILI	TIOOOUSD TO TOTAL
SSTDEEVASSLTLQPMTGIPAVEST	NEVECTE:
ONTHSTIGATSPETPEFLVOORWGA	MEASCLEI
OSPSSCADSOSOIMEYIHKIEADLE	HLKKVEE
SYTILCQRLAGSALTDKHSDKS	

SeQ III DNO of peptide sequence of the sequenc			1 14 .	1 000	Deadlesed	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucleotide seq. USSN 09/496 porter contraction of the contraction of t	SEQ ID	SEQ ID	Mct	SEQ	Predicted	1	D-Americ Acid F=Glutemic Acid
USSN   05496   09496	1	1	hod	1		1	E-Phenylalanine G-Glygine H-Histidine
sequence once of the property		peptide			l =:		F=Filenylaiannie, O=Grychie, ri=ristidine,
uence    14	eotide	seq-		1			I=Isoleucine, K=Lysine, L=Leucine,
914   ag to first samine acid residue of peptide sequence   914   ag to first samine acid residue of peptide sequence   7-Threadine, V-Valine, W-Trytophan, Y-Tyrosine, X-Eukinowa, *-Stop codon, Possible mulceloide design, Valine	seq-	uence	1	09/496	correspondi		
1331		į.		914	ng to first	acid residue	
Peptide			Ì	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Peptide	ļ	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1331	ł	ł		1	}	1	/=possible nucleotide deletion, \=possible
1331   2681   A   10353   I   2160   AAGQOPAPDKSKETKTONTEAPYTKIELD   SYSTATLIDEPTEVDPPWNLPTLQDSGIKWES   RDTKGKILFPQGIGRLILLIGELYPYCSLDL   SSAFQL VGGKMAGGFFSNSSIMSPILLGLVIG   VLYTVLYQSSTTSTILVLILLIGELYPYCSLDL   SSAFQL VGGKMAGGFFSNSSIMSPILLGLVIG   VLYTVLYQSSTTSTILVLIPPEVATHYLEITOL   VLYTVLYQSSTTSTILVLIPPEVATHYLEITOL   VLYTVLYQSSTTSTILVLIPPEVATHYLEITOL   VLYTVLYQSSTTSTILVLIPPEVATHYLEITOL   VLYTVLYGSSTTSTILVLIPPEVATHYLEITOL   VLYTVLYGSSTTSTILVPEVATHYLEITOL   VLYTVLYGSSTTSTILVGLDK   KVISQJAMNDEKAKINSLVIKWCKTETTIKTO   VLYTVLYSTANCTSPSL CWTDGJONWTAKNIVT   VYESHAKCCHIFNINFIDLA VYTILLISLLV   VLYTVLSTANCTSPSL CWTDGJONWTAKNIVT   VYESHAKCCHIFNINFIDLA VYTILLISLLV   VLYTVLSTANCTSPSL CWTDGJONWTAKNIVT   VYESHAKCCHIFNINFIDLA VYTILLISLLV   VLYTVLSTANCTSPSL CWTDGJONWTAKNIVT   VYESHAKCCHIFNINGLL WYPPT   VLYTVLSSINGTTTAIL AAL   ASKGNALRSSL QUAL CHEFFINISGL   VYESHAM   VYES	ł	1					
AAGQQPTAPDKSKETNKTDNTEAPTYTKILLY SYSTATLIDEPTEVDPWNLPTLODSGIKWSE RITKGKILCFFQGGGLILLLGFLYFFVCSLDIV SAFQLVGGKMAGGFSNSSIMSPRILGJUG ULVTVLVQSSSTSTISIVVSMVSSSLITVRAADI INGANATGSTISTIVALMQVGDRSFFRAFA GATYHDFFNMLSVLVLLYEVATHYLEITTQL VESFHKNGEDAPLLKVTIKFTLIVQLDK KVISQIAMMERAKNKSLVKIWCKTFTIKTYT NIVTVPSTANCTSSSICWTDGGINGTMKINTY YKENIAKCQHIFVKFHLPDLAVGTILLISLLV LCGLIMIVKLIGSVLKGOVATVKKITTINKTYT YKENIAKCQHIFVKFHLPDLAVGTILLISLLV LCGLIMIVKLIGSVLKGOVATVKKITTINKTYT YKENIAKCQHIFVKFHLPDLAVGTILLISLLV LCGCLIMIVKLIGSVLKGOVATVKINTDFP FPFAWLTGYLAILVGAGMTFIVGSSSVFTSAL PILIGIGVTIERAYPLTLGSNIGTTTAILAAL ASPGNALRSSLQIALCHFFRISGELLWYPIFFLIP LTYPGLSLAGWRVLVOVGPVVFIILIVLCL CGPKCCCSKCCEDLEAGAGGQVYVKAPET FINITISREAGGEVPASDSKTECTAL LQSRCFRVLPKKQNWFPLPWMRSLKFW DAVVSKTTGCFGMRCCCCCRVCCRACCLLC GCPKCCCSKCCEDLEAGAGGGVYVKAPET FINITISREAGGEVPASDSKTECTAL CGPKCCCSKCCEDLEAGAGGGVYVKAPET FINITISREAGGEVPASDSKTECTAL SGOGSPHROGPPSLTAPHSELDPALPFGGR SGOGKLRRVLVPMSVEPSWGPGPSEGVTAV TSDLGGEHNWTELLDLFNHTLSECHVELSQST KRVVLFALYLAMFVVGLVENLLVICVNWME VTLDYTWLWGSFSCRTTHYFYFVNMYSSFF LVCLSVGRYTLTSASPSWGRVGHVRRAM CAGIWVLSAIPLPEVVHIQLVEGPEPMCLFM APFETTSTWALAVALSTTLICHLEVHLYLFPLUTVTN VLTACRLROPGOPKSRRICLLLCAYVAVFV MCWLPYHTVLLILTHGTHISLICHYHLYLT FFYDVIDCFSMLHCVINPLYNTLSPHERGRLL NAVWHYPKDGTAGGAGSSSCTGHSUIT KGDSQPAAAPHPEPSLSFQAHHLLPNTSPISP TQPLTPS  1333 2683 A 10358 2 884 AAGAGADGREPASERASRAEPFAVAMGGNL LAGSGFKTLAGALTUVWLFANDYSAFWT VLTACRLROPGOPKSRRÄCLLLCAYVAVFV MCWLPYHTVLLILTHGTHISLIFVANLCSTLL LAESRSGKSMRAGVPTMRSSSRKQYMOLGG RVLLVIMFMTLHEDASFFSIVQNIVGTAMV LVAIGFKTELAALITUVWLFANTVYFNAFWT IPVYKMHDPLKYDFGTMSVIGGLLLVVAL SSFVFILLIGQLTCOVLVLSRRYCYQALFGGLF GIIALQTIAYSILWDLKFLMRMSLLIKELIKELM LAESRSGKSMRAGVPTMRSSSRKYMYMAGALAGGGLLLVVAL GFGGVSMDEKKKEW SALAVELLGFERFHALIOKRSFRSLPELKDAV UNGGSGFGGFCAVALIVVYFNAFSSKS WRCCSQEEGKELLCHTLCDILESACCDHSGS ALGGFGGFCAVALIVVYFNAFSSKS WRCCSQEEGKELLCHTLCDILESACCDHSGS SALAVELGGEGFFTHALIOKRSFRSLPELKDAV UNGGRESGRKALLGHINGACHTIME LVWGTKSSFGLSDTIFCKWTGCFVFSSEGGS VCLVSWIRGKTTETETASISGSPASSCOVEHS SALAVELGFGEFFTALIOKRSFRSLPELKDAV UNGGRESGRKALLGHINGAVCHERINK EIEDASE		0.00	<del> </del>	10252		2100	
SYSTATLIDEPTEVDDPWALPTLQDSGIKWSE BRITKGKRILCFPGGGGRILLLIGET, FFFVCSLDIL SSAFQLVGGKMAGGFFSNSSIMSNPLLGLUG U.VTVLVQSSSTSTISVSMYMSSLLTVRAAIP IIMGANIGTSTINTIVALMQVGDRSEFRRAFA GATVHDFFNNLSVLVLLPVSVATIVELITQL IVESPHFKNGEDAPDLLKVTIKFFTKLIVQLDR KVISQIAMDERAKNSLVLIWCFFTINTQ INVTVSTANCTSPSLCWTDGIGNWTMKNVT YKENIARCQHIFVSHIPDLAWGTHISHLULLU LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP PFPAWLTGYLAILUGAGMTFIVOSSYFTSAL TPLIGIGWTIERAYPLTLGSNIGTTTTAILAAL ASPGNALRSSLQLALCHFFENISGILWYPIPFT RLPRMAKGLGHISAVXWFWAVPYLIIFFILI LTVGTSLAGWRVLVQVGVPVYLIFFILI LTVGTSLAGWRVLVQVGVPVYLIFFILI LTVGTSLAGWRVLVQVGVPVYLIFFILI LTVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVLVQVGVPVYLIFFILI TVGTSLAGWRVGCCCCCRVCCCACCLU GCPKCCCSCCCEDLERAGGQDVPVKAPET RLPRMAKGLGHISAVXWFVAWGPVGCCCCRVCCACCLU GCPKCCCSCCCEDLERAGGGDVPVKAPET TSDLGGEIRWVTLAGASDSCCTALE SQCGSGPHROVPVRASSSCCTALE TVGTSLAGWRVGCCCCCRVCCACCLU GCPKCCCCSCCCEDLERAGGGOVPVKAPET TSDLGGEIRWVTLAGAGGGGVPVARGAGGAGGGGPHRVVTNAMSSUFF LVCLSVDRYVTLTSASPSWORYOGRVVRAF SQCGSGRHRVLVFNAVSVPSWGPGSEGVTAVP TSDLGGEIRWVTGLLDLFTNLTCVNWGG SQCAGLMVLVTNAMALDGGVLLVCNWGG SQCAGLMVLVTNAMALDGGVLLVCNWGG SQCAGLMVLVTNAMALGGVLLVGNVVV MCWLPYHVTLLLTLHGTHSISLCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLLY FYYDVDCFSMLHCUNPULNTLSCCHLVHLL FYYDRAMAHALGGGLLLVAL SKYPENLIGGLTCOCH VLSNRYVQ'NACFGLF GIIALQTIAYSLWDLAGRGGNGVTMRSSPRQYMGGG RVLLVLMFMTLHFDASFSTSIQNIVCTALM LVAIGHTSCAGAGGAGGAGGGGRGFTHLTYVRYAFAFWI IPYYRMHDERAYDFCTMSVIGGLLLVAL GGGGVSMDEKKKR SARAVANGCHLCVVLLFSSEGS VCLVSWLGKTTTETTTASISGSPASSCOVEHS SALAVELGGEGFCHALIQKRSFRSLPELKDAV VDGGBGEGGFCAVALIGVYDFCHNKG ELVWGTKSSPGLDTHCCRWTQSFNSSLPELKDAV VDGGBGEGGFCAVALIGVYDFCHNKG ELVWGTKSSPGLDTHCCRWTGSFNS	1331	2681	A	10353	1 1	2100	A COOPTADDY SYSTEM TONTS APVIKIBLED
RITKOKILCFFQGGGLILLLGFLYFFVCSLD/USSARQOFFSNSSIMSPRILGILVIG SAAPQLVGGKMAGGFSNSSIMSPRILGILVIG VLVTVLVQSSSTSTISIVVSMVSSSLITVRAAPJ IIMGANGTSTINTIVALMQVGGREFRAFA GATVHDFFNWLSVLVLLPVEVATHYLEITTQL KVISQIAMDEKAKNKSLVKIWCKTFTINKTQ INTYPYSTANCTSSICWTDGIGNOTHKENVT YKENIAKCQHIEVNFHLPDLAVGTILLISLLVIQLDK KVISQIAMDEKAKNKSLVKIWCKTFTINKTQ INTYPYSTANCTSSICWTDGIGNOTHKENVT YKENIAKCQHIEVNFHLPDLAVGTILLISLLVIQLDK KVISQIAMDEKAKNKSLVKIWCKTFTINKTQ INTYPYSTANCTSSICWTDGIGNOTHLANDLY LCGCLIMIVILLGSVLKGVATVIKTINTDFP FPFAWLTGYLAILVGAOMTFIVQSSSVFTSAL TPLIGIGVTTERAYPLTUGSNIGTTALLAL ASPONALRSSLQIALCHFFRISGILWYPIFLIFPEP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPPP RIPTRIAGAGGAISAYYRWFAVFYLIFPEPPP RIPTRIAGAGGAISAYAWFAVFYLIFPEPPP RIPTRIAGAGGAISAYAWFAVFYLIFPEPPP RIPTRIAGAGGAISAYAWFAVFYLIFPEPPP RIPTRIAGAGGAISAYAWFAVFYLIFPEPPP RIPTRIAGAGGAISAYAWFAVFYLIFPEPPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFAYAWFAVFYLIFYBPP RIPTRIAGAGGAISAYAWFAVFAYAWFAVFAYAWFAVFAYFAYAWFAVFAYFAYFAYAWFAYFAYFAYFAYAWFAYFAYFAYFAYAWFAYFAYFAYFAYFAYAWFAYFAYFAYFAYFAYFAYFAYFAYFAYFAYFAYFAYFAYF	1	ł	Ì	{	4	1	AAGQQFTAFDKSKETIKTDIVIEAT VIKILLET
SSAPQL/GGKMAGGFFSNSSMSNPLLGL/NAAIP ULV-VLVQSSSTSTINVSM/MSSSLITVRAAIP UMGANIGTSTIN/TWALMQ/GGRSEFRRAFA GATYMDFFNNLS/ULV_LPVEVAHTYLEITIQL UVESPHFKNGEDAPDLLKVTKPFTKLIVQLDK KVIQQIAMDBEKAKNSLVIWLGTTILISLLV LVGGLIMIVKLIGSVLKGQVATVIKKTINTDFP FPRAWLTGYLAIL/VQAOMTEVASSVFTSAL TPLIGIGOTITERAYPLTILISRIGTTITALLAAL ASPGNALRSSLQIALCHFFNISGBLWYPIPFI ELTVFGI.SLAGWRVLVQVQFVVFIILVLLCL GCPKCCKSKCCDLEAQEGQOVPVKAPET FINITISREAQGEVPASDSXTECTAL GGPKCCCKSKCCDLEAQEGQOVPVKAPET FINITISREAQGEVPASDSXTECTAL TSLGGEHNWTELLDFALPFGFR GSQGKLRRVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRRVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRRVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRAVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRAVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRRVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRRVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALPFGFR GSQGKLRRVLVPMSVEPSWGPGFSEGVTAVP TSDLGGEHNWTELLDLFALFFGFRL ASPETSTWALAAVASTILLGLFALWHLY FFYDVIDCFSMLRAVSTRIPPFVVIMISSFPHFLIVTN VLTACRLRQPGQPKSRRRICLLCAVAVEV MCWLPYHYTILLTHGTHSILFICH WILLY FFYDVIDCFSMLRCVNPHLYNTLSPHFRGRLL NAVVHYLFROQTKAGTCASSSCSTQHSUBLIT KGDSQFAAAAPHFPSILSFQAHLLLNGTLINGL TLAGGLIGLUVLSRNFVQYACTGLIG TLAGGRAPHARANGVGPTARSSSFRQYMQLGFL GIGLQTTAYSTWALAVGFGPTSUSTGAHLLPNTSPISP TQPLTPS 1333 2683 A 10358 2 884 AGGGGADGREPASERASRAEPFAVAMGQND LMGTAEDFADQFLRVTKQYLPHVARLCLIST LLEGGIRMPGVBGRQDVIDTHVARLCLIST FLEGGIRMPGVBGRQDVIDTHVARLCLIST LLEGGIRMPGVBGRQDVIDTHVARLCLIST LLEGGRAPHAPHGASFSTSVQHACGSLL LAESRSEGKSMFAGVPTMRSSSRQYMCYSLLVAL GPGGVSMDEKKKEW QWSMGVLGVALFFFTASSSGSPASRAAVFQLLFP ELPHPYOGESARRSARRFLIMSELTKELLVAL GPGGVSMDEKKKEW GWSMGVRGVTLFTANSGERSSCQVEHS SALAVELLGFEGFRALICKRSFRSEPELKOA LDQYSMGNKFGVLFLTNSVLTKTGERIKN EIEDASEPLIDPVYGHGSQSLINLLTGHAMSE LVWGTKSSRGLSDTECRWTOGOTYFESEDS LLQFEGGPCAVLJENSKLLTKGERIKN EIEDASEPLIDPVYGHGSQSLINLLTGHAMSE KRUCKVGSYLKISKRYLDCLASETHLIVTKR EIEDASEPLIDPVYGHGSGSLINLLTGHAMSE KRUCKVGSYLKISKRYLDCLASETHLIVTKR EIEDASEPLIDPVYGHGSGSLINLLTGHAMS NVMGGREGKGRACHATOTYPEENGFIPE	Ļ	İ	1			1	SYSTATLIDEPTEVDDPWNLPTLQDSGIRWSE
VLVTVLVQSSSTSTISIVVSMVSSSLLTVRAAP    IMGANGTSTINTIVALMQVGDRSEPRAFA    GATVHDFFNWLSVLVLLPVEVATHYLEITQL    VESPHENGBLABOLLKVTIKSPLIVQLDK    KVISQIAMNDEKAKNKSLVKIWCKTFINKTIVQLDK    KVISQIAMNDEKAKNKSLVKIWCKTFINKTIVQLDK    KVISQIAMNDEKAKNKSLVKIWCKTFINKTIVQLDK    KVISQIAMNDEKAKNKSLVKIWCKTFINKTIVQLDK    VESPHARCQHIPVAFHLPDLAYGTILLISLIVQLDK   LCQCLIMIVKLLGSVLKGQVATVKITILTPE    FFRAWLIGYLAILVGAOMTFIVQSSSYSTISLAAL   TPLIGICVITIERAYPLTLIGSNIGTTALIAAL   ASPONALRSSLQIALCHFFFNISGILLWYPIFIPF    RLIPRMAKGLORISAKYRWAVPYLIHFPLP    LTVPGISLAGWRVLVOVOVPYVFIHLVLLX    LLQSRCFRVLFKKLQNNNFLPLWMRSLXPW    DAVVSKFTGCFGMRCCCCCRVCCACCLLC    GCPKCCKCSKCCEDLEEAQFGQDVFVKAPET    FINNITISEAQGEVASDSSKTECTLIV   GCPKCKCKSKCCEDLEEAQFGQDVFVKAPET    FINNITISEAQGEVASDSSKTECTLIV   GSQGKLRRVLVFMSSLSSKTCHTVFYVNMSSIFF    LVCLSVDRYVTLISASSSVQRYQHRVRRAM    CAGIWVLSAIPLPEVVIIQLVEGEPMCLFM    APFETYSTWALAVALSTITLGFLLPFPLIVFN    VLTACRLRQFQGPGSRRRICLLLCVINWEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGLIMNLYLINMAIADLGIVLSLPVWMEG    SGRAGADGREFASERASRAEPFAVAMGQND    LNAGRETKLALUTVWMFANTSPHFGRILL    NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT    KGDSGPAAAAPHFPESISSTQAHLFNSFINSTPHSTPSISTPHELGGILTAGVLVINSRNFWQYACFGLILVSLUTLSLPFTTNTGYLLAGGLLLL    LAESREGGRAMFAGWPTMRESSPKQYMQLGLLLVALLGGLLLL    LAESREGGRAMFAGWPTMRESSPKQYMQLGLLLVALLGGLLLL    LAESREGGRAMFAGWPTMRESSPKQYMQLGLLLVALLLLLLLSSEKSSS    WRDCSQEEGGRAUTVALLFSSEKSS    WRDCSQEEGGRAUTVALLFSSEKSS    WRDCSQEEGGRAUTVALLFSSEKSS    WRDCSQEEGGRAUTVALLFSSEKSSS    WRDCSQEEGGRAUTVALLTSSEKSS    WRDCSQEEGGRAUTVALLTSSEKSSS    WRDCSQEEGGRAUTVALLTSSEKSS    WRDCSQEEGGRAUTVALLTSSEKSS    WRDCSQEEGGRAUTVALLTSSEKSS    WRDCSQEEGGRAUTVALLTSSEKSS    WRDCSQEE		1					
IIMGANGTSITNTIVALMQVOGRSEFERAFA GATVEDFFNUS.VLVLLPVENTHVLEITQL IVESPHEKNGEDAPDLLKVITKFFTKLYQLDK KVISQIAMIDEKAKNSLVKLWCKTFTINKTO INVTYPSTANCTISPLCWTDGIQNWTMKNYT YEENIAKCQHPVFNFH.PDLAVGAWCTILLISLU LCGCLIMIVKLIGSVLKGQVATVIKKTINTDFP FPFAWLTGYLAHLVGAGMTFIVLLUSSSYFTSAL TPLIGGGYTTERAYPLTLGSNIGTITTALLAAL ASPGNAR,RSLQALACHFFFNISQILWYPIPFT RIPRIMAKGLONISAKYRWFAVPYLIEFFLIP LTVFGLSLAGWRVLVOVGVPVFIILLYCLCR LQSCRPVLYRKLQNWINPLHVMRSLKPW DAVVSKFTGCFQMRCCCCRVCCRACCLLC GCPKCCRCSKCEDLEEAQGEDPVFXAPFT TELLIGGGYTTSALAAL ASPGNAR,RSLQALACHFFFNISQILWYPIPFFLIP LTVFGLSLAGWRVLVOVGVPVFIILLYCLCR LQSCRYPLTREBLDPALPPGFR GSQGKLRRVLVPMSVRSWGPGFSSCVTAVF TSDLGEHINVTELDLFPHTILSECHVELSQST KRVVLFALYLAMFVVGLVENLLVICVNWGG SGRAGLMNLYHMSVRSWGPGFSSCVTAVF TSDLGEHINVTELDLFPHTILSECHVELSQST KRVVLFALYLAMFVVGLVENLLVICVNWGG SGRAGLMNLYHLINMAIADLGIVSLFVWMGE SGRAGLMNLYHLINMAIADLGIVSLFVWMGE VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF LVCLSVDRYVTILSASPSWGRYGHRVRAMA CAGIWVLSAIPLPEVVHQLVGLVGEPEMCLFM AFFETYSTWALAVALSTTLGHCHLVHLLY FFYDVIDCFSMLHCVNDPLYNFLSPFFRCRIL NAVVHYLPKDQTKAGTCASSSSCSTOHSUIT KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP TQPLTPS  1333 2683 A 10358 2 884 AAGGAGDGREPASERASRAEPFAVAMGQND LMGTAEDFAGVERSGRYDTHTWGGYLLA SSFYFINLLGQLTGCVLVLSRNFVQYACGGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLGQLTGCVLVLSRNFVQYACFGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLAGLTGCVVLVSRNFVQYACFGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLAGLTGCVLVLSRNFVQYACFGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLAGLTGCVLVLSRNFVQYACFGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLAGLTGCVLVLSRNFVQYACFGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLAGLTGCVLVLSRNFVQYACFGLF GIILQTIAYSILWDLKFLMRITWGGYLLA SSFYFINLLAGLTGCVLVSRSSSSS WRCSQGEGKELLCHTLCDILESACCDSSSS VCLVSWLRGKTTETASISGSPASSCQVEHS SALAVEELGFERRHALIQKSFRSLFLEKDAV LQCYSMWGNKKGVGLTLINEA ELVSWLSGSYLLGHTERQSGLINLLLTIGHANSN VWDGDRECSGMRULGHTERGASGLINLLTTRIAVSN VWDGDRECSGMRULGHTERGASGLINLLTTVFTA KDMALVAPEAPSEQARRYCTJTDPENOFPT	ł						SSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIG
GATVHDFNWLSVLVLLPVEVATHYLEITOL     VESFHEKNGEAPPLLKVTKPFTKLIVQLOK     KVISQIAMNJEKAKNKSLVKIWCKTFTIKTO      IVEYSPHAKNEQAPPLLKVTKSPTKLIVQLOK     KVISQIAMNJEKAKNKSLVKIWCKTFTIKTO      IVEYPSTANCTSPSLCWTLOSIQNWTMKNVT     YKENIAKCQHFFVNFHLPLAVGTILLISLIV     LCGCLIMIVKILGSVLKGQWATIKLISLIV     LCGCLIMIVKILGSVLKGQWATIKLISLIV     LCGCLIMIVKILGSVLKGQWATIKLATILAL     ASPGNALRSSLQIALCHFFFINISGILWYPIPFT     RLPRMAKGLGNISAKYRWFAVFYLIIFFEIP     LTVFGLSLAGWRVLVGVGYDYVPIIILVLCLR     LLQSRCPVLPKKLQNWNFLPLWMSSLKPW     DAVYSKFTGCGQMCCCCCVCCRACCLLC     GCPKCCRCSKCCEDLEEAQEGQDVPVAPET     LLQSRCPVLPKKLQNWNFLPLWMSSLKPW     DAVYSKFTGCGPWACCCCVCCRACCLL     GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET     FINITISSEAQEGVPASDSKTECTAL     LLQSRCPVLPKKLQNWNFLPLWMSSLKPW     DAVYSKFTGCGPWACCCCVCCRACCLL     GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET     FINITISSEAQEGVPASDSKTECTAL     SQQGSQFHRQGPPSLLTAPHSLDLPALPPGR     GSGKLRRVLVPMSVKPSWGPSECTAL     SQQGSQFHRQGPPSLLTAPHSLDLPALPPGR     GSGKLRRVLVPMSVKPST     SQCGSQFHRQGPPSLLTAPHSLDLPALPPGR     SGRGKLRRVLAPMSVKPST     SQCGSQFHRQGPPSLLTAPHSLDLPALPPGR     SGRGKLRRVLAPMSVKPST     SQCGSQFHRQGPPSLLTAPHSLDLPALPPGR     SGRGKLRRVLAPMSVLTAPHSLAP     SQCGSQFHRQGPPSLLTAPHSLDLPALPPGR     SGRGKLRRVLAPMSVLTAPHSLAP     SQCGSQFHRQGPPSLLTAPHSLDLPALPPGR     SGRGKLRRVLAPMSVLTAPHSLAP     SQCGSGRLRRVLAPMSVLTAPHSLAP     SQCGSGRALAPHSVLTAPHSLDLPALPPGR     SGRGKLRRVLLAPMSVLTAPHSLAP     SQCGSGRALAPHSLAP     SACHTLAPHSLAP     SCRCHCHT     SQCGSGRALAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SCRCHCHT     SQCGSGRALAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAPHSLAP     SACHTLAP     SACHTLAPHSLAP	1		}	ł	1		VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIP
GATVHDFNWLSVLVLLPVEVATHYLEITOL				}			IIMGANIGTSITNTIVALMQVGDRSEFRRAFA
IVESFHERNGEDAPDLLKVITKFFTKLYQLDK   KVISQIAMNDEKAKNISLIVKIJCKIFTINKTQ   INVTVPSTANCTSPSLCWTDGIQNWTMKNT   YKENIAKCQHIPVFHH.PDLAUCHLLISLIV   LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP   FPFAWLTGYLAILVGAQMTIVQSSSYFTSAL   TPLIGIGVTIERAVPTLLISRIVATURIAL   ASPGNALRSSLQIALCHFFINISGILL WYIPPT   RLPRIMAKGI, GNISAKY RWA-NYFVLIEFFLIP   LTVGLSLAGWRVLVGYGVPVFIILVLCLR   LQSRCPNLYRKLQNWNPLLYLLCR   LQSRCPNLYRKLQNWNPLLYLLCR   LQSRCPNLYRKLQNWNPLLYLLCR   LQSRCPNLYRKLQNWNPLLYLLCR   LQSRCPNLYRKLQNWNPLLPLWMRSLKPW   DAVVSKTGCFQMRCCCCRVCCRACCLLC   GCPKCCRCSKCEDLERAGEGQDVPVKAPET   FDNITISREAGGEVPASDSKTECTAL   SQQGSQPHRQGPPSLTAPHSLDLPALPPGPR   GSQKLRRVLVPMSVKPSWGPGFSGOYTAVP   TSDLGEIHNWTELLDLFNHTLSECHVELSQNT   KRVVLFALYLAMFVGLVENHLVICVNWRG   SGRACLMNLYILMMAIADLGIVLSLPVWMLE   VTLDYTWL WGSSCRFTHYFYNMYSSFF   LVCLSVDRYVTLTSASPSWQRYQHRVCHVNWS   CAGIWLSAILPLEVHULDVCHWRAG   SGRACLMNLYILLMGTHUSLCHVLSLPVWMLE   VTLDYTWL WGSSCRFTHYFYNMYSSFF   LVCLSVDRYVTLTSASPSWQRYQHRVCHRWAG   GAGIWLSAILPLEVHULDVCHWRAG   GAGIWLSAILPLEVHULDVCHPREMGLL   NAVHYLPKDQTKAGTCASSSSCSTQHSIIT   KGDSQPAAAAPHPESLSFQAHHLLPNTSPISP   TQPLTPS   AAGAGADGREPASRAAEPAVAMGQND   LMGTAEDFADQFLRVTKQYLPHVARLCLLST   FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA   SSFVFLMLLGQLTGCVLVLSRBNFVQVACGGLL   GIIALQTIAYSIL WDLKFLMRNLALGGGLLLL   LAERSSGKSKAFAQVTPMSSFKQYMQLGG   RVLLVLMFMTLLHFDASFFSIVQNIVGTALM   LVAIGFKTRLAALTLVVWLFANDYFAFWY   TPVYKPMHDELKVDFFQTMSVIGGLLLVVAL   GROGVSMBEKKEW   GRAVLLVLWFANTVAFAFWY   TPVYKPMHDELKVDFFQTMSVIGGLLLVVAL   GROGVSMBEKKEW   GRAVELQVLSTFFFPASFSNSFAAAVPQLLFF   ELPLPHYPQGSAKRSARRILMSELLTKELM   ELVWGTKSSFGLISTHTCRWTYGFYFSSEGS   ALGPEGGPCAVIAPVQAFLLKKLLFSSKSS   WRDCSGEGGLICHTILDELSACCDHSGS   CLVSWLRGKTTEETASIGSPAESSCOVEHS   SALAVELGFERFHALIQKRSFRSLPELKDAV   LDQYSMWGNKFGVLLFTYSVLTKGIENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   EIEDASEPLIDPVYGHOSSISILLTGENIKN   E	1						GATVHDFFNWLSVLVLLPVEVATHYLEIITQL
KVISQIAMDEKAKNSLVKIWCKIFTINTÖ   INVIPSTANCISPELGWIDGINWITMKNYT   YERINAKCQHIFVNIHLDLAVGIILLISLLV   LGGCLIMIVKILGSVLKGOVATVIKKITIDFF   FPFAWLTGYLAILVGAGMTPIVQSSSYFTSAL   TPLIGGVITEBAYPLICASIGLLWYPIPFT   RLPRMAKGLONISAKYRWFAVFYLIFFIPFIP   LTVFGLSLAGWRVLVGVGYPVFIIILVLCLR   LLQSRCRVLPKKLQNWNILPLWMSLKPW   DAVVSKFTGCFQMRCCCCCYCCRACCLLC   GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET   FINITISREAQGEVPASDSKTECTAL   LGSRCRVLPKKLQNWNILPLWMSLKPW   DAVVSKFTGCOPYCCACCACLLC   GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET   FINITISREAQGEVPASDSKTECTAL   SQGGSQFHRQOPPSLLTAPHSLDLPALPPGFR   GSGGKLRRUVHMSVKPSWGPSEGVTAVPY   TSDLGEIHNVTELLDLFNITLSECHVELSQST   KRVLFALYLAMPVGLVEHYMYSSFF   LVCLSVDRYVTLTSASPSWQRVQHBVRRAM   CAGIWVLSAIPLPEVVHIQLVGGPEPMCLFM   APFETYSTWALAVALSTTILGFLLPFPLITVFN   VLTACRIRQPGQPKSSRRHCLLLCAYVAVPV   MCWLPYHYTLLLILLITAHTSHCHLLLAYVAVPV   MCWLPYHYTLLLILLITAHTSHCHLLLAYVAVPV   MCWLPYHYTLLLILLITAHTSHCHLLLAYVAVPV   MCWLPYHYTLLLILLITAHTSHCHLLLAYVAVPV   MCWLPYHYTLLILLITAHTSHCHLLLAYVAVPV   MCWLPYHYTLLILLITAHTSHCRILLITAHTSHCRILLITAHTSHCHL   KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP   TQPLTPS 	Į.						IVESFHEKNGEDAPDLLKVITKPFTKLIVOLDK
INVTVPSTANCTSPSLCWTDGIQNYMKNNT YKENIAKCOHIFVNFHLPDLAVGTILLIISLLV LCGCLIMIVKILGSVLKGQVATVIKKTNTDP FPFAWLTGYLAILVGAGMTAVKKTNTDP FPFAWLTGYLAILVGAGMTAVKKTNTDP FPFAWLTGYLAILVGAGMTAVKTNTDP FPFAWLTGYLAILVGAGMTAVAVFVLIFFFLIP LTVGGLSLAGWRVLVGVGYPVVFIIIIVLCLR LLQSRCPRVLPKKLQNWFIPTIWLCLR LLQSRCPRVLPKKLQNWFIPTIWLCLR LLQSRCPRVLPKKLQNWFIPTIWLCLR LLQSRCPRVLPKKLQNWFIPTIWLCLR LLQSRCPRVLPKKLQNWFIPTIWMSSLKPW DAVVSKFTGCFQMRCCCCGRVCCRCCLLC GCPKCCRCSKCCEDLEAGEGQDVPVKAPET FDNITISREAQGEVPASDSKTECTAL LLQSRCPRVLPKSDDPALPPGPR GSQGKLRRVLVPMSVKPSWOPGPSEGVTAVP TSDLGEINWTELLDLTANESCHVELSQST KRVVLFALYLAMFVVGLVENULVICVNWSG SGRAGLMNLVILMAGPSCHTLSCHVELSQST KRVVLFALYLAMFVVGLVENULVICVNWSG SGRAGLMNLVILMAGSSCRTHFYFTVNMYSSIFF LVCLSVDRVYTLTSASPSWQRYQHRVRRAM CAGIWVLSAIHPPEVVHIQEPEMCLFM APFETYSTWALAVALSTTILGFLLPFLITVFN VLTACRLRQPQGPKSRRFICLLLCAYVAVFV MCWLPYHVTLLLILTHGTHISLHCHL.WHLLY FFYDVUCFSSCHMLCVINPIN-SEPHERGRLL NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP TOPLTPS  1333 2683 A 10358 2 884 AAGGAGAGREPASERASRAEPPAVAMGQND LMGTAEDFADQFLRVTKQVLPHVARLCLIST FLEDGIRMWFQWSEQRDYDDTTWNGYLLA SSSVENLILGQLTGCVLVLSRNFVQYACFGLE GIIALOTIAYSILWDLKFLMRNLALGGILLL LAESRSGCKSKMFAGYPTNAFSSFKQYMQLGG RVLLVLMFMTLLHFDASFFSIVONIVGTALM LVAIGFKTRLAAITLVVMRSSSKRYMQLGG RVLLVLMFMTLLFIDASFFSIVONIVGTALM LVAIGFKTRLAAITLVVMRSSKRYMQLGG RVLLVLMFMTLLFIDASFFSIVONIVGTALM LVAIGFKTRLAAITLVVMRSSKRYMQLGG RVLLVLMFFRTLASIGSPALSSCSCS WRCSQEGGELICHTLCDILESACCDHSOS YCL VSWLRGKTTEETASIGSPALSSCOVEHS SALAVELGFERFHALIORSFSSLSQFLIKEM EIEDASEPLIDDVYGHGSQSLINLLTIGHAVSN VWDCDBRECSGMKLLGHRVASFSSLSPLKMAV LDQYSMWGNKRGVLLFLYSVLTKGIENIKN EIEDASEPLIDDVYGHGSQSLINLLTIGHAVSN VWDCDBRECSGMKLLGHREQAAVGFLITMEA LRYCKVGSVLKISKPYLDCLASETHLTVFFA KDMALVAPPAPSEQARRYTOTYPEDNOFIP	1	1		1	1		KVISOIAMNDEK AKNKSI VKIWCKTETNKTO
YKENIAKCQHIFVIFH,DLAVGTILLISLLV LCGCLIMIVKLIGSVIKGQVATVIKKTINTDFP FPFAWLTGYLAILUGAGMTFIVQSSSYFTSAL TPILGIGVITIERAYPLTILGSNIGTTTTAILAAL ASPGNALRSSLQIALCHFFINISGILLWYPIPFT R.PJRMAKGLGNISAKYRWFAVFYLHIFFILIP LTVFGLSLAGWRVLVGVGYPVVFIIILVLCLR LLQSRCPRVLPKKLQNWFILPLWMSSLKPW DAVVSKTGCFGMRCCCCCCCCCCCCCCCCCLC GCPKCCCSKCCEDLEEAQEGQDYVKAPET FIDNITISREAGGEVASDSKTECTAL  1332 2682 A 10354 30 1377 SQQGSQPHRQGPPSLTAPPISCDLPALPPGPR GSQGKLRRVLYPMSVKPSWGPGPSEGVTAVP TSDLGEHNWTELLDLFNHISECHVELSQST KRVVLFALVLAMFVVGLVENLLVICNWRG SGRAGLMNI,VILNMAHADLGIVLSLPVWMLE VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF LVCLSVDRYVILTISASPSWGRYQHRVRRAM CAGWVLSAIPLPEVVHIQLVEGPEPMCLFM APPETYSTW ALAVALSTILLIGHPFILITVFN VLTACRLQPGQPKSRRFICLLCAYVAVFV MCWLPYHVTILLIHGTHISLHCHLVHLLY FFYDVIDCFSMLHCVINPILNTFLSPHFRGILL NAVVHYLPKDQTKAGTCASSSTGHSIIT KGDSQPAAAAPHEPESLSFQAHHLLINTSPISE TOPLITE  1333 2683 A 10358 2 884 AGAGAGDGREPASERASRAEPPAVAMGQND LMGTAEDFADOFLRVTKQVLPHVAILCLIST FLEDGIRMWFQWSGQRDYDTTWNGGYLLA SSFVEINLLQLTGCVLVLSRNFVQYACFGLF GIIALQTIAYSILWDLKFLMRNLALGGGLLL LAESRSECKSKMFAGYPTMRESSFKQYMQLGG RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI LVAIGFKTKLAALTILVVWLFAINVYFNAFWT IPVYKPMHDFLKYDFGTMSSVIGGLLLVVAL GPQGVSMDGKKKEW ALAQFECGREVATQGFTMSSTGGSLINSLTIKELM ELDASSFLIDDEVYGHGSQSLINGLTIKEN ELDASSFLIDDEVYGHGSQSLINGLTKENN ELDASSFLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTKENN ELEDASEPLIDDEVYGHGSQSLINGLTGHAVSN VWDGDRECSGMALLGHIRGAAVGFLTLMEA LRYCKVGSYLKISKRYLDCLASETHITVFFA KDMALVAPPAFEGARRYGTYTDDEDNOFIP			1		1		DIVINOCIANCISPEI CWINGIONWIMKNVI
LCGCLIMIVKILGSVLKQQVATVIKKINTDFF FFPRAWLTGYLAILVQAGMTFIVQSSSYFTSAL TPLGIGVITIERAYPLTLGSNIGTTTAILAAL ASPGNALRSS QIALCHFFRISTGILWYPIPT RLPIRMAKGLGNISAKYRWFAAVFVLIIFFILD LTVFGLSLAGWRVLVQVQVYVVPIIILVLCLR LLQSRCPRVLPKKLQNWYPLPLWMRSLKFW DAVVSKFTGCFOMRCCCCCRVCCRACCLLC GCPKCCRCSKCCEDLEAGPGQDVPVKAPET FDNITISREAQGEVPASDSKTECTAL SQGSQPHRQGPSLLTAPHSLDLPALPPGPR GSGKLRRVLVPMSVPSWGPGFSEQVTAVP TSDLGEIHINVTELLDLFNISCHVELSQST KRVVLFALVLAMPVGLVSNLVLCVNWRG SGRAGLMNLVILMMALADLGIVLSLPVWMLE VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF LVCLSVDRVVTLTSASPSWGRYGHRVRAM CAGIWVLSAIHIPPEVVHQLVEGPEPMCLPM APFETYSTWALAVALSTITLGFLLPFLLTVFN VLTACRLRQPGQPKSRRFICLLLCAYVAVFV MCWLPYHVTLLLLTHGTHISLHCHLVHLLY FFYDVIDCFSMLHCVINPILVNFLSPHFRGRLL NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT KGDSQPAAAPHFEPSLSFQAHHLLPNTSPISP TQPLTPS  1333 2683 A 10358 2 884 AAGAGADGREPASERASRAEPPAVAMGQND LWAGFSKTKLGQLTGCVLVJCSRFFVQYACFGLF GIIALQTIAYSILWDLKFLMRNLALGGGLLL LAESRSEGKSKFAGVPTINGYLLARFWTYNAFWT IPVYKPMHDFLKYDFQTMSGGLLLVAL GFGGVSMDEKKKEW ALAGFSKTKLAALTLVVWLFAINVYFNAFWT IPVYKPMHDFLKYDFQTMSSFRQVMQLGG RVLLVLMFMTLHFDASFFSIVONYGTALMT LVAGFSKTKLAALTLVVWLFAINVYFNAFWT IPVYKPMHDFLKYDFQTMSSSKQVGHISTWCGALLFV ELPJHPHVPGQESAKRSSARRFLIMSESKSS WRCSQEGGEGLLCHTLGDLESSACCDHSOS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEELGFERFHALIORKSFSSLPELKIAN LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASFPLIDDVYGHGSQSLJNLLLTGHANSN VWDGDRECSGMKLLGHRQAAVGFLITMEA LRYCKVGSYLKISKIPYLDCLASETHITNFFA KDMALVAPPAPSGAMRTYGTYDPEDNOFIP			1				TWO THE TAKE COMPANIENT DOLLAR
FFFAWLTGYLAILVGAGMTFIVGSSYSTSAL TPILGIGVTIERAYPLTIGSNIGTTTAILAAL ASPGNALRSSI QIALCHFFFNISGILWYPIPFT RLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP LTVFGLSLAGWRVLVQVOVVVFIIILVLCLR LLQSRCPRVLPKKLQNWFLPLWMRSLKPW DAVVSKTGCFGMRCCCCCRVCCRACCLLC GCPKCCCSKCCEDLEEAQEGQDYVKAPET FINITISREAGGEVFASDSKTECTAL  1332 2682 A 10354 30 1377 SQGGSQPHRQGFPSLTAPPISLDLPALPPGPR GSQGKLRRVLVPMSVKPVGOFSEGVTAVP TSDLGEHNWTELLDLFNHTLSECHVELSQST KRVLFALVLAMFVVGLVENLLVICVNWGG SGRAGLMNI,VILNMALADLGIVLSLPVWMLE VTLDYTWLWGSFSCRFTHYFYFVMMLE VTLDYTWLWGSFSCRFTHYFFVFWMLE VTLDYTWLWGSFSCRFTHYFFVFWMLE VTLDYTWLLWGSFSCRFTHYFFVFWMLE VTLDYTWLLWGSFSCRFTHYFFFVMMLSH APFETYSTWALAVALSTIFLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLLCAYVAVFV MCWLPYHYTLLLTLHGFLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLLCAYVAVFV MCWLPYHYTLLLTLHGFLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLLCAYVAVFV MCWLPYHYTLLLTLHGFLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLLCAYVAVFV MCWLPYHYTLLLTLHGFLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLCAYVAVFV MCWLPYHYTLLLTLHGFLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLCAYVAVFV MCWLPYHYTLLLTLHGGLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLCAYVAVFV MCWLPYHYTLLLTLHGGLJFPFLITVFN VLTACRLRQPGQPKSRRFICLLCAYVAVFV MCWLPYHYTLLLTHGJFFFTVWNGSPKCHULL NAVVHYLPKDQTKAGTCASSSSCSTHSIIIT KGDSQPAAAAPHEPESLSFQAHHLLPNTSPISS TQPLITS  484 AAGAGAGDREPASERASRAEPPAVAMGQND LMGTAEDFADQFLRVTKQVLPHVACLCLIST FLEDGRRWWQWSGRQRDYDTTWNGGYLLA SSFVFLNLLGQLTGCVLVLSRNFVQVACFGLF GIIALQTTAYSILWDLKFLMRNLALGGLLLL LAESRSECKSKMFAGVPTNMFSSFKQYMQLG RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI LVAIGFKTKLAALTLVVVLFANVYFNAFWT IPVYKPMHDFLKYDFQTMSSSFKAAMPQLLEP ELPLPHVPQGESAKRRSARRFLINSTELKLM ELEDASFPLIDPVYGHGSQSLINLLTLITGENIKN ELEDASFPLIDPVYGHGSQSLINLLTLITGENIKN ELEDASFPLIDPVYGHGSQSLINLLTLITGHAVSN VWDGDRECSGMKLLGHTLOTILESACCDHSGS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEL GFERFHALIQNEGAAVGFLITMEA LRYCKVGSVLKISKBYLDCAASETHLTVFTA KDMALVAPPESDARRYGTYTDEDNOFIP						1	YKENIAKCOHIFYNFHLPDLAYGIICLICSLLY
TPLIGIGYTIERAYPLTLGSNIGTTTTAILAAL ASPONALRSSLQIALCHFFNISGILL WYPPFFT RLPRMAKGLGNISAKYRWFAVFYLIEFFLIP LTVFGLSLAGWRVLVGVGVVVFIILVLCLR LLQSRCPRVLPKKLQNWNFLPLWMRSLKPW DAVVSKFTGCFQMRCCCCRVCCACCLLCL GCPKCCCSKCCEDLEEAQEGQDVPVKAPET FDNITISREAQGEVPASDSKTECTAL  1332 2682 A 10354 30 1377 SQQSG9PRGOPPSLFAPSLDLPALPPGPR GSQGKLRRVLVPMSVKPSWGPGPSEGVTAVP TSDLGEINNWTELLDLFNHTLSECHVELSQST KRVVLFALYLAMFVVGLVENLLVICVNWRG SGRAGLMMLYILMMAIADLGIVLSLPVWMLE VTLDYTWL WGSSCRAFTYFYFVMNYSSIFF LVCLSVDRYVTLTSASPSWGRYQHRVRRAM CAGIWVLSAITPLEVVHIQLVSGPEPMCLFM APFETYSTWALAVALSTTILGFLLPPFLITVFN VLTACRLRQPGQPKSRRHCLLAYVAVFV MCWLPFHYTLLLITLHGTHISLHCHLVHLLY FFYDVIDCFSMLHCVNPPLYNFLSHFRGRLL NAVVHYJPKDQTKAGTSSSSCSTQHHLLPNTSPISF TQPLTFS TQPLTFS TQPLTFS TELDGIRMWFQWSSCRDYIDITTWNCGYLLA SSSVFLNLLGQLTGCVLVLSRNFVQYACFGLE GIIALCTHAYSILWDLKFMNLALGGGLLLU LAESRSGKSMFAGVYPMRESSPKQYMQLGG RVLLVLMFMTLLHFDASFFSIVONVCGTALM LVAIGSKTKLAALTLVVWLFAINVYFNAFWT IPVYKPMHDFLKVDFFQTMSVIGGLLLVVAL GPGGVSMDEKKEW GRAGAGAGAGREPASFRASRAFLMSGLLLLVVAL GPGGVSMDEKKEW SQCGQEQELLCHTLCDLESACCDHSGS YCLVSWLRGKTTETASISGSPASAVPQLEF LPLPHYPQGGSAKRSARFLIMSELTKELM ELVWGTKSSPGLSDTIFCRWTQGFVFSSEGS ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS WRDCSQEQKELLCHTLCDLESACCDHSGS YCLVSWLRGKTTETASISGSFRSLPELKDAV LDQYSMWGNKFGVLLFLSVLLTKGIENIKN EIEDASEPLIDPVYGHGSSGLNILLTGHAVSN VWDGDRECSGMKLLGIHEQAAVGFLTMEA LRYKVGSYLKISKIPYLDCLASSTELLTVFRA			1	1		1	LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP
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RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI LVAIGFKTKLAALTLVVWLFAINVYFNAFWT iPVYKPMHDFLKYDFFQTMSVIGGLLLVVAL GPGGVSMDEKKKEW  1334  2684  A 10367  59  1562  QAWSLQVALSPFFFPASPSNSFAAAVPQLLFP ELPLPHVPGQESAKRSARRFLIMSELTKELM ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS WRDCSQEEQKELLCHTLCDILESACCDHSGS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEELGFERFHALIQKRSFRSLPELKDAV LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN VWDGDRECSGMKLLGIHEQAAVGFLTLMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA KDMALVAPEAPSEQARRVFQTYDPEDNGFIP		1				1	I AESDSEGK SMEAGVPTMRESSPK OVMOLGG
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ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS  ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS WRDCSQEEQKELLCHTLCDILESACCDHSGS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEELGFERFHALIQKRSFRSLPELKDAV LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN VWDGDRECSGMKLLGIHEQAAVGFLTLMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA KDMALVAPEAPSEQARRVFQTYDPEDNGFIP	1554	2007	(''	1330.	1		ELPLPHVPGQESAKRRSARRFLIMSELTKELM
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EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN VWDGDRECSGMKLLGIHEQAAVGFLTLMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA KDMALVAPEAPSEQARRVFQTYDPEDNGFIP		1	1	-	1	1	LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN
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QID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
icl-	peptide		in	nucleotide	location	F=Phenylalanine, U=Olyclic, H=Historic,
tide	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
	,		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
q-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	l		314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ŀ	{	1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	}	1	Ì	1	sequence	/-possible nucleotide deletion, \-possible
	}	}	1	peptide	1	nucleotide insertion
	1	1		sequence		LGIILLGPFLQEFFPDQGSSGPESFTVYHYNGL
	<del> </del>					KQSNYNEKVMYVEGTAVVMGFEDPMLQTD
	1	1	1	1		KOSNYNEK VM I VEGTAV VMGI EDITAL
		1	1	1		DTPIKRCLQTKWPYIELLWTTDRSPSLN
	2685	A	10375	82	2929	TRTKRRLGREKAMASPPRGWGCGELLLPFMI
335	2005	^	10373	52	Ì	LGTLCEPGSGQIRYSMPEELDKGSFVGNIAKD
	1	1	i		1	I GI FPOFLAERGVRIVSRGRTQLFALNPKSGS
	1			}		T VTA GRIDREEL CAOSPLCVVNFNILVENKM
	}	1	1		1	KIVGVEVEIDINDNFPRFRDEELKVKVNENA
	1	1		1		AAGTRLVLPFARDADVGVNSLRSYQLSSNLH
	1	}	1	· ·		FSLDVVSGTDGQKYPELVLEQPLDREKETVH
		ł	1	1	1	DLLLTALDGGDPVLSGTTHIRVTVLDANDNA
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		1		l		GINGKLTYSFRNEEEKISETFQLDSNLGEISTL
		1	}	}	l	QSLDYEESRFYLMEVVAQDGGALVASAKVV
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	1	1	- [	Į.	1	LFSVHDGDSGENGEIACSIPRNLPFKLEKSVD
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	j	ļ	ļ	ł	ł	VGLHTGEVRTARALLDRDALKQSLVVAVED
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	1	1	l l		-	IDPEDLDLTLYLVVAVAAVSCVFLAFVIVLL
	-	l.		\		LRLRRWHKSRLLQAEGSRLAGVPASHFVGV
	}	1	1			DCVRAFLOTYSHEVSLTADSRKSHLIFFQFN
	1		1			ADTI LSEESCEKSEPLLMSDKVDANKEEKK
	1		- 1			OCAPPNITOWRESOAORPGTSGSQNGDDIGI
	1	- 1	- 1	1	ŀ	WPNNOFDTEMLOAMILASASEAADGSSILU
	-	1	1	}		GAGTMGLSARYGPQFTLQHVLQGELGSDYI
		)	j			QNVYIPGSNATLTNAAGKRDGKAPAGGNG
		ļ	1			KKKSGKKEKK
	l l	l	1			RPRRQPSFSCRVLVLEDPPCFRFTNSMNQE
1226	2686	A	10379	1	557	RPRRRQPSFSCRVLVLEDPFCFRFTMSMTQL
1336	2000	1	102/		1	LAKLQAQVRIGGKGTARRKKKVVHRTATA
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	1				1262	TPGSTISWSPAAARGLSVCRCCRLHPASAML
1337	2687	A	10380	1	1263	FGDLPEPERSPRPAAGKEAQKGPLLFDDLPP
		1	}	1	ł	SSTDSGSGGPLLFDDLPPASSGDSGSLATSIS
						MVKTEGKGAKRKTSEEEKNGSEELVEKKV
		- [		1		MVKIEGKGAKKKISEEEKNOSEELVEKKV
						KASSVIFGLKGYVAERKGEREEMQDAHVIL
		)	1			DITEECRPPSSLITRVSYFAVFDGHGGIRASK
		1	1			A A ONT HONLIRK FPK GDVISVEKTVKRCLL
	-		}			TEKHTDEFFI KOASSOKPAWKDGSTATOVI
	1	1	1	1	1	VIDNII VIANI GDSRAIL CRYNEES QKHAALS
	1		1	}	}	SKEHNPTQYEERMRIQKAGGNVRDGRVLG
	Í	1	1	l	1	LEVSRSIGDGQYKRCGVTSVPDIRRCQLTPN
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		1	ļ	1		RFILLACDGLFKVFTPEEAVNFILSCLEDEKI
	1					TREGKSAADARYEAACNRLANKAVQRGSA
		- [	1	1		MVTVMVVRIGH
					690	GPSOSMAAGELEGGKPLSGLLNALAQDIFF
1338	2688	A	1038	5 3	589	VPGITEELLRSOLYPEVPPEEFRPFLAKMKU
		1		1		KSIASADMDFNQLEAFLTAQTKKQGGITSD
						AAVISKF WKSHKTKIRESLMNQSRWNSGLE
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	ļ	İ	ļ	}		QESEFLCLEFDEVKVNQILKTLSEVEESISTL

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, O=Olycine, 11=11300me,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	delice	{	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	1 214	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	Ì		sequence	/-possible nucleotide deletion, \-possible
			1	peptide	i	nucleotide insertion
		ļ	_	sequence		
	+	<del>                                     </del>				QPN CFKCDC
1339	2689	A	10386	50	390	LGAMAKHHPDLIFCRKQAGVAIGRLCEKCDG
1339	2009	1	10500	}		KCVICDSYVRPCTLVRICDECNYGSYQGRCVI
				1		CGGPGVSDAYYCKECTIQEKDRDGCPKIVNL
		1	ĺ	1	ļ	GSSKTDLFYERKKYGFKKR
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1340	2690	Α	10388	113	3472	RPSWMVDNKRMRTASNFQWLLSTFILLYLM
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		)	ì	1		NQVNSQKKGAPHDLKCVTNNLQVWNCSWK
i	1	ľ	1	1	}	APSGTGRGTDYEVCIENRSRSCYQLEKTSIKIP
						ALSHGDYEITINSLHDFGSSTSKFTLNEQNVSL
	1	1				IPDTPEILNLSADFSTSTLYLKWNDRGSVFPHR
1	1		}	}		SNVIWEIKVLRKESMELVKLVTHNTTLNGKD
ļ	1	}		}		TLHHWSWASDMPLECAIHFVEIRCYIDNLHFS
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1				1		GLEEWSDWSPVKNISWIPDSQTKVFPQDKVIL
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	i	1	1	į.		AGYPPDTPQQLNCETHDLKEIICSWNPGRVTA
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1		ļ	1			KNLIIYWKPLPINEANGKILSYNVSCSSDEETQ
1	1	1	- 1			SLSEIPDPOHKAEIRLDKNDYIISVVAKNSVGS
1	1		1	į		SPPSKIASMEIPNDDLKIEQVVGMGKGILLTW
		1	1	1		HYDPNMTCDYVIKWCNSSRSEPCLMDWRKV
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	ı	}	1	ì		QLLRSMIGYIEELAPIVAPNFTVEDTSADSILV
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1	į.	1	İ	1		HAILIPVAVAVIVGVVTSILCYRKREWIKETFY
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					5057	MI PPKHLSATKPKKSWAPNLYELDSDLTKEP
1341	2691	A	10392	1	5057	DVIIGEGPTDSEFFHQRFRNLIYVEFVGPRKTL
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				1	1	The major of the August CACCAT WOIEI HIDEI GV
				ì	1	SGLDNSLSWAAVGIVISCVLWDIELIIIDI EGV
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						ATKSVSTHAOGDAAQGLGGTIVRMWARDSN
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSODAESYONVVDLAEDRKPHNTIQD
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMFNYRKLLSLGVOLAEDDGHSHMTQGHSS
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRRYHFDTDGK
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRRYHFDTDGK GSIHDOKGCPRKKPFECGSEMRKAMSVSSLS
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRYHFDTDGK GSIHDQKGCPRKKPFECGSEMRKAMSVSSLS SI SSPSTESOPIDFGAMPYVCDECGRSFSVIS
						ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRRYHFDTDGK

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			CE C	D== d: ni= d	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Mct	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ıcl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	Į	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
-q-	uence	\	09/496	correspondi	acid residue	O=Glutamine R=Arginine, S=Serine,
ence		)	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Ì	!	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
	ĺ	ļ		peptide		nucleotide insertion
	j		\	sequence	ļ	SQVGGKRFECKDCGETFNKSAALAEHRKIHA
						RGYLVECKNQECEEAFMPSPTFSELQKIYGK
	1	1				DKFYECRVCKETFLHSSALIEHQKIHFGDDKD
	Ì	ļ			j	NEREHERERERGETFRPSPALNEFQKMYG
	}	ĺ	i			KEKMYECKVCGETFLHSSSLKEHQKIHTRGN
	ì	1	1		1	PFENKGKVCEETFIPGQSLKRRQKTYNKEKLC
	ì	1	(			DFTDGRDAFMQSSELSEHQKIHSRKNLFEGR
			1			GYEKSVIHSGPFTESQKSHTITRPLESDEDEKA
		Ì				FTISSNPYENQKIPTKENVYEAKSYERSVIHSL
		1			Ì	ASVEAQKSHSVAGPSKPKVMAESTIQSFDAIN
	1	1	ì			HQRVRAGGNTSEGREYSRSVIHSLVASKPPRS
	1	1	ł		i	HOKVKAGGNISEGKE I SKSVINSE VISSE I I
	1	1				HNGNELVESNEKGESSIYISDLNDKRQKIPAR ENPCEGGSKNRNYEDSVIQSVFRAKPQKSVP
	1				1	GEGSGEFKKDGEFSVPSSNVREYQKARAKKK
	1				}	GEGSGEFKKDGEFSVPSSNVKE I QKARARIUS YIEHRSNETSVIHSLPFGEQTFRPRGMLYECQ
	1				1	PIEHRSNETSVIHSLPFGEQTFR KOMETECQ ECGECFAHSSDLTEHQKIHDREKPSGERNYE
			}			WSVIRSLAPTDPQTSYAQEQYAKEQARNKCK
	1		ı			DFRQFFATSEDLNTNQKIYDQEKSHGEESQGE
	l		1			NTDGEETHSEETHGQETIEDPVIQGSDMEDPQ
	Ì	l	ì			KDDPDDKIYECEDCGLGFVDLTDLTDHQKVH
	1	1		1		SRKCLVDSREYTHSVIHTHSISEYQRDYTGEQ
		- 1				LYECPKCGESFIHSSFLFEHQRIHEQDQLYSM
	Ì	- (	į	1	ŀ	KGCDDGFIALLPMKPRRNRAAERNPALAGSA
	1	1		Ì		IRCLLCGQGFIHSSALNEHMRLHREDDLLEQS
	Ì	1	Ì	ļ	ļ	QMAEEAIIPGLALTEFQRSQTEERLFECAVCG
		1	ł			ESFVNPAELADHVTVHKNEPYEYGSSYTHTS
			ļ.			FLTEPLKGAIPFYECKDCGKSFIHSTVLTKHKE
	1	1		1		LHLEEEEEDEAAAAAAAAAQEVEANVHVPQ
		1	1			VVLRIQGLNVEAAEPEVEAAEPEVEAAEPEV
			l	<b>†</b>		EAAEPNGEAEGPDGEAAEPIGEAGQPNGEAE
	ļ	-			j	QPNGDADEPDGAGIEDPEERAEEPEGKAEEPE
						GDADEPDGVGIEDPEEGEDQEIQVEEPYYDC
	1	l	l	ì	1	HECTETFTSSTAFSEHLKTHASMIFEPANAFG
		ı				ECSGYIERASTSTGGANQADEKYFKCDVCGQ
		1	i			ECSGYIERASISIUOANQADERIIREDIO
		ì	Į.			LENDHL SLARHQNTHTG
1342	2692	A	10393	2	1350	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSA
1342	2072	1		1		ASRRSPAARPPVPAPPALPRGRPGTEGSTSLS
		}				APAVLVVAVAVVVVVVSAVAWAMANYIHV
		-	ļ			PPGSPEVPKLNVTVQDQEEHRCREGALSLLQ
	1	İ	[			HLRPHWDPQEVTLQLFTDGITNKLIGCYVGN
	1		l l			TMEDVVLVRIYGNKTELLVDRDEEVKSFRVL
		Ì		1		QAHGCAPQLYCTFNNGLCYEFIQGEALDPKH
		1	ļ			VCNPAIFRLIARQLAKIHAIHAHNGWIPKSNL
		- 1				WLKMGKYFSLIPTGFADEDINKRFLSDIPSSQI
		}	)			LQEEMTWMKEILSNLGSPVVLCHNDLLCKNII
		ļ		ļ		VNEKOGDVOFIDYEYSGYNYLAYDIGNHENE
		- 1		}		FAGVSDVDYSLYPDRELOSQWLRAYLEAYK
						FEKGEGTEVTEKEVEILFIOVNOFALASHFFW
		1	i	1	1	GLWALIQAKYSTEFDFLGYAIVRFNQYFKM
					1	KPEVTALKVPE
			1.556	<del>-   102</del>	839	PEAOTSAVLAREKGHLPTMRHEAPMQMASA
1343	2693	A	10394	102	633	ODARYGOKDSSDONFDYMFKLLIIGNSSVGK
i		ĺ				TSFLERVADDSFTSAFVSTVGIDFKVKTVFKN
]						EKRIKLQIWDTAGQERYRTITTAYYRGAMGF
1		- 1		1		LMYDITNEESFNAVQDWSTQIKTYSWDNAQ
ļ		1				VILVONK COMEDER VISTERGOHLGEOLGFE
1					-	FFETSAKDNINVKQTFERLVDIICDKMSESLET
1				}		DPAITAAKQNTRLKETPPPPQPNCAC
i			1			DRPPWNSRVDDFVTNLIHLSSKGHISPAKDTS
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1344	2694	A	10395	2	4136	LQQRTPAEMSPVLHFYVRPSGHEGAASGHTR

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5E O TO 1	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		l	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
00.100				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	}			residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide	-	nucleotide insertion
		1		sequence		RKLQGKLPELQGVETELCYNVNWTAEALPSA
						EETKKLMWLFGCPLLLDDVARESWLLPGSN
	ł	1			1	DLLLEVGPRLNFSTPTSTNIVSVCRATGLGPV
	1	1				DRVETTRRYRLSFAHPPSAEVEAIALATLHDR
	1					MTEQHFPHPIQSFSPESMPEPLNGPINILGEGR
		1	ļ	1		LALEKANQELGLALDSWDLDFYTKRFQELQR
		1				NIDSTVE A FDI AOSNSEHSRHWEFKGULHVDG
		1	1			OKI VHSI FESIMSTOESSNPNNVLKFCDNSSA
	Ì	1				LOCKEVREL RPEDPTRPSRFOOQQGLKHVVFI
		ł	1		1	AETHNEPTGVCPFSGATTGTGGRIRDVQCTG
		l	· I		j	PGAHVVAGTAGYCFGNLHIPGYNLPWEDLSF
		1			1	OVECNEARPLEVAIEASNGASDYGNKEGEPV
		1		1		I AGEARSI GLOT PDGORREWIKPIMESUGIUS
						MEADHICKEAPEPGMEVVKVGGPVYKIGVGO
		ł				GAASSVOVOGDNTSDLDFGAVQRGDPEMEQ
		1			Ţ	KMNRVIRACVEAPKGNPICSLHDQGAGGNG
	1					NOT KEI SDPAGAIIYTSRFOLGDPILNALLIW
						GAEYQESNALLLRSPNRDFLTHVSARERCPA
		- 1	İ			CFVGTITGDRRIVLVDDRECPVRRNGQGDAP
						PTPPPTPVDLELEWVLGKMPRKEFFLQRKPP
		ı				MLQPLALPPGLSVHQALERVLRLPAVASKRY
		- 1				LTNKVDRSVGGLVAQQQCVGPLQTPLADVA
ı			l			VVALSHEELIGAATALGEQPVKSLLDPKVAA
			1			RLAVAEALTNLVFALVTDLRDVKCSGNWM WAAKLPGEGAALADACEAMVAVMAALGVA
		i	1			VDGGKDSLSMAARVGTETVRAPGSLVISAYA
		-				VDGGKDSLSMAARVGTETVRATUSEVIST VCPDITATVTPDLKHPEGRGHLLYVALSPGQ
						HRLGGTALAQCFSQLGEHPPDLDLPENLVRA
		ł				FSITQGLLKDRLLCSGHDVSDGGLVTCLLEM
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			<b>\</b>	}		I PPTFPK ASVPREPGGPSPRVAILKEEGSNGDK
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		1	ţ			DACARI DDERKRPDTFSLGVCNGCULLALLU
	1	Ì		l	}	WVCCDPNEDAAEMGPDSOPARPGLEERINE
1	į		l l	\	\	SCRVESRWASVRVGPGPALMLKUMEUAVLI
			1			VVVSAHGEGYVAESSPELOAOIEARGLAPLHW
ļ		ļ	l		<b>\</b>	ADDDGNPTEOYPLNPNGSPGGVAGICSCDGK
		}	}		1	HIAVMPHPERAVRPWQWAWRPPPFDILIIS
		1		1		DWI OI FINARNWTLEGSC
L		_+-	1020	6 65	642	GVPGEWAGTMASRAGPRAAGTDGSDFQHRE
1345	2695	Α	1039	ده ا		PVAMHYOMSVTLKYEIKKLIYVHLVIWLLLV
ļ		1				AVMSVGHIRLLSHDOVAMPYQWEYPYLLSI
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	. [	Ì				VCSMEMEPAAOOLYRHGKAYRFLFGFSAVSI
ļ		ì	1	ļ		MYLVLVLAVQVHAWQLYYSKKLLDSWFTST
		1				OEKKHK
			1020	8 1	718	DDFVRCGPQSAAMGASARLLRAVIMGAPGS
1346	2696	_   A	1039	0 1	1	CVCTVSSRITTHFELKHLSSGDLLRDNMLRG
1			1	-		FIGULAKAFIDOGKLIPDDVMTRLALHELKINI
1		Ì		)		TOVEWLI DGFPRTLPOAEALDRAYQIDTVINI
1		1				NVPFEVIKORLTARWIHPASGRVYNIEFNPPA
		1	}			TVGIDDI TGFPLIOREDDKPETVIKRLKAYED
				1		OTKPVLEYYQKKGVLETFSGTETNKIWPYVY
	ŀ		-	1	1	A ET OTK VPOR SOK ASVTP
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1347	269	7 /	1040	153	1969	KHRQENNALDMAPEIHMTGPMCLIENTNGEL VANPEALKILSAITQPVVVVAIVGLYRTGKSY

					D 1: 1 3 and	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-Aspartic Acid E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
eq-	1 0000	ļ	914	ng to first	acid residue	Q=Glutamine, K=Argittine, S=Serine,
ience	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	{	i		peptide	•	/=possible nucleotide deletion, \=possible
	1	1		sequence		nucleotide insertion
			<b></b>	Sequence	<del> </del>	L MONK LAGKNIKGESLGSTVKSHTKGIWMWCV
		1	-			DUDKKDEHTI.VI.I.DTEGLGDVKKGDNQNDS
	· ·	1	ì	]		I WHETE A VITT SSTILVYNSMGTINQQAMDQLI I
		1	l			VTELTHRIRSKSSPDENENEDSADFVSFFPDFV
	Į.	1	1	ļ		WTLRDFSLDLEADGQPLTPDEYLEYSLKLTQ
	ł	i	(	(		GTSQKDKNFNLPRLCIRKFFPKKKCFVFDLPI
	1	į .	1	1		GISQKDKNFNLFRECIRG TIRGUES TO SEE TO
	}	1	ł	l		HRRKLAQLEKLQDEELDPEFVQQVADFCSYI
	1	1	1	į	ĺ	FSNSKTKTLSGGIKVNGPRLESLVLTYINAISR
	1	1				GDLPCMENAVLALAQIENSAAVQKAIAHYD
	1	1	1	1		QQMGQKVQLPAETLQELLDLHRVSEREATEV
	1	1	1	1		VARVICEK DVDHI FOKKLAAULUKARUUFCA
	1	1		1		QNQEASSDRCSALLQVIFSPLEEEVKAGIYSK
	1		1			DCGVCI FIOKLODLEKKYYEEPRKGIQAEEIL
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	1	1	1	1		I VORTIVE OF TERMERERAULLEEUEK IL I SAL
	1	1	l	1	}	QEQARVLKERCQGESTQLQNEIQKLQKTLKK
	1			1		KTKRYMSHKLKI
		}	l l			TQLPAPLSGVLSRLQLGSGAPLLTWVQETAG
1348	2698	A	10404	5	892	VAGGAPRRTPVTMWRLLARASAPLLRVPLS
1340	2070	1	1			DSWALLPASAGVKTLLPVPSFEDVSIPEKPKL
	}	. ]	1			DSWALLPASAGVATLLE VISITED VOIL DE LE VISITE
	1	1	l l	ļ		RFIERAPLVPKVRREPKNLSDIRGPSTEATEFT
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	1	- [	-	1	1	DPKNMFAIWRVPAPFKPITRKSVGHRMGGGK
1		į	1	1		GAIDHYVTPVKAGRLVVEMGGRCEFEEVQG
	- {		1	1	[	LEI DONALIKI PEAAKAVSKUI LEKNIKALIQUE
	ł		1			RERNNONPWTFERIATANMLGIRKVLSPIDL
	1	1				L TUVCKVWGKFYMPKRV
	1	1			1184	T PRICEAL GGI FOTHSDMKGSYPV WEDFINK
1349	2699	A	10409	59	1104	A GRI OSOI RTTVVAAAAFLDAFQKVADMA
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1	1	1	{	1		EYKKARQEIKKKSSDTLKLQKKAKKGRGDIQ
1	l l	Ì	İ			PQLDSALQDVNDKYLLLEETEKQAVRKALIE
}	}	1	1			ERGRECTFISMLRPVIEEEISMLGEITHLQTISE
1						EKOKI CI FISMLKI VILEELISMEGETTIBQXIS
				-		DLKSLTMDPHKLPSSSEQVILDLKGSDYSWS DLKSLTMDPHKLPSSSEQVILDLKGSDYSWS
}		Ì				YQTPPSSPSTTMSRKSSVCSSLNSVNSSDSRS
	1	l	1			GSHSHSPSSHYRYRSSNLAQQAPVRLSSVSSH
1			1	ŀ		DSGFISODAFOSKSPSPMPPEAPNQRIALEAL
1	1	1			1	DEDNIC COPTT A SGPPA A A LLAUKYKOM
				<del></del>	958	- LCDCCDCVDVSWSSGPGSPGOTORRSWVKS
1350	2700	A	10410	511	930	D CUSSI I PPSODEVAGLSVILRGTVDDKLNW
						A TAIT VIDENT NIK DECITIVE EMILDIMASI YUMMU
		1	l			KYTYPALREEAPREHVESFFQKMDRNKDGV
1	1	1	- 1			VTIEEFIESCQKDENIMRSMQLFDNVI
1	1					LAPETE EDIE CONTINUE NUMBER NOT DISTRIBUTE

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

Pages 340 to 1963 of this application contain amino acid sequence listings. They can be obtained at the address given below.

Les pages 340 to 1963 de cette demande contiennent des listages des séquences d'acides aminés. Elles peuvent être obtenues à l'adresse indiquée ci-dessous.

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(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.